

GenCore version 5.1.4\_p5\_4578  
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# 3M protein - protein search, using sw model

Run on: April 4, 2003, 08:36:10 ; Search time 25.9677 seconds  
(without alignments)  
71.839 Million cell updates/sec

Title: US-09-779-703-1

Perfect score: 81  
Sequence: 1 QRETPGCAKAPWY 14

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :  
A\_Geneseq\_101002:\*

1:	/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT:*
2:	/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*
3:	/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT:*
4:	/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:*
5:	/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1984.DAT:*
6:	/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1985.DAT:*
7:	/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1986.DAT:*
8:	/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1987.DAT:*
9:	/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1988.DAT:*
10:	/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1989.DAT:*
11:	/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1990.DAT:*
12:	/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1991.DAT:*
13:	/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1992.DAT:*
14:	/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1993.DAT:*
15:	/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1994.DAT:*
16:	/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1995.DAT:*
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18:	/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1997.DAT:*
19:	/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1998.DAT:*
20:	/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT:*
21:	/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT:*
22:	/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT:*
23:	/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	81	100.0	14	21	AA82194
2	81	100.0	17	11	AA805469
3	81	100.0	17	15	AA860233
4	81	100.0	17	21	AA82196
5	81	100.0	25	11	AA80513
6	81	100.0	140	16	AA872456
7	81	100.0	145	9	AA82043
8	81	100.0	147	9	AA81853
9	81	100.0	147	22	AA867245
10	81	100.0	147	22	AA871982

11	81	100.0	149	10	AA891635
12	81	100.0	149	11	AA805612
13	81	100.0	150	8	AA870528
14	81	100.0	150	8	AA871245
15	81	100.0	150	9	AA881236
16	81	100.0	150	9	AA882190
17	81	100.0	150	9	AA882303
18	81	100.0	150	9	AA881066
19	81	100.0	150	9	AA881068
20	81	100.0	150	10	AA895660
21	81	100.0	150	11	AA805286
22	81	100.0	150	11	AA808151
23	81	100.0	150	12	AA811011
24	81	100.0	150	12	AA811723
25	81	100.0	150	13	AA829808
26	81	100.0	150	13	AA829809
27	81	100.0	150	13	AA822311
28	81	100.0	150	13	AA869584
29	81	100.0	150	15	AA869579
30	81	100.0	150	15	AA869580
31	81	100.0	150	15	AA869581
32	81	100.0	150	15	AA869582
33	81	100.0	150	15	AA869583
34	81	100.0	151	9	AA881251
35	81	100.0	151	9	AA881233
36	81	100.0	151	9	AA881231
37	81	100.0	151	10	AA893187
38	81	100.0	151	11	AA805865
39	81	100.0	151	11	AA807900
40	81	100.0	151	11	AA811615
41	81	100.0	151	12	AA811703
42	81	100.0	151	12	AA811613
43	81	100.0	151	12	AA811714
44	81	100.0	151	12	AA811860
45	81	100.0	151	12	AA811861

## ALIGNMENTS

RESULT 1  
AA82194  
ID AA82194 standard; peptide; 14 AA.  
AC AA82194;  
DE 08-TUN-2000 (first entry)  
DT  
XX Tumour necrosis factor alpha derived peptide #1.  
XX Tumour necrosis factor alpha; TNF-alpha; human; mouse; oedema;  
KW Proinflammatory; pulmonary oedema.  
OS Homo sapiens.  
XX  
XX MO200009145-A1.  
XX  
XX 24-FEB-2000.  
XX  
XX 10-AUG-1999; 99MO-EP05806.  
XX  
XX 14-AUG-1998; 98EP-0870180.  
XX 18-SEP-1998; 98EP-0870198.  
XX 21-OCT-1998; 98EP-0870222.  
XX  
XX (INNO-) INNOGENETICS NV.  
XX Lucas R, De Betseller P, Pugin J, Bloc A, Fransen L;  
XX WPI; 2000-282855/24.  
XX  
XX Use of peptides derived from human OR mouse tissue necrosis  
XX factor-alpha (TNF-alpha), and comprising 7-17 contiguous amino acids,  
XX PT

for preventing or treating oedema -  
Claim 5; Page 16; 26pp; English.

The present invention describes the use of peptides comprising a chain of 7-17 contiguous amino acids derived from the Ser100-Glu116 region of human tumour necrosis factor-alpha (TNF-alpha), or Ser99-Glu115 region of mouse TNF-alpha, for treating oedema. The peptides form pharmaceutical compositions for treating oedema, especially pulmonary oedema. The peptides are non-toxic, whilst retaining the oedema resorption-inducing capacity as TNF. The present sequence represents a specifically claimed TNF-alpha peptide from the present invention.

Sequence 14 AA:

Query Match 100.0%; Score 81; DB 21; Length 14;  
Best Local Similarity 100.0%; Pred. No. 7.2e-07;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 QRETPGAEAKPMY 14  
|||||  
1 QRETPGAEAKPMY 14

SUIT 2  
R05469

AAR05469 standard; protein; 17 AA.

AAR05469;

23-OCT-1990 (first entry)

Tumour necrosis factor derived peptide.

Tumour necrosis factor; TNF; neoplastic disease; autoimmune disease; infection; inflammation; transplant rejection.

Synthetic.

DE3841759-A.

13-JUN-1990.

12-DEC-1988; 88DE-3841759.

12-DEC-1988; 88DE-3841759.

(BADI ) BASF AG.

Bohm HJ, Daum L, Haupt A, Schmied B, Walker N, Zechel JC;

WPI; 1990-186576/25.

New tumour necrosis factor derived peptides- for treating or preventing neoplastic and autoimmune diseases, infection, inflammation and transplant rejection.

Example 1; Page 7; 16pp; German.

To residue S1 is attached Ac and to residue T17 NH2.

This peptide is an example of a highly generic sequence of the formula X-A-Y.

A-QRETPGAEAKP, HRETPGAEAKP, HRETPGAEAKP, PROTPGAEAKP, PGLQEP, PGHOGP or PGLQGP;

X-G-NH-CHM-CO, G-NH-CHM-CO-W, G-R-NH-CHM-CO or G-R-NH-CHM-CO-W; Y-Z, NH-CHO-COZ, V-NH-CHO-COZ, NH-CHO-CO-U-Z or V-NH-CHO-CO-U-Z;

Z-OH or an amino protecting group;

R, U, V and W= peptide chains of 1-4 naturally occurring alpha aminoacids;

M and O= H, isopropyl, CHMe, Et, phenyl, CH(OH), 3-indolyl- or 4-imidazolyl-methyl or (CH2)bt; D=1-6;

T-OH, MeO, MeS, isopropyl, phenyl (opt. 4-OH, substd.), HS, NH2, COOH,

CC CONH2, or NH2 C (NH) NH; or  
CC M ans O together are (CH2)C-S-S-(CH2)d, (CH2)eCO NH-(CH2)f or  
CC (CH)2eNH CO(CH2)gNH CO(CH2)h; c and d=1-4; e and f=1-6; g=1-12.  
CC The peptide is a low mol. wt. deriv. of TNF.  
CC See also DE3841753-55, DE3841759, DE3841761-64, DE3841767-68.  
XX

Sequence 17 AA:

Query Match 100.0%; Score 81; DB 11; Length 17;  
Best Local Similarity 100.0%; Pred. No. 8.9e-07;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRETPGAEAKPMY 14  
|||||  
Db 4 QRETPGAEAKPMY 17

RESULT 3  
AAR60233  
ID AAR60233 standard; peptide; 17 AA.

XX AAR60233;

AC 16-MAR-1995 (first entry)

DE hTNF-alpha tip.

XX

TNF-alpha; tumor necrosis factor-alpha; tip peptide; mutein; cancer; sepsis; inflammation; cytokine; metastasis; lectin; adhesion; mutagenesis; trypanoside.

XX Synthetic.

XX Key Location/Qualifiers

FT Msc-difference 1 /note= "N-terminal biotin Gly-Gly"

XX MO9418325-A.

PD 18-AUG-1994.

PF 02-FEB-1994; 94MO-EP00286.

XX 03-FEB-1993; 93EP-0400262.

XX (INNO-) INNOGENETICS NV SA.

PI De Baetselier P, Franssen L, Lucas R, Sablon E;

XX WPI; 1994-279746/34.

PT New tumour necrosis factor -alpha muteins, antibodies and

PT antisense peptide(s) - used in the treatment of diseases and

PT conditions associated with the in vivo activities of TNF-A eg

XX cancer, sepsis, inflammation, etc

PS Disclosure; Page 61; 132pp; English.

XX The TNF-alpha tip peptides given in AAR60232-42 were modified with

XX N-terminal biotin-Gly-Gly moieties and were used to demonstrate

XX CC that the tip region of mouse and human TNF-alpha contains the

XX CC trypanosomal and lectin-like activities of the molecule and is

XX CC is involved in TNF-induced lethal shock.

Sequence 17 AA:  
Query Match 100.0%; Score 81; DB 15; Length 17;  
Best Local Similarity 100.0%; Pred. No. 8.9e-07;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRETPGAEAKPMY 14  
|||||  
Db 3 QRETPGAEAKPMY 16

RESULT 4  
 ID AAY82196  
 AC AAY82196 standard; peptide; 17 AA.  
 XX  
 DT 08-JUN-2000 (first entry)  
 DE Tumour necrosis factor alpha derived circularised peptide #1.  
 XX  
 KW Tumour necrosis factor alpha; TNF-alpha; human; mouse; oedema;  
 XX proinflammatory; pulmonary oedema; cyclic.  
 OS Homo sapiens.  
 FH Key Location/Qualifiers  
 FT Disulfide-bond 1..17  
 PN WO200009149-A1.  
 PD 24-FEB-2000.  
 PF 10-AUG-1999; 99WO-EP05806.  
 XX  
 PR 14-AUG-1998; 98EP-0870180.  
 PR 18-SEP-1998; 98EP-0870198.  
 PR 21-OCT-1998; 98EP-0870222.  
 XX  
 PA (INNO-) INNOGENETICS NV.  
 XX  
 PI Lucas R, De Baetselier P, Pugin J, Bloc A, Fransen L;  
 DR WPI; 2000-282855/24.  
 XX  
 PT Use of peptides derived from human or mouse tissue necrosis  
 PT factor-alpha (TNF-alpha), and comprising 7-17 contiguous amino acids,  
 PT for preventing or treating oedema  
 XX  
 PS Claim 8; Page 16; 26pp; English.  
 XX  
 CC The present invention describes the use of peptides comprising a chain  
 CC of 7-17 contiguous amino acids derived from the Ser100-Glu116 region  
 CC of human tumour necrosis factor-alpha (TNF-alpha), or Ser99-Glu115  
 CC region of mouse TNF-alpha, for treating oedema. The peptides form  
 CC pharmaceutical compositions for treating oedema, especially pulmonary  
 CC oedema. The peptides are non-toxic, whilst retaining the oedema  
 CC resorption-inducing capacity as TNF. The present sequence represents  
 CC a specifically claimed TNF-alpha circularised peptide from the present  
 CC invention.  
 XX  
 SQ Sequence 17 AA;  
 QY  
 Db 1 QRETPGAEAKPMY 14  
 3 QRETPGAEAKPMY 16  
 Query Match 100.0%; Score 81; DB 21; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 8.9e-07;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

KW Tumour necrosis factor; TNF; neoplastic disease; autoimmune  
 XX disease; infection; inflammation; transplant rejection.  
 XX  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 4..4  
 FT /label=OTHER  
 FT /note="Ornithine"  
 XX  
 PN DE3841759-A.  
 XX  
 PD 13-JUN-1990.  
 XX  
 PF 12-DEC-1988; 88DE-3841759.  
 XX  
 PR 12-DEC-1988; 88DE-3841759.  
 XX  
 PA (BADI ) BASF AG.  
 XX  
 PI Bolm HJ, Daum L, Haupt A, Schmied B, Walker N, Zechel JC;  
 DR WPI; 1990-186576/25.  
 XX  
 PT New tumour necrosis factor derived peptides- for treating or preventing  
 PT neoplastic and autoimmune diseases, infection, inflammation and  
 PT transplant rejection.  
 XX  
 PS Example 37; Page 12; 16pp; German.  
 XX  
 CC To residue S1 is attached Ac and to residue Y22 NH2.  
 CC Residues Orn4 and Asp22 together form a covalent bond.  
 CC This peptide is an example of a highly generic sequence of the  
 CC formula X-A-Y  
 CC A- QRETPGAEAKP; HRETPEAEAKP, HRETPEAEAPMA, PRDTPGAEAKP, PGLQEP,  
 CC PGPQGP or PGLQGP;  
 CC X- G-NH-CHM-CO, G-NH-CHM-CO-W, G-R-NH-CHM-CO or G-R-NH-CHM-CO-W;  
 CC Y- Z, NH-CHO-CO2, V-NH-CHO-CO2, NH-CHO-CO-U-Z or V-NH-CHO-CO-U-Z;  
 CC G- H or an amino protecting group;  
 CC Z- OH, NH2 or carboxy protecting group; or G and Z together are a  
 CC covalent bond or the gp. CO(CH2)aNH; a=1-12;  
 CC R, U, V and W= peptide chains of 1-4 naturally occurring alpha aminoacids;  
 CC M and Q= H, isopropyl, CHMe, Et, phenyl, CH(OH), 3-indolyl- or  
 CC 4-imidazolyl-methyl or (CH2)br; b=1-6;  
 CC T= OH, MeO, MeS, isopropyl, phenyl (opt. 4-OH, substd.), HS, NH2, COOH,  
 CC CONH2, or NH2 C (NH) NH; or  
 CC M and Q together are (CH2)c-S-S-(CH2)d, (CH2)eCO NH-(CH2)f or  
 CC (CH)2eNH CO(CH2)gNH CO(CH2) f; c and d=1-4; e and f=1-6; g=1-12.  
 CC The peptide is a low mol. wt. deriv. of TNF.  
 CC See also DE3841753-55, DE3841759, DE3841761-64, DE3841767-68.  
 XX  
 SQ Sequence 25 AA;  
 QY  
 Db 1 QRETPGAEAKPMY 14  
 8 QRETPGAEAKPMY 21  
 Query Match 100.0%; Score 81; DB 11; Length 25;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-06;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 6  
 ID AAR72456  
 AC AAR72456 standard; protein; 140 AA.  
 XX  
 DT 19-DEC-1995 (first entry)  
 DE Tumour necrosis factor-alpha 4th exon fragment.  
 XX  
 KW Tumour necrosis factor; fusion protein; metastasis; inhibition.

Synthetic.

Key Location/Qualifiers

Misc-difference 1 /note- "This residue has the peptide AAR72454 attached at the N-terminus"

TW239078-A.

21-JAN-1995.

12-OCT-1993; 93TW-0108498.

29-SEP-1993; 93JP-0020556.

(MIZU/) MIZUNO D.  
(SONA/) SONAMOTO I.

Sonamoto I;

WPI; 1995-168947/22.

Pharmaceutical and veterinary composition for inhibiting metastasis - can be made into tablet form

Disclosure; Page 5; 14pp; Chinese.

The amino acid sequence of a part of the 4th exon from the tumour necrosis factor (TNF)-alpha. The protein has the peptide AAR72454 attached to the N-terminal amino acid. The fusion protein can be used in pharmaceutical compositions for inhibiting metastasis.

Sequence 140 AA;

Query Match 100.0%; Score 81; DB 16; Length 140;

Best Local Similarity 100.0%; Pred. No. 8.4e-06;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 ORETPGAEAKPMW 14

|||||

85 ORETPGAEAKPMW 98

JULT 7

AAP82043 standard; protein; 145 AA.

AAP82043;

12-DEC-1990 (first entry)

Sequence of new tumour necrosis factor (TNF).

Anticancer drug; lymphokine; antitumour.

Homo sapiens.

JP63032486-A.

12-FEB-1988.

25-JUL-1986; 86JP-0173822.

25-JUL-1986; 86JP-0173822.

(TEIJ ) TEIJIN KK.

WPI; 1988-080331/12.

New biologically active polypeptide - useful as anticancer agent

Claim 2(1); Page 547; 17pp; Japanese.

XX

CC New biologically active polypeptide has cytotoxic activity specifically  
CC for tumour cells and therefore, is expected to be used as an anticancer  
CC drug. It is derived from human TNF by deleting 11 N-terminal AAs. (See  
CC also J63188396, AAN81624 and AAP81236).

SQ Sequence 145 AA;

Query Match 100.0%; Score 81; DB 9; Length 145;

Best Local Similarity 100.0%; Pred. No. 8.7e-06;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ORETPGAEAKPMW 14

DB 91 ORETPGAEAKPMW 104

RESULT 8

AAP81853 standard; protein; 147 AA.

AAP81853;

17-DEC-1990 (first entry)

Sequence of modified human tumour necrosis factor (hTNF).

Antitumour; anticancer; cytostatic.

Homo sapiens.

JP62272991-A.

27-NOV-1987.

21-MAY-1986; 86JP-0114754.

21-MAY-1986; 86JP-0114754.

(TEIJ ) TEIJIN KK.

WPI; 1988-010365/02.

N-PSDB; AAN82306.

New bioactive polypeptide -

PT has antitumour activity, and is obtd. by culturing bacteria

transformed with plasmid contg. DNA sequence of the polypeptide

Claim 2(1); Page 761; 20pp; Japanese.

DNA sequence encoding hTNF was synthesised chemically and inserted into

vector plasmid. Recombinant plasmid was cut with restriction enzyme and

DNA fragment coding for new bioactive polypeptide was obtd. The new

bioactive polypeptide has ten N-terminal AAs deleted. It has antitumour

CC activity greater than hTNF and can be produced by culturing bacteria

transformed with a plasmid contg. DNA encoding the polypeptide.

SQ Sequence 147 AA;

Query Match 100.0%; Score 81; DB 9; Length 147;

Best Local Similarity 100.0%; Pred. No. 8.9e-06;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ORETPGAEAKPMW 14

DB 92 ORETPGAEAKPMW 105

RESULT 9

AAB67245 standard; protein; 147 AA.

AAB67245;



```

XX 18-APR-2001 (first entry)
DT
XX
DE Human tumour necrosis factor alpha.
XX
KW Human; Apo2 ligand; divalent metal ions; viral infection; cancer.
XX
OS Homo sapiens.
XX
PN WO200100832-A1.
XX
PD 04-JAN-2001.
XX
PE 26-JUN-2000; 2000WO-US17579.
XX
PR 28-JUN-1999; 99US-0141342.
XX
PA (GETH ) GENENTECH INC.
XX
PI Ashkenazi AJ, Hymowitz S, Kelley RF, Koumenis I, Leung S;
PI O'Connell M, Pai R, Shahrokh Z, Simmons L;
XX
DR WPI; 2001-123012/13.
XX
PT Use of divalent metal ions for making Apo-2 ligand and in formulations
PT containing Apo-2 ligand for increasing yield and stability of ligand
PT trimers, useful for therapeutic applications -
XX
PS Disclosure; Fig 3; 60pp; English.
XX
CC The present invention relates to a formulation comprising Apo-2
CC ligand and divalent metal ions. Apo-2 ligand and the formulation
CC are useful for treating cancers and viral infections. Addition
CC of divalent metal ions for making Apo-2 ligand and formulations
CC containing Apo-2 ligand results in increased yield and stability
CC of Apo-2 ligand trimers.
XX
SQ Sequence 147 AA;

Query Match 100.0%; Score 81; DB 22; Length 147;
Best Local Similarity 100.0%; Pred. No. 8.9e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRETPGAEAKPMY 14
DB 92 QRETPGAEAKPMY 105

RESULT 10
AAY71982
ID AAY71982 standard; Protein; 147 AA.
XX
AC AAY71982;
XX
DT 28-MAR-2001 (first entry)
DT
XX
DE C-terminal region of human Tumour Necrosis Factor (TNF).
XX
KW Human; Tumour Necrosis Factor; TNF; Immunosuppressant; TALL-1;
KW Tumour necrosis factor and Apol-related leucocyte expressed ligand 1;
KW therapy; autoimmune disorder; rheumatoid arthritis; multiple sclerosis;
KW systemic lupus erythematosus; SLE; insulin dependent diabetes mellitus;
KW thrombocytopenia purpura; acute rheumatic fever; myasthenia gravis;
KW haemolytic anaemia; Grave's disease; Goodpasture's syndrome;
KW post-streptococcal glomerulonephritis; polyarteritis nodosa; BCMA;
KW B cell maturation factor; pemphigus vulgaris; B-lymphocyte proliferation.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FH Region 2..8
FH /label= Beta_strand
FT Region 16..18

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FT /label= Beta_strand
FT Region 26..28
FT /label= Beta_strand
FT Region 31..34
FT /label= Beta_strand
FT Region 37..40
FT /label= Beta_strand
FT Region 45..56
FT /label= Beta_strand
FT Region 66..71
FT /label= Beta_strand
FT Region 80..90
FT /label= Beta_strand
FT Region 104..114
FT /label= Beta_strand
FT Region 119..127
FT /label= Beta_strand
FT Region 140..147
FT /label= Beta_strand
XX
PN WO200068378-A1.
XX
PD 16-NOV-2000.
XX
PE 05-MAY-2000; 2000WO-US12266.
XX
PR 06-MAY-1999; 99US-0132892.
XX
PR 01-MAY-2000; 2000US-0201012.
XX
PA (NAJE-) NAT JEWISH MEDICAL & RES CENT.
XX
PI Shu HS.
XX
DR WPI; 2001-016094/02.
XX
PT Isolated TALL-1 protein is used to identify compounds that regulate B
PT lymphocyte proliferation, used to treat B lymphocyte associated
PT autoimmune disorders -
XX
PS Example 1; Fig 1b; 112pp; English.
XX
CC The present invention relates to Tumour necrosis factor (TNF) and
CC Apol-related leucocyte expressed ligand 1 (TALL-1) nucleic acid
CC molecules, proteins (including homologues), and their antibodies. The
CC invention in particular relates to methods for regulating the
CC interaction between TALL-1 and TALL-1 receptors (BCMA referred as B cell
CC maturation factor) to regulate monocyte, macrophage and B lymphocyte
CC mediated immune responses. TALL-1 protein is useful for identifying
CC compounds that regulate B lymphocyte proliferation. It is also useful for
CC treating B lymphocyte associated autoimmune disorders like rheumatoid
CC arthritis, systemic lupus erythematosus (SLE), insulin dependent diabetes
CC mellitus, multiple sclerosis, myasthenia gravis, Grave's disease,
CC autoimmune haemolytic anaemia, autoimmune thrombocytopenia purpura,
CC Goodpasture's syndrome, pemphigus vulgaris, acute rheumatic fever,
CC post-streptococcal glomerulonephritis or polyarteritis nodosa.
CC The TALL-1 protein and its corresponding nucleic acid sequence are also
CC useful in diagnostic assays.
CC The present sequence is a C-terminal region of human Tumour necrosis
CC factor (TNF) which has 20-25% sequence identity with C-terminal region of
CC human TALL-1 protein extracellular domain.
XX
SQ Sequence 147 AA;

Query Match 100.0%; Score 81; DB 22; Length 147;
Best Local Similarity 100.0%; Pred. No. 8.9e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRETPGAEAKPMY 14
DB 92 QRETPGAEAKPMY 105

RESULT 11

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AAP91635

AAP91635 standard; protein; 149 AA.

AAP91635;

25-JUN-1990 (first entry)

Polypeptide derived from human tumour necrosis factor.

Tumour necrosis factor; antitumour activity; pTNF482.

Homo sapiens.

JP01023898-A.

26-JAN-1989.

17-JUL-1987; 87JP-0177284.

17-JUL-1987; 87JP-0177284.

(TEIJ ) TEIJIN KK.

WPI: 1989-072158/10.

N-PSDB: AAN94432.

New physiologically active polypeptide - with antitumour activity.

Claim 1; page 1; 18pp; Japanese.

The recombinant polypeptide expressed by E.coli transformed with pTNF482, has antitumour activity with greater specific activity and stability than natural h-TNF, and which causes less side effects.

Sequence 149 AA;

Query Match 100.0%; Score 81; DB 10; Length 149;

Best Local Similarity 100.0%; Pred. No. 9e-06; Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 QRETPGAEAKPMY 14

|||||

94 QRETPGAEAKPMY 107

JUL 12

105612

AAR05612 standard; protein; 149 AA.

AAR05612;

29-OCT-1990 (first entry)

Antitumour peptide.

Antitumour; cancer; tumour necrosis factor; ds.

Synthetic.

JP02128696-A.

17-MAY-1990.

09-NOV-1988; 88JP-0281364.

09-NOV-1988; 88JP-0281364.

(TEIJ ) TEIJIN KK.

WPI: 1990-196692/26.

N-PSDB: AAO05038.

New physiologically active polypeptide -

PT contains specific amino acid sequence, shows antitumour effect and has low side effect.

XX

PS

Disclosure; 18pp; Japanese.

XX

CC DNA is synthesised from 17 oligonucleotides TNF-1 to TNF-17.

CC The gene product may be truncated by 12 N-terminal AAs, and

CC

residue Leu-157 may be replaced by Phe

XX

SQ Sequence 149 AA;

Query Match 100.0%; Score 81; DB 11; Length 149;

Best Local Similarity 100.0%; Pred. No. 9e-06;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRETPGAEAKPMY 14

|||||

Db 95 QRETPGAEAKPMY 108

RESULT 13

AAP70528

ID AAP70528 standard; protein; 150 AA.

XX AAP70528;

DT 30-JAN-1991 (first entry)

DE Synthetic tumour necrosis factor mutant.

XX Tumour necrosis factor; mutant; antitumour agent; vector pTNF 416;

XX JP62248498-A.

PD 29-OCT-1987.

PE 21-APR-1986; 86JP-0090087.

PR 21-APR-1986; 86JP-0090087.

XX (TEIJ ) TEIJIN KK.

DR WPI: 1987-345004/49.

DR N-PSDB: AAN70852.

XX

PT New bioactive polypeptide - having antitumour activity and higher activity than human tumour necrosis factor.

PS Claim 1; page 623; 18pp; Japanese.

XX

CC The mutant of tumour necrosis factor (TNF) is constructed by modifying the sequence of human TNF and deleting 7 N-terminal amino acids. The mutant has activity 2.8 times that of human TNF.

CC It is expressed using expression vector pTNF 416 in E.coli.

CC The cells are then cultured to give the mutant in an amt. of 15.5%

CC of total proteins. The antitumour activity of this protein was

CC measured using mouse L-929 fibroblast cells. 100 micro litres of

CC E.coli lysate contg. 0.00006 units had specific activity of the

CC

SQ Sequence 150 AA;

Query Match 100.0%; Score 81; DB 8; Length 150;

Best Local Similarity 100.0%; Pred. No. 9.1e-06; Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRETPGAEAKPMY 14

|||||

Db 95 QRETPGAEAKPMY 108

RESULT 14

AAP71245



GenCore version 5.1.4-p5\_4578  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 4, 2003, 08:37:36 ; Search time 10.1613 Seconds  
(Without alignments)  
132.452 Million cell updates/sec

Title: US-09-779-703-1

Perfect score: 81

Sequence: 1 ORETEGAEAKPMY 14

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

1: PIR1:\*  
2: PIR2:\*  
3: PIR3:\*  
4: PIR4:\*

Pred. No. is the number of results predicted to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	81	100.0	232	1	SI2606
2	81	100.0	233	1	QMHUN
3	81	100.0	233	1	S22052
4	81	100.0	233	2	SI1688
5	68	84.0	185	2	S52715
6	68	84.0	233	1	S24642
7	66	81.5	234	1	JH0529
8	65	80.2	235	1	QMHNS
9	65	80.2	235	2	JU0029
10	65	80.2	235	2	I54490
11	59.5	73.5	193	1	S06192
12	59.5	72.8	234	1	J01344
13	49	60.5	234	1	A25451
14	47	58.0	711	2	F75440
15	45	55.6	469	2	F48783
16	44	54.3	713	2	G98286
17	44	54.3	713	2	AB2997
18	43	53.1	157	2	AF3344
19	43	53.1	289	2	AH0060
20	43	53.1	733	2	B40595
21	43	53.1	1021	2	F82230
22	43	53.1	1677	2	T14267
23	42	51.9	142	2	A47169
24	42	51.9	187	2	C75136
25	42	51.9	350	2	A10924
26	42	51.9	800	1	S31575
27	42	51.9	1539	2	G70630
28	41.5	51.2	347	2	D69373
29	41	50.6	331	2	A83678

30	41	50.6	712	2	A96023	probable methylal
31	41	50.6	730	2	A13351	methylmalonyl-CoA
32	41	50.6	774	1	QRECFR	iron(III) diclrat
33	40	49.4	184	2	H72414	hypothetical prote
34	40	49.4	259	1	B42379	bis(5'-nucleosyl)-
35	40	49.4	280	1	A64726	bis(5'-nucleosyl)-
36	40	49.4	282	2	F85486	bis(5'-nucleosyl)-
37	40	49.4	282	2	F90635	bis(5'-nucleosyl)-
38	40	49.4	455	2	S39663	aminopeptidase hom
39	40	49.4	647	2	G75060	hydrogenase-4 comp
40	40	49.4	758	2	H87133	methylmalonyl-CoA
41	40	49.4	909	2	AC3419	phage host specif
42	40	49.4	1236	1	VHMVME	structural polypro
43	40	49.4	1239	1	VHMVEV	structural polypro
44	40	49.4	1240	1	VHMVEV	structural polypro
45	40	49.4	1241	2	S26373	genome polyprotein

#### ALIGNMENTS

##### RESULT 1

SI2606 tumor necrosis factor alpha precursor - pig

C:Species: Sus scrofa domestica (domestic pig)

C>Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 04-Feb-2000

C:Accession: SI2606; SI7290; SI8965; I46659

R:Diwrs, R.T.; Coffee, B.W.; Prestwood, A.K.; McGraw, R.A.

Nucleic Acids Res. 18, 5564, 1990

A:Title: Gene sequence of porcine tumor necrosis factor alpha.

A:Reference number: SI2606; MUID:91016861; PMID:2216741

A:Accession: SI2606

A:Molecule type: DNA

A:Residues: 1-232 <DRE>

A:Cross-references: EMBL:X54001; NID:q2135; PIDN:CAA37949.1; PID:q2136

R:Kuhnert, P.; Wuehrlich, C.; Peterhans, E.; Pauli, U.

Gene 102, 171-178, 1991

A:Title: The porcine tumor necrosis factor-encoding genes: sequence and comparative a

A:Reference number: SI7289; MUID:91340150; PMID:1874444

A:Accession: SI7290

A:Molecule type: DNA

A:Residues: 1-232 <KUH>

A:Cross-references: EMBL:X54859; NID:q2137; PIDN:CAA38639.1; PID:q2134

R:Choi, C.S.; Mollitor, T.W.; Lhn, G.F.; Murtough, M.P.

submitted to the EMBL Data Library, January 1991

A:Description: Complete nucleotide sequence of a cDNA encoding porcine tumor necrosis

A:Reference number: SI8965

A:Accession: SI8965

A:Molecule type: mRNA

A:Residues: 1-232 <CHO>

A:Cross-references: EMBL:X57321; NID:q2137; PIDN:CAA40591.1; PID:q2138

R:Pauli, U.; Beutler, B.; Peterhans, E.

Gene 81, 185-191, 1989

A:Title: Porcine tumor necrosis factor alpha: Cloning with the polymerase chain react

A:Reference number: I46659; MUID:90034181; PMID:2478420

A:Accession: I46659

A:Molecule type: mRNA

A:Residues: 44-232 <PAU>

A:Cross-references: GB:M29079; NID:q164694; PIDN:AAA31128.1; PID:q164695

C:Genetics:

A:Insertions: 62/3; 78/1; 93/1

C:Superfamily: tumor necrosis factor

C:Keywords: cytokine; cytotoxin; glycoprotein; lipoprotein; lymphokine; macrophage; m

F:1-77/Domain: propeptide #status predicted <PRO>

F:78-232/Product: tumor necrosis factor alpha #status predicted <MAT>

F:13/20/Binding site: myristate (lys) (covalent) #status predicted

F:81/Binding site: carbohydrate (Ser) (covalent) #status predicted

F:144-176/Disulfide bonds: #status predicted

Query Match 100.0%; Score 81; DB 1; Length 232;

Best Local Similarity 100.0%; Pred. No. 66-06;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 QRETPGCAKPMW 14  
|||||

177 QRETPGCAKPMW 190

SQUL 2

Human factor alpha precursor [validated] - human  
Alternate names: cachectin; TNFA

Species: Homo sapiens (man)  
Date: 28-Aug-1985 #sequence\_revision 28-Aug-1985 #text\_change 08-Dec-2000  
Accession: A93585; S36153; A93351; A44189; B61478; I53311; S62610; I54522; A01646; B23  
Addn, G.E.; Naylor, S.L.; Sakaguchi, A.Y.; Smith, D.; Jarrett-Nedwin, J.; Pennica, D.  
Jelic Acids Res. 13, 6361-6373, 1985

Title: Human lymphotoxin and tumor necrosis factor genes: structure, homology and chr  
Reference number: A93585; MUID:86016093; PMID:2959927

Accession: A93585

Molecule type: DNA

Residues: 1-233 <NED>

Cross-references: GB:X02910; GB:X02159; NID:g37209; PIDN:CAA26669.1; PID:g37210  
Rits, F.J.M.; Bougueleret, L.; Prieur, S.; Caterina, D.; Primas, G.; Perrot, V.; Jurke  
ture Genet. 3, 137-145, 1993

Title: Dense Ala clustering and a potential new member of the NF-kappaB family within a  
Reference number: S36152; MUID:93272029; PMID:8499947

Accession: S36153

Status: nucleic acid sequence not shown; translation not shown

Molecule type: DNA

Residues: 1-233 <IRI>

Cross-references: EMBL:215026; NID:g37211; PIDN:CAA78745.1; PID:g37212  
Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1992

Pennica, D.; Nedwin, G.E.; Hayflick, J.S.; Seeburg, P.H.; Derynck, R.; Palladino, M.A.  
ture 312, 724-729, 1984

Title: Human tumour necrosis factor: precursor structure, expression and homology to 1  
Reference number: A93351; MUID:85086244; PMID:6392892

Accession: A93351

Molecule type: mRNA

Residues: 1-233 <PEN>

Cross-references: GB:X02910; GB:X02159; NID:g37209; PIDN:CAA26669.1; PID:g37210  
Note: this protein was isolated from the monocytic-like cell line HL-60 from a promyeloc  
nang, A.M.; Creasey, A.A.; Lahnner, M.B.; Lin, L.S.; Strickler, J.; Van Arsdel, J.N.;  
lence 228, 149-154, 1985

Title: Molecular cloning of the complementary DNA for human tumor necrosis factor.  
Reference number: A44189; MUID:85142190; PMID:3856324

Accession: A44189

Molecule type: mRNA

Residues: 1-62, 'S', 64-233 <WAN>

Cross-references: GB:M10988; NID:g339737; PIDN:AAA61198.1; PID:g339738  
Fukuda, S.; Ando, S.; Sanou, O.; Tanai, M.; Fujii, M.; Masaki, N.; Nakamura, K.I.; An  
phokine Res. 7, 175-185, 1988

Title: Simultaneous production of natural human tumor necrosis factor-alpha, -beta and  
Reference number: A61478; MUID:88301617; PMID:2841543

Accession: B61478

Molecule type: protein

Residues: 83-102;109-119;121-128, 'X', 130-131;142-144, 'X', 146, 'xxx', 150-152;159-174;180  
Karmenout, A.; Fransen, L.; Tavernier, J.; Van Der Heyden, J.; Tizard, R.; Kawashima,  
r. J. Biochem. 152, 515-522, 1985

Title: Molecular cloning and expression of human tumor necrosis factor and comparison  
Reference number: I53311; MUID:86030296; PMID:3932069

Accession: I53311

Status: translated from GB/EMBL/DBJ

Molecule type: DNA

Residues: 1-233 <MAR>

Cross-references: GB:M26331; NID:g339763; PIDN:AAA36758.1; PID:g339764  
Experimental source: U-937 cells

Takakura-Yamamoto, R.; Yamamoto, S.; Fukuda, S.; Kurimoto, M.  
r. J. Biochem. 235, 431-437, 1996

Title: O-Glycosylated species of natural human tumor-necrosis factor-alpha.  
Reference number: S62610; MUID:96202967; PMID:8631363

Accession: S62610

Molecule type: protein

Residues: 77-99 <TAK>

R.D'Alfonso, S.; Richiardi, P.M.  
Immunogenetics 39, 150-154, 1994

A>Title: A polymorphic variation in a putative regulation box of the TNFA promoter re  
A:Reference number: I54522; MUID:94102809; PMID:7903959

A:Accession: I54522

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-8 <DAL>

A:Cross-references: GB:S68530; NID:g544751  
R.Stevenson, F.T.; Birsten, S.L.; Locksley, R.M.; Lovett, D.H.  
J. Exp. Med. 176, 1053-1062, 1992

A>Title: Myristyl acylation of the tumor necrosis factor alpha precursor on specific  
A:Reference number: A59163; MUID:93018820; PMID:1402651

A:Contents: annotation: identification of myristylated lysines  
R.aggart, B.B.; Kohr, W.J.; Haas, P.E.; Moffit, B.; Spencer, S.A.; Henzel, W.J.; Br  
J. Biol. Chem. 260, 2345-2354, 1985

A>Title: Human tumor necrosis factor: Production, purification, and characterization.  
A:Reference number: A92511; MUID:85130974; PMID:3871770

A:Contents: annotation: disulfide bond  
C:Comment: Secreted from mitogen-activated macrophages within 4-24 hours after induc  
C:Comment: TNF-alpha and -beta (lymphotoxin) are the products of different genes clos  
ut are produced by different cell types and have different induction kinetics.

C:Genetics:

A:Gene: GDB:TNF; TNFA

A:Cross-references: GDB:120441; OMIM:191160

A:Map position: 6p21.3-6p21.3

A:Introns: 62/3; 78/1; 94/1

C:Complex: homotrimer

C:Superfamily: tumor necrosis factor

C:Keywords: cytokine; cytotoxin; glycoprotein; homotrimer; lipoprotein; lymphokine; m  
F:-76/Domain: propeptide #status predicted <PRO>

F:17-233/Product: tumor necrosis factor #status experimental <MNT>

F:19,20/Binding site: myristate (Lys) (covalent) #status experimental

F:81/Binding site: carbohydrate (Ser) (covalent) (partial) #status experimental

F:145-177/Disulfide bonds: #status experimental

Query Match 100.0%; Score 81; DB 1; Length 233;  
Best Local Similarity 100.0%; Pred. No. 66-06;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 178 QRETPGCAKPMW 191  
|||||

RESULT 3

S22052

Tumor necrosis factor alpha precursor - baboon

C:Species: Papio sp. (baboon)

C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 04-Feb-2000

C:Accession: S22052

R:Sanjanwala, M.; Edwards, A.  
submitted to the EMBL Data Library, September 1991

A:Description: Baboon Tumor Necrosis Factor Derived from Sequences of Genomic DNA.  
A:Reference number: S22052

A:Accession: S22052

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-233 <SAN>

A:Cross-references: EMBL:X62141; NID:g38159; PIDN:CAA44068.1; PID:g38160

C:Genetics:

A:Introns: 62/3; 78/1; 94/1

C:Superfamily: tumor necrosis factor

C:Keywords: glycoprotein; lipoprotein; myristylation; transmembrane protein  
F:19,20/Binding site: myristate (Lys) (covalent) #status predicted

F:81/Binding site: carbohydrate (Ser) (covalent) #status predicted

F:145-177/Disulfide bonds: #status predicted

Query Match 100.0%; Score 81; DB 1; Length 233;  
Best Local Similarity 100.0%; Pred. No. 66-06;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

## QY 1 QRETEGAEAKPMY 14

Db 178 QRETEGAEAKPMY 191

## RESULT 4

S11688

tumor necrosis factor alpha precursor - cat  
 C:Species: Felis silvestris catus (domestic cat)  
 C:Date: 21-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 04-Feb-2000  
 C:Accession: S11688  
 R:McGraw, R.A.; Coffee, B.W.; Otto, C.M.; Drews, R.T.; Rawlings, C.A.  
 Nucleic Acids Res. 18, 5563, 1990  
 A:Title: Gene sequence of feline tumor necrosis factor alpha.  
 A:Reference number: S11688; MUID:91016860; PMID:2216740  
 A:Accession: S11688  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-233 <MCG>  
 A:Cross-references: EMBL:X54000; NID:91084; PIDN:CAA37948.1; PID:g295777  
 C:Genetics:  
 A:Introns: 62/3; 78/1; 94/1  
 C:Superfamily: tumor necrosis factor  
 C:Keywords: glycoprotein; lipoprotein; myristylation; transmembrane protein  
 F:19/20/Binding site: myristate (Lys) (covalent) #status predicted  
 F:81/Binding site: carbohydrate (Ser) (covalent) #status predicted  
 F:145-177/Disulfide bonds: #status predicted

## Query Match

Best Local Similarity 100.0%; Score 81; DB 2; Length 233;  
 Pred. No. 66-06;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

## QY 1 QRETEGAEAKPMY 14

Db 178 QRETEGAEAKPMY 191

## RESULT 5

S52715

tumor necrosis factor alpha precursor - bovine (fragment)  
 C:Species: Bos primigenius taurus (cattle)  
 C:Date: 19-May-1995 #sequence\_revision 21-Jul-1995 #text\_change 04-Feb-2000  
 C:Accession: S52715  
 R:Wenters, B.; Gaidulis, L.  
 submitted to the EMBL Data Library, March 1995  
 A:Description: Cloning and sequence analysis of cDNAs encoding bovine CD40 ligand and bc  
 A:Reference number: S52715  
 A:Accession: S52715  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-185 <MER>  
 A:Cross-references: EMBL:Z48808; NID:9755701; PIDN:CAA88743.1; PID:g755702  
 C:Superfamily: tumor necrosis factor  
 C:Keywords: glycoprotein  
 F:33/Binding site: carbohydrate (Ser) (covalent) #status predicted  
 F:97-129/Disulfide bonds: #status predicted

## Query Match

Best Local Similarity 84.0%; Score 68; DB 2; Length 185;  
 Pred. No. 0.00069;  
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

## QY 2 RETPEGAERAKPMY 14

Db 131 RETPEGAERAKPMY 143

## RESULT 6

S24642

tumor necrosis factor alpha precursor - bovine  
 C:Species: Bos primigenius taurus (cattle)  
 C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 04-Feb-2000  
 C:Accession: I46047; S24642  
 R:Cludts, I.; Cleuter, Y.; Kettmann, R.; Burny, A.; Droogmans, L.

## Cytokine 5, 336-341, 1993

A:Title: Cloning and characterization of the tandemly arranged bovine lymphotoxin and  
 A:Reference number: I46046; MUID:94083525; PMID:8260599  
 A:Accession: I46047  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-233 <CL2>  
 A:Cross-references: EMBL:Z14137; NID:9796; PIDN:CAA78511.1; PID:g798  
 C:Genetics:  
 A:Gene: TNFA  
 A:Introns: 62/3; 78/1; 94/1  
 C:Superfamily: tumor necrosis factor  
 C:Keywords: glycoprotein; lipoprotein; myristylation; transmembrane protein  
 F:20/Binding site: myristate (Lys) (covalent) #status predicted  
 F:81/Binding site: carbohydrate (Ser) (covalent) #status predicted  
 F:145-177/Disulfide bonds: #status predicted

## Query Match

Best Local Similarity 84.0%; Score 68; DB 1; Length 233;  
 Pred. No. 0.00088;  
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

## QY 2 RETPEGAERAKPMY 14

Db 179 RETPEGAERAKPMY 191

## RESULT 7

JH0529

tumor necrosis factor alpha precursor - sheep  
 N:Alternate names: cachectin; TNF alpha  
 C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)  
 C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 04-Feb-2000  
 C:Accession: JH0529; S48118; S13114; S20661  
 R:Green, I.R.; Sargan, D.R.  
 Gene 109, 203-210, 1991  
 A:Title: Sequence of the cDNA encoding ovine tumor necrosis factor-alpha: problems wi  
 A:Reference number: JH0529; MUID:92112044; PMID:1765267  
 A:Accession: JH0529  
 A:Molecule type: mRNA  
 A:Residues: 1-234 <GRD>  
 A:Cross-references: EMBL:X55152; NID:91405; PIDN:CAA38952.1; PID:g1406  
 A:Experimental source: alveolar macrophage  
 R:Nash, A.D.; Barclay, G.J.; Brandon, M.R.; Andrews, A.E.  
 Immunol. Cell Biol. 69, 273-283, 1991  
 A:Title: Molecular cloning, expression and characterization of ovine TNF-alpha.  
 A:Reference number: S48118; MUID:92155784; PMID:1786996  
 A:Accession: S48118  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-234 <NAS>  
 A:Cross-references: EMBL:X56756; NID:9297806; PIDN:CAA40076.1; PID:g297807  
 R:Young, A.J.; Hay, J.B.; Chan, J.Y.C.  
 Nucleic Acids Res. 18, 6723, 1990  
 A:Title: Primary structure of ovine tumor necrosis factor alpha cDNA.  
 A:Reference number: S13114; MUID:91067496; PMID:2251151  
 A:Accession: S13114  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-62, 64-234 <YON>  
 A:Cross-references: EMBL:X55966; NID:91403; PIDN:CAA39437.1; PID:g1404  
 A>Note: comparison with the introns of homologous sequences suggest that this is prob  
 C:Superfamily: tumor necrosis factor  
 C:Keywords: alternative splicing; cytokine; cyclooxin; glycoprotein; lipoprotein; lym  
 F:1-77/Domain: propeptide #status predicted <PRO>  
 F:78-234/Product: tumor necrosis factor alpha #status predicted <TNF>  
 F:20/Binding site: myristate (Lys) (covalent) #status predicted  
 F:82/Binding site: carbohydrate (Ser) (covalent) #status predicted  
 F:96/Binding site: carbohydrate (Asn) (covalent) #status predicted  
 F:146-178/Disulfide bonds: #status predicted

## Query Match

Best Local Similarity 81.5%; Score 66; DB 1; Length 234;  
 Pred. No. 0.0019;  
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

2 RETPEGAEKAPMW 14
||| |||||
180 RETPEGAEKAPMW 192

3JUL 8
/MSN
tumor necrosis factor alpha precursor - mouse
Alternate names: cachectin; TNF alpha
Species: Mus musculus (house mouse)
Date: 31-Mar-1988 #sequence, revision 31-Mar-1988 #text, change 04-Feb-2000
Accession: A22908; S03791; A27303; A25164; A34251; I59058; A36696
Shirai, T.; Shimizu, N.; Shiojiri, S.; Horiguchi, S.; Ito, H.
A 7, 193-201, 1988
Title: Cloning and expression in Escherichia coli of the gene for mouse tumor necrosis
Reference number: A22908; MUID:88224564; PMID:2836146
Accession: A22908
Molecule type: DNA
Residues: 1-235 <SHI>
Cross-references: GB:M20155
Shakhov, A.N.; Nedospasov, S.A.
org. Khim. 13, 701-705, 1987
Title: Molecular cloning of the genes coding for tumor necrosis factors: complete nucl
Reference number: S03791; MUID:87298639; PMID:3040015
Accession: S03791
Molecule type: DNA
Residues: 1-235 <SHA>
Cross-references: GB:M38296; NID:9202086; PIDN:AAA0459.1; PID:9202087
Note: article in Russian with English abstract
Semion, D.; Kawashima, E.; Jongeneel, C.V.; Shakhov, A.N.; Nedospasov, S.A.
cleic Acids Res. 15, 9083-9084, 1987
Title: Nucleotide sequence of the murine TNF locus, including the TNF-alpha (tumor nec
Reference number: A03679; MUID:88067722; PMID:3684584
Accession: A27303
Molecule type: DNA
Residues: 1-235 <SEK>
Cross-references: GB:Y00467; NID:954830; PIDN:CAA6530.1; PID:954832
Pennica, D.; Hayflick, J.S.; Brinman, T.S.; Palladino, M.A.; Goeddel, D.V.
oc. Natl. Acad. Sci. U.S.A. 82, 6060-6064, 1985
Title: Molecular cloning of mouse tumor necrosis factor cDNA and its eukaryotic expre
Reference number: A25164; MUID:85298296; PMID:3898078
Accession: A25164
Molecule type: mRNA
Residues: 1-235 <PEN>
Cross-references: GB:M11731; NID:9202084; PIDN:AAA0458.1; PID:9202085
Franssen, L.; Muller, R.; Marmenout, A.; Tavernier, J.; van der Heyden, J.; Kawashima,
cleic Acids Res. 13, 4417-4429, 1985
Title: Molecular cloning of mouse tumor necrosis factor cDNA and its eukaryotic expre
Reference number: A23127; MUID:85242112; PMID:2989794
Accession: A23127
Molecule type: mRNA
Residues: 1-235 <FRA>
Cross-references: GB:X02611; NID:954844; PIDN:CAA26457.1; PID:954845
Cseh, K.; Beutler, B.
Biol. Chem. 264, 16256-16260, 1989
Title: Alternative cleavage of the cachectin/tumor necrosis factor propeptide results
Reference number: A34251; MUID:89380231; PMID:2777790
Accession: A34251
Molecule type: protein
Residues: 70-87 <CSE>
Caput, D.; Beutler, B.; Hartog, K.; Thayer, R.; Brown-Shimer, S.L.; Cerami, A.
oc. Natl. Acad. Sci. U.S.A. 83, 1670-1674, 1986
Title: Identification of a common nucleotide sequence in the 3'-untranslated region of
Reference number: I59058; MUID:86149365; PMID:2419912
Accession: I59058
Status: preliminary; translated from GB/EMBL/DBJ
Molecule type: mRNA
Residues: 1-230, 'R', 232-235 <RES>
Cross-references: GB:M3049; NID:9202082; PIDN:AAA0457.1; PID:9202083
Sherry, B.; Jue, D.M.; Zentella, A.; Cerami, A.
chem. Biophys. Res. Commun. 173, 1072-1078, 1990
Title: Characterization of high molecular weight glycosylated forms of murine tumor ne

```

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A:Reference number: A36696; MUID:91097531; PMID:2268312
A:Accession: A36696
A:Molecule type: protein
A:Residues: 80-85, 'X', 87-99 <SHE>
C:Genetics:
A:Introns: 62/3; 81/1; 97/1
A:Note: the first intron occurs in the 5'-untranslated region
C:Superfamily: tumor necrosis factor
C:Keywords: cytokine; cytotoxin; glycoprotein; lipoprotein; lymphokine; macrophage; m
F:80-235/Product: tumor necrosis factor #status experimental <MAT>
F:20/Binding site: myristate (Lys) (covalent) #status predicted
F:84/Binding site: carbohydrate (Ser) (covalent) #status predicted
F:148-179/Disulfide bonds: #status predicted

Query Match          80.2%; Score 65; DB 1; Length 235;
Best local Similarity 76.9%; Pred. No. 0.0028;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      2 RETPEGAEKAPMW 14
Db      181 KDRPEGAEKAPMW 193

RESULT 9
JU0029
tumor necrosis factor alpha precursor - rat
N:Alternate names: cachectin; TNF alpha
C:Species: Rattus norvegicus (Norway rat)
C:Date: 07-Jun-1990 #sequence, revision 07-Jun-1990 #text, change 04-Feb-2000
C:Accession: JU0029; JN0868; S21674
R:Shirai, T.; Shimizu, N.; Horiguchi, S.; Ito, H.
Agric. Biol. Chem. 53, 1733-1736, 1989
A:Title: Cloning and expression in Escherichia coli of the gene for rat tumor necrosi
A:Reference number: JU0029
A:Accession: JU0029
A:Molecule type: DNA
A:Residues: 1-235 <KWO>
R:Kwon, J.; Chung, I.Y.; Benveniste, E.N.
Gene 132, 227-230, 1993
A:Title: Cloning and sequence analysis of the rat tumor necrosis factor-encoding gene
A:Reference number: JN0868; MUID:94040766; PMID:8224868
Accession: JN0868
A:Molecule type: DNA
A:Residues: 1-235 <KWO>
A:Cross-references: GB:I00981; NID:9205253; PIDN:AAA16275.1; PID:9205254
R:Stiller, H.C.; Greve, M.; Gausling, R.; Pavlovic, M.; Decker, K.
Biol. Chem. Hoppe-Seyler 373, 271-281, 1992
A:Title: Rat tumor necrosis factor-alpha. Transcription in rat Kupffer cells and in v
A:Reference number: S21674; MUID:92329007; PMID:1627266
Accession: S21674
A:Molecule type: mRNA
A:Residues: 1-38, 'P', 40-162, 'T', 164-201, 'S', 203-235 <RST>
A:Cross-references: GB:X66539; NID:9395369; PIDN:CAA7146.1; PID:9395370
C:Comment: Tumor necrosis factor is secreted by macrophages in response to endotoxin
C:Genetics:
A:Gene: TNF-alpha
A:Introns: 62/3; 81/1; 97/1
C:Superfamily: tumor necrosis factor
C:Keywords: cytokine; cytotoxin; glycoprotein; lipoprotein; lymphokine; macrophage; m
F:80-235/Product: tumor necrosis factor #status predicted <MAT>
F:9,20/Binding site: myristate (Lys) (covalent) #status predicted
F:84/Binding site: carbohydrate (Ser) (covalent) #status predicted
F:148-179/Disulfide bonds: #status predicted

Query Match          80.2%; Score 65; DB 2; Length 235;
Best local Similarity 76.9%; Pred. No. 0.0028;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      2 RETPEGAEKAPMW 14
Db      181 KDRPEGAEKAPMW 193

```

## RESULT 10

I54490

tumor necrosis factor alpha precursor - white-footed mouse

C/Species: Peromyscus leucopus (white-footed mouse)

C/Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 04-Feb-2000

C/Accession: I54490

R:Grew, M.D.; Filipowsky, M.E.

Immunogenetics 35, 351-353, 1992

A&gt;Title: Sequence of the tumor necrosis factor/cachectin (TNF) gene from Peromyscus leuc

A/Reference number: I54490; MUID:92218012; PMID:1348497

A/Accession: I54490

A&gt;Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-235 &lt;RES&gt;

A/Cross-references: GB:M59233; NID:g202506; PIDN:AAA40596.1; PID:g202507

C/Genetics:

A:Gene: TNF

A/Introns: 62/3; 81/1; 97/1

C/Superfamily: tumor necrosis factor

C/Keywords: cytokine; lipoprotein; myristylation

F:19/20/Binding site: myristate (Lys) (covalent) #status predicted

F:84/Binding site: carbonylrate (Ser) (covalent) #status predicted

## Query Match

Best Local Similarity 80.2%; Score 65; DB 2; Length 235;

Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 REPPEGAERKPMY 14

Db 181 KETPESELEKPMY 193

## RESULT 11

S06192

tumor necrosis factor alpha precursor - goat (fragment)

N/Alternate names: cachectin; TNF alpha

C/Species: Capra aegagrus hircus (domestic goat)

C/Date: 28-Feb-1990 #sequence\_revision 28-Feb-1990 #text\_change 31-Jan-2000

C/Accession: S06192; S41867

R:Goldstein, I.M.; Henner, D.; Talhouk, A.

submitted to the EMBL Data Library, March 1989

A/Reference number: S06192

A/Accession: S06192

A/Molecule type: mRNA

A/Residues: 1-193 &lt;GOL&gt;

A/Cross-references: EMBL:X14828; NID:g9992; PIDN:CAA32937.1; PID:g993

R:Rimstad, E. submitted to the EMBL Data Library, January 1994

A/Reference number: S41867

A/Accession: S41867

A&gt;Status: preliminary

A/Molecule type: mRNA

A/Residues: 36-38, 'S', 'A', '80-88', 'N', '90-114', 'O', '116-123', 'D', '125-144', 'G', '145-173', 'L'

A/Cross-references: EMBL:X77317; NID:g452607; PIDN:CAA54523.1; PID:g452608

C/Superfamily: tumor necrosis factor

C/Keywords: cytokine; cytolysin; glycoprotein; lymphokine; macrophage; membrane protein

F:42/Binding site: carbonylrate (Ser) (covalent) #status predicted

F:106-138/Disulfide bonds: #status predicted

## Query Match

Best Local Similarity 73.5%; Score 59.5; DB 2; Length 193;

Matches 12; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 2 REPPEGAERKPMY 14

Db 140 REPPE-ARAKPMY 151

## RESULT 12

J01344

tumor necrosis factor alpha precursor - horse

N/Alternate names: cachectin; TNF alpha

C/Species: Equus caballus (domestic horse)

C/Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 04-Feb-2000

C/Accession: J01344

R:Su, X.; Morris, D.D.; McGraw, R.A.

Gene 107, 319-321, 1991

A&gt;Title: Cloning and characterization of gene TNF alpha encoding equine tumor necrosi

A/Reference number: J01344; MUID:92084125; PMID:1748301

A/Accession: J01344

A/Molecule type: DNA

A/Residues: 1-234 &lt;SU&gt;

A/Cross-references: GB:M64087; NID:g164244; PIDN:AAA30959.1; PID:g164245

C/Comment: This protein is an important proximal mediator of endotoxemia.

C/Genetics:

A:Gene: TNF-alpha

A/Introns: 62/3; 79/1; 95/1

C/Superfamily: tumor necrosis factor

C/Keywords: cytokine; cytolysin; glycoprotein; lipoprotein; lymphokine; macrophage; m

F:78-234/Product: tumor necrosis factor alpha #status predicted &lt;TUM&gt;

F:19/20/Binding site: myristate (Lys) (covalent) #status predicted

F:82/Binding site: carbonylrate (Ser) (covalent) #status predicted

F:146-178/Disulfide bonds: #status predicted

## Query Match

Best Local Similarity 72.8%; Score 59; DB 1; Length 234;

Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 REPPEGAERKPMY 14

Db 181 ESPPEGAERKPMY 192

## RESULT 13

A25451

tumor necrosis factor alpha precursor - rabbit

N/Alternate names: cachectin; TNF alpha

C/Species: Oryctolagus cuniculus (domestic rabbit)

C/Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 04-Feb-2000

C/Accession: A25454; A25451; J50727

R:Itto, H.; Yamamoto, S.; Kuroda, S.; Sakamoto, H.; Kajihara, J.; Kiyota, T.; Hayashi,

DNA 5, 149-156, 1986

A&gt;Title: Molecular cloning and expression in Escherichia coli of the cDNA coding for

A/Reference number: A25454; MUID:86219711; PMID:3519137

A/Accession: A25454

A/Molecule type: mRNA

A/Residues: 1-234 &lt;ITO&gt;

A/Cross-references: GB:M12845; NID:g165759; PIDN:AAA31486.1; PID:g165760

R:Itto, H.; Shirai, T.; Yamamoto, S.; Akita, M.; Kawahara, S.; Todd, C.W.; Wallace, R.

DNA 5, 157-165, 1986

A&gt;Title: Molecular cloning of the gene encoding rabbit tumor necrosis factor.

A/Reference number: A25451; MUID:86219712; PMID:3519138

A/Accession: A25451

A/Molecule type: DNA

A/Residues: 1-234 &lt;ITT&gt;

A/Note: this sequence differs from that shown in having a Gln inserted between residu

R:Shahov, A.N.; Kiprash, D.V.; Azizov, M.M.; Jongeneel, C.V.; Nedospasov, S.A.

Gene 95, 215-221, 1990

A&gt;Title: Structural analysis of the rabbit TNF locus, containing the genes encoding T

A/Reference number: JH0309; MUID:91065534; PMID:2249779

A/Accession: J50727

A/Molecule type: DNA

A/Residues: 1-62, 'O', '63-234 &lt;SHA&gt;

A/Cross-references: GB:M0340; GB:M5326; NID:g165754; PIDN:AAA31484.1; PID:g165756

C/Genetics:

A:Introns: 62/3; 80/1; 96/1

C/Superfamily: tumor necrosis factor

C/Keywords: cytokine; cytolysin; glycoprotein; lipoprotein; lymphokine; macrophage; m

F:82-234/Product: tumor necrosis factor #status predicted &lt;PRO&gt;

F:19/20/Binding site: myristate (Lys) (covalent) #status predicted &lt;MAT&gt;

F:83/Binding site: carbonylrate (Ser) (covalent) #status predicted

F:147-178/Disulfide bonds: #status predicted



Job time : 12.1613 secs

Query Match 60.5%; Score 49; DB 1; Length 234;  
 Best Local Similarity 69.2%; Pred. No. 1.3;  
 Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

2 RETPEGAERKPMY 14  
 ||||| || ||  
 180 RETPEGAERKPMY 192

SU.T 14  
 5440

ethylmalonyl-CoA mutase, beta subunit - Deinococcus radiodurans (strain R1)  
 Species: Deinococcus radiodurans  
 Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 17-Mar-2000  
 Accession: F75440  
 White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;  
 M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma  
 ; Smith, H.O.; Venter, J.C.; Fraser, C.M.  
 lence 286, 1571-1577, 1999  
 Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.  
 Reference number: A75250; MUID:20036896; PMID:10567266  
 Accession: F75440

Status: Preliminary  
 Molecule type: DNA  
 Residues: 1-711 <WHI>  
 Cross-references: GB:AE001958; GB:AE000513; NID:g6458805; PIDN:AAF10655.1; PID:g645881  
 Experimental source: strain R1  
 Genetics:

Gene: DR1084  
 Map position: 1  
 Superfamily: human methylmalonyl-CoA mutase; cobalamin-binding homology

Query Match 58.0%; Score 47; DB 2; Length 711;  
 Best Local Similarity 69.2%; Pred. No. 9.1;  
 Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

2 RETPEGAERKPMY 14  
 ||||| || ||  
 31 RETPEGLTLKPLY 43

SU.T 15  
 8783

lated to SG11 protein [imported] - Neurospora crassa  
 Alternate names: protein 13E11.310  
 Species: Neurospora crassa

Date: 05-May-2000 #sequence\_revision 05-May-2000 #text\_change 05-May-2000  
 Accession: T48783  
 Schulte, U.; Algn, V.; Hohnsels, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura,  
 blimited to the Protein Sequence Database, April 2000  
 Reference number: Z24541  
 Accession: T48783

Status: Preliminary  
 Molecule type: DNA  
 Residues: 1-469 <SCH>  
 Cross-references: EMBL:AL353820; GSPDB:GN00112; NCSP:13E11.310  
 Experimental source: cosmid contig 13E11; strain 74  
 Genetics:  
 Gene: NCSP:13E11.310  
 Map position: 2  
 Introns: 277/3

Query Match 55.6%; Score 45; DB 2; Length 469;  
 Best Local Similarity 77.8%; Pred. No. 13;  
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

5 PEGAEKPM 13  
 ||| ||||  
 459 PEGVEKPM 467

arch completed: April 4, 2003, 08:42:56

GenCore version 5.1.4.p5.4578  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 4, 2003, 08:36:51 ; Search time 5.64516 seconds

(without alignments) 102.861 Million cell updates/sec

Title: US-09-779-703-1

Perfect score: 81

Sequence: 1 QRETPGAEKPMV 14

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs., 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 0%

Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	81	100.0	232	1	TNFA_PIG
2	81	100.0	233	1	TNFA_PIG
3	81	100.0	233	1	TNFA_PIG
4	81	100.0	233	1	TNFA_PIG
5	81	100.0	233	1	TNFA_PIG
6	81	100.0	233	1	TNFA_PIG
7	81	100.0	233	1	TNFA_PIG
8	81	100.0	233	1	TNFA_PIG
9	81	100.0	233	1	TNFA_PIG
10	81	100.0	233	1	TNFA_PIG
11	81	100.0	233	1	TNFA_PIG
12	81	100.0	233	1	TNFA_PIG
13	81	100.0	233	1	TNFA_PIG
14	81	100.0	233	1	TNFA_PIG
15	81	100.0	233	1	TNFA_PIG
16	81	100.0	233	1	TNFA_PIG
17	81	100.0	233	1	TNFA_PIG
18	81	100.0	233	1	TNFA_PIG
19	81	100.0	233	1	TNFA_PIG
20	81	100.0	233	1	TNFA_PIG
21	81	100.0	233	1	TNFA_PIG
22	81	100.0	233	1	TNFA_PIG
23	81	100.0	233	1	TNFA_PIG
24	81	100.0	233	1	TNFA_PIG
25	81	100.0	233	1	TNFA_PIG
26	81	100.0	233	1	TNFA_PIG
27	81	100.0	233	1	TNFA_PIG
28	81	100.0	233	1	TNFA_PIG
29	81	100.0	233	1	TNFA_PIG
30	81	100.0	233	1	TNFA_PIG
31	81	100.0	233	1	TNFA_PIG
32	81	100.0	233	1	TNFA_PIG
33	81	100.0	233	1	TNFA_PIG

34	40	49.4	1236	1	POLN_EEVE
35	40	49.4	1239	1	POLN_EEVE
36	40	49.4	1240	1	POLN_EEVE
37	39.5	48.8	233	1	TNFA_PIG
38	39	48.1	239	1	TNFA_PIG
39	39	48.1	356	1	GLN3_ORYSA
40	39	48.1	462	1	YD36_YEAST
41	39	48.1	496	1	SRM_MOUSE
42	39	48.1	536	1	GAG_FSYMD
43	39	48.1	580	1	GAG_FTV
44	39	48.1	589	1	MAYS_YEAST
45	39	48.1	589	1	MAYS_YEAST

## ALIGNMENTS

RESULT 1	ID	STANDARD:	PRT:	232 AA.
TNFA_PIG	1			
AC	P23563			
DT	01-NOV-1991 (Rel. 20, Created)			
DT	01-NOV-1991 (Rel. 20, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor ligand superfamily member 2) (cachectin).			
DE	TNF OR TNFSF2 OR TNFA.			
OS	Sus scrofa (Pig).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.			
OX	NCBI_Taxid=9823;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=91016861; PubMed=2216741;			
RA	Drews R.T., Coffee B.W., Prestwood A.K., McGraw R.A.;			
RL	"Gene sequence of porcine tumor necrosis factor alpha.";			
RL	Nucleic Acids Res. 18:5564-5564(1990).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	TISSUE=Liver;			
RA	MEDLINE=9140150; PubMed=1874444;			
RL	Kuhert P., Wethrich C., Peterhans E., Pauli U.;			
RL	"The porcine tumor necrosis factor-encoding genes: sequence and comparative analysis.";			
RL	Gene 102:171-178(1991).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RX	TISSUE=Macrophage;			
RA	Choi C.S., Mollitor T.W., Lin G.F., Murtough M.P.;			
RL	"Complete nucleotide sequence of a cDNA encoding porcine tumor necrosis factor-alpha.";			
RL	Anim. Biotechnol. 2:97-105(1991).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RX	STRAIN=Large white; TISSUE=Fibroblast;			
RA	MEDLINE=21108615; PubMed=11169259;			
RL	Chardon P., Rogel-Gallard C., Catolico L., Duprat S., Vaitman M., Renard C.;			
RL	"Sequence of the swine major histocompatibility complex region containing all non-classical class I genes.";			
RL	Tissue Antigens 57:55-65(2001).			
RN	[5]			
RP	SEQUENCE OF 44-232 FROM N.A.			
RX	MEDLINE=90034181; PubMed=2478420;			
RA	Pauli U., Beutler B., Peterhans E.;			
RL	"Porcine tumor necrosis factor alpha: cloning with the polymerase chain reaction and determination of the nucleotide sequence.";			
RL	Gene 81:185-191(1989).			
CC	-I- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and TNFRSF1B/TNFR2. It is mainly secreted by macrophages and can induce cell death of certain tumor cell lines. It is potent pyrogen causing fever by direct action or by stimulation of interleukin 1 secretion and is implicated in the induction of			

cachexia, under certain conditions it can stimulate cell proliferation and induce cell differentiation.

- 1- SUBUNIT: Homotrimer (By similarity).
- 1- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an extracellular soluble form (By similarity).
- 1- PTM: The soluble form derives from the membrane form by proteolytic processing (By similarity).
- 1- PTM: The membrane form, but not the soluble form, is phosphorylated on serine residues. Dephosphorylation of the membrane form occurs by binding to soluble TNFRSF1A/TNFR1 (By similarity).
- 1- DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF DISEASES, INCLUDING CANCER AND INFECTION, AND IS CHARACTERIZED BY GENERAL ILL HEALTH AND MALNUTRITION.
- 1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.

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EMBL: X54001; CAJ37949.1; -  
 EMBL: X54859; CAJ38639.1; -  
 EMBL: X57321; CAJ40591.1; -  
 EMBL: AJ251914; CAB63852.1; -  
 EMBL: M29079; AAA31128.1; -  
 PIR: S12606; S12606.  
 PIR: S17290; S17290.  
 PIR: S18965; S18965.  
 HSSP: P01375; ATSV.  
 InterPro: IPR003636; TNF\_abc.  
 InterPro: IPR000478; TNF\_family.  
 Pfam: PF00229; TNF\_1.  
 PRINTS: PR01234; TNFCROSISCT.  
 ProDom: PD002012; TNF\_abc; 1.  
 SMART: SM00207; TNF\_1.  
 PROSITE: PS00251; TNF\_1; 1.  
 PROSITE: PS50049; TNF\_2; 1.  
 Cytokine; Cytotoxin; Transmembrane; Phosphorylation; Signal-anchor.  
 CHAIN 1 232 TUMOR NECROSIS FACTOR, MEMBRANE FORM.  
 DOMAIN 77 232 CYTOPLASMIC (POTENTIAL).  
 TRANSMEM 36 56 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN) (POTENTIAL).  
 DOMAIN 57 232 EXTRACELLULAR (POTENTIAL).  
 SITE 76 77 CLEAVAGE (BY ADAM17) (BY SIMILARITY).  
 MOD\_RES 2 2 PHOSPHORYLATION (BY CK1) (BY SIMILARITY).  
 DISULFID 144 176 BY SIMILARITY.  
 SEQUENCE 232 AA; 25254 MW; 65B28F702D9C8BE CRC64;

Query Match 100.0%; Score 81; DB 1; Length 232;  
 Best Local Similarity 100.0%; Pred. No. 4.2e-06;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 QRETPGAEAKPW 14  
 ||||||||||||  
 177 QRETPGAEAKPW 190

UNT 2  
 A.DELLE  
 TNFA\_DELLE STANDARD; PRT; 233 AA.  
 OSMMRI:  
 15-JUN-2002 (Rel. 41, Created)  
 15-JUN-2002 (Rel. 41, Last sequence update)  
 15-JUN-2002 (Rel. 41, Last annotation update)  
 Tumor necrosis factor precursor (TNF-alpha) (tumor necrosis factor ligand superfamily member 2) (cachectin).  
 TNF OR TNFSF2 OR TNFA.  
 Delphinapterus leucas (Beluga whale).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Cetacea; Odontoceti;  
 OC Monodonta; Delphinapterus.  
 OC NCBI\_TaxID=9749;  
 RX [1]  
 RX SEQUENCE FROM N.A.  
 RX PubMed=11768130.  
 RA Denis F., Archambault D.;  
 RT "Molecular cloning and characterization of beluga whale  
 (Delphinapterus leucas) interleukin-1beta and tumor necrosis  
 factor-alpha."  
 RL Can. J. Vet. Res. 65:233-240(2001).  
 CC -1- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and  
 TNFRSF1B/TNFR2. It is mainly secreted by macrophages and can  
 induce cell death of certain tumor cell lines. It is potent  
 pyrogen causing fever by direct action or by stimulation of  
 interleukin 1 secretion and is implicated in the induction of  
 cachexia, under certain conditions it can stimulate cell  
 proliferation and induce cell differentiation (By similarity).  
 CC -1- SUBUNIT: Homotrimer (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an  
 extracellular soluble form (By similarity).  
 CC -1- PTM: The soluble form derives from the membrane form by  
 proteolytic processing (By similarity).  
 CC -1- PTM: The membrane form, but not the soluble form, is  
 phosphorylated on serine residues. Dephosphorylation of the  
 membrane form occurs by binding to soluble TNFRSF1A/TNFR1 (By  
 similarity).  
 CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

EMBL: AF320323; AAL56946.1; -  
 InterPro: IPR003636; TNF\_abc.  
 InterPro: IPR000478; TNF\_family.  
 Pfam: PF00229; TNF\_1.  
 PRINTS: PR01234; TNFCROSISCT.  
 ProDom: PD002012; TNF\_abc; 1.  
 SMART: SM00207; TNF\_1.  
 PROSITE: PS00251; TNF\_1; 1.  
 PROSITE: PS50049; TNF\_2; 1.  
 DR Cytokine; Cytotoxin; Transmembrane; Glycoprotein; Phosphorylation;  
 DR Signal-anchor.  
 CHAIN 1 233 TUMOR NECROSIS FACTOR, MEMBRANE FORM.  
 DOMAIN 78 233 CYTOPLASMIC (POTENTIAL).  
 TRANSMEM 36 56 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN) (POTENTIAL).  
 DOMAIN 57 233 EXTRACELLULAR (POTENTIAL).  
 SITE 77 78 CLEAVAGE (BY ADAM17) (BY SIMILARITY).  
 MOD\_RES 2 2 PHOSPHORYLATION (BY CK1) (BY SIMILARITY).  
 FT DISULFID 145 177 BY SIMILARITY.  
 FT CARBOHYD 95 95 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 233 AA; 25420 MW; 2DE37DCB2BC9E961 CRC64;

Query Match 100.0%; Score 81; DB 1; Length 233;  
 Best Local Similarity 100.0%; Pred. No. 4.2e-06;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 QRETPGAEAKPW 14  
 ||||||||||||  
 DB 178 QRETPGAEAKPW 191

RESULT 3  
 TNFA\_FEICA  
 ID TNFA\_FEICA STANDARD; PRT; 233 AA.

AC P19101;  
 DT 01-NOV-1990 (Rel. 16, Created)  
 DT 01-NOV-1990 (Rel. 16, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor  
 ligand superfamily member 2) (Cachectin).  
 GN TNF OR TNFSF2 OR TNFA.  
 OS Felis silvestris catus (Cat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 NC Mammalia; Eutheria; Carnivora; Pissipedia; Felidae; Felis.  
 NCBI\_TaxID=9685;  
 RN  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-Blood;  
 RX MEDLINE=91016860; PubMed=2216740;  
 RA McGraw R.A., Coffee B.W., Otto C.M., Drews R.T., Rawlings C.A.;  
 RT "Gene sequence of feline tumor necrosis factor alpha.";  
 RN Nucleic Acids Res. 18:5563-5563(1990).  
 [2]  
 RC SEQUENCE FROM N.A.  
 RC TISSUE-Bone marrow;  
 RA Daniel S.L., Brenner C.A., Legendre A.M., Solomon A., Rouse B.T.;  
 RL Submitted (XXX-1993) to the EMBL/GenBank/DBJ databases.  
 CC  
 CC -1- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and  
 TNFRSF1B/TNFR. It is mainly secreted by macrophages and can  
 induce cell death of certain tumor cell lines. It is potent  
 pyrogen causing fever by direct action or by stimulation of  
 interleukin 1 secretion and is implicated in the induction of  
 cachexia. Under certain conditions it can stimulate cell  
 proliferation and induce cell differentiation.  
 CC  
 CC -1- SUBUNIT: Homotrimer (By similarity).  
 CC  
 CC -1- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an  
 extracellular soluble form (By similarity).  
 CC  
 CC -1- PTM: The soluble form derives from the membrane form by  
 proteolytic processing (By similarity).  
 CC  
 CC -1- PTM: The membrane form, but not the soluble form, is  
 phosphorylated on serine residues. Dephosphorylation of the  
 membrane form occurs by binding to soluble TNFRSF1A/TNFR1 (By  
 similarity).  
 CC  
 CC -1- DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF DISEASES, INCLUDING  
 CANCER AND INFECTION, AND IS CHARACTERIZED BY GENERAL ILL HEALTH  
 AND MALNUTRITION.  
 CC  
 CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.  
 CC  
 CC -----  
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 or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
 CC -----  
 DR EMBL; X54000; AAA37948.1; -;  
 DR EMBL; M92061; AAA30818.1; -;  
 DR PIR; S11688; S11688.  
 DR HSSP: P01375; 4TSV.  
 DR InterPro; IPR003636; TNF\_abc.  
 DR InterPro; IPR00478; TNF\_Family.  
 DR Pfam; PF00229; TNF; 1.  
 DR PRINTS; PR0134; TNECROSISFCT.  
 DR PRODOM; PD002012; TNEC\_abc; 1.  
 DR SMART; SM00207; TNF; 1.  
 DR PROSITE; PS00251; TNF\_1; 1.  
 DR PROSITE; PS50049; TNF\_2; 1.  
 CC Cytokine; Cytotoxin; Transmembrane; Phosphorylation; Signal-anchor.  
 FT CHAIN 1 233 TUMOR NECROSIS FACTOR, MEMBRANE FORM.  
 FT CHAIN 77 233 TUMOR NECROSIS FACTOR, SOLUBLE FORM.  
 FT DOMAIN 1 35 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 36 56 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)  
 FT (POTENTIAL).  
 FT EXTRACELLULAR (POTENTIAL).  
 FT SITE 76 77 CLEAVAGE (BY ADAM17) (BY SIMILARITY).  
 FT MOD\_RES 2 2 PHOSPHORYLATION (BY CK1) (BY SIMILARITY).

FT DISULFID 145 177 BY SIMILARITY.  
 FT CONFLICT 28 G -> R (IN REF. 2).  
 FT CONFLICT 104 104 R -> W (IN REF. 2).  
 FT CONFLICT 151 151 L -> H (IN REF. 2).  
 FT CONFLICT 155 155 A -> T (IN REF. 2).  
 FT CONFLICT 210 210 T -> A (IN REF. 2).  
 SQ SEQUENCE 233 AA; 25322 MW; 434D239567862506 CRC64;  
 Query Match 100.0%; Score 81; DB 1; Length 233;  
 Best Local Similarity 100.0%; Pred. No. 4.2e-06;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 QRETEPGAEAKPMY 14  
 Db 178 QRETEPGAEAKPMY 191  
 |||||  
 ID TNFA\_HUMAN STANDARD; PRT; 233 AA.  
 AC P01375;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor  
 ligand superfamily member 2) (Cachectin).  
 GN TNF OR TNFSF2 OR TNFA.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 NC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 NCBI\_TaxID=9606;  
 RN  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=87217060; PubMed=3555974;  
 RA Nedospasov S.A., Shakhov A.N., Turetskaya R.L., Mett V.A.,  
 RA Azizov M.M., Georgiev G.P., Korobko V.G., Dodyrin V.N.,  
 RA Filippov S.A., Bystryov N.S., Boldyreva E.F., Chuvpilo S.A.,  
 RA Chumakov A.M., Shingarova L.N., Ovchinnikov Y.A.;  
 RT "Tandem arrangement of genes coding for tumor necrosis factor (TNF-  
 alpha) and lymphotoxin (TNF-beta) in the human genome.";  
 RL Cold Spring Harb. Symp. Quant. Biol. 51:611-624(1986).  
 RN  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=85086244; PubMed=6392892;  
 RA Penica D., Nedwin G.E., Hayflick J.S., Seeburg P.H., Derynck R.,  
 RA Palladino M.A., Kohr W.J., Aggarwal B.B., Goeddel D.V.;  
 RT "Human tumor necrosis factor: precursor structure, expression and  
 homology to lymphotoxin.";  
 RL Nature 312:724-729(1984).  
 RN  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=85137898; PubMed=3883195;  
 RA Shirai T., Yamaguchi H., Ito H., Todd C.W., Wallace R.B.,  
 RT "Cloning and expression in Escherichia coli of the gene for human  
 tumour necrosis factor.";  
 RL Nature 313:803-806(1985).  
 RN  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=86016093; PubMed=2995927;  
 RA Nedwin G.E., Naylor S.L., Sakaguchi A.Y., Smith D.H.,  
 RA Jarrett-Nedwin J., Penica D., Goeddel D.V., Gray P.W.;  
 RT "Human lymphotoxin and tumor necrosis factor genes: structure,  
 homology and chromosomal localization.";  
 RL Nucleic Acids Res. 13:6361-6373(1985).  
 RN  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=85142190; PubMed=3856324;  
 RA Wang A.M., Cressey A.A., Laddner M.B., Lin L.S., Strickler J.,  
 RA van Arsdell J.N., Yamamoto R., Mark D.F.;  
 RT "Molecular cloning of the complementary DNA for human tumor necrosis  
 factor.";  
 RL Science 228:149-154(1985).  
 [6]

SEQUENCE FROM N.A.  
MEDLINE-86030296; PubMed-3932069;  
Marmenout A., Franssen L., Tavernier J., van der Heyden J., Tizard R.,  
Kawashima E., Shaw A., Johnson M.J., Semon D., Mueller R.,  
Ruysschaert M.R., van Vliet A., Fiers W.;  
"Molecular cloning and expression of human tumor necrosis factor and  
comparison with mouse tumor necrosis factor.";  
Eur. J. Biochem. 152:515-522(1985).  
(7)  
SEQUENCE FROM N.A.  
MEDLINE-93272029; PubMed-8499947;  
Iris F.J.M., Bougueleret L., Prieur S., Caterina D., Primas G.,  
Perrot V., Jurka J., Rodriguez-Tome P., Claverie J.-M., Dussset J.,  
Cohen D.;  
"Denise Aliu clustering and a potential new member of the NF kappa B  
family within a 90 kilobase HLA class III segment.";  
Nat. Genet. 3:137-145(1993).  
(8)  
SEQUENCE FROM N.A.  
Rowen L., Madan A., Qin S., Shaffer T., James R., Ratcliffe A.,  
Abdasi N., Dickhoff R., Loretz C., Madan A., Dors M., Young J.,  
Lasky S., Hood L.;  
"Sequence of the human major histocompatibility complex class III  
region.";  
Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.  
(9)  
SEQUENCE FROM N.A.  
Shima S., Tamiya G., Oka A., Inoko H.;  
"Homo sapiens 2,229,817bp genomic DNA of 6p21.3 HLA class I region.";  
Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.  
(10)  
SEQUENCE FROM N.A.  
Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poel C.L., Yi Q.,  
Nickerson D.A.;  
Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.  
(11)  
SEQUENCE FROM N.A.  
Tissot-Blood;  
Strausberg R.;  
Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.  
(12)  
PHOSPHORYLATION (MEMBRANE FORM).  
PubMed-8597870;  
Pocsik E., Duda E., Wallach D.;  
"Phosphorylation of the 26 kDa TNF precursor in monocytic cells and in  
transfected HeLa cells.";  
J. Inflamm. 45:152-160(1995).  
(13)  
PHOSPHORYLATION BY CK1, AND DEPHOSPHORYLATION.  
PubMed-10205166;  
Watts A.D., Hunt N.H., Manigasekara Y., Bloomfield G., Wallach D.,  
Roufogalis B.D., Chaudhuri G.;  
"A casein kinase I motif present in the cytoplasmic domain of members  
of the tumor necrosis factor ligand family is implicated in 'reverse  
signaling'.";  
EMBO J. 18:2119-2126(1999).  
(14)  
MUTAGENESIS.  
MEDLINE-91184128; PubMed-2009860;  
Ostade X.V., Tavernier J., Prange T., Fiers W.;  
"Localization of the active site of human tumour necrosis factor  
(TNF) by mutational analysis.";  
EMBO J. 10:827-836(1991).  
(15)  
MYRISTOYLATION.  
MEDLINE-93018820; PubMed-1402651;  
Stevenson F.T., Bursten S.L., Locksley R.M., Lovett D.H.;  
"Myristic acylation of the tumor necrosis factor alpha precursor on  
specific lysine residues.";  
J. Exp. Med. 176:1053-1062(1992).  
(16)  
CLEAVAGE BY ADAM17.  
MEDLINE-97186575; PubMed-9034191;

Query Match 100.0%; Score 81; DB 1; Length 233;  
 Best Local Similarity 100.0%; Pred. No. 4.2e-06;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ORETEGAACKPMY 14  
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 DB 178 ORETEGAACKPMY 191

## RESULT 5

TNFA\_MACFA STANDARD; PRT; 233 AA.  
 AC P79337;  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor  
 DE ligand superfamily member 2) (Cachectin).  
 GN TNF OR TNFSF2 OR TNFA.  
 OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
 OC Cercopithecinae; Macaca.  
 NCBI\_TaxID=9541;  
 RX [1]  
 RN SEQUENCE FROM N.A.  
 RC TISSUE=Lymphocytes;  
 RL Tatum M.;  
 Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and  
 CC TNFRSF1B/TNFR. It is mainly secreted by macrophages and can  
 CC induce cell death of certain tumor cell lines. It is potent  
 CC pyrogen causing fever by direct action or by stimulation of  
 CC interleukin 1 secretion and is implicated in the induction of  
 CC cachexia, under certain conditions it can stimulate cell  
 CC proliferation and induce cell differentiation.  
 CC -1- SUBUNIT: Homotrimer (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an  
 CC extracellular soluble form (By similarity).  
 CC -1- PTM: The soluble form derives from the membrane form by  
 CC proteolytic processing (By similarity).  
 CC -1- PTM: The membrane form, but not the soluble form, is  
 CC phosphorylated on serine residues. Dephosphorylation of the  
 CC membrane form occurs by binding to soluble TNFRSF1A/TNFR1 (By  
 CC similarity).  
 CC -1- DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF DISEASES, INCLUDING  
 CC CANCER AND INFECTION, AND IS CHARACTERIZED BY GENERAL ILL HEALTH  
 CC AND MALNUTRITION.  
 CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL: AB000513; BAA19131.1; -  
 DR HSSP: P01375; 4TSV.  
 DR InterPro: IPR003636; TNF\_abc.  
 DR InterPro: IPR000478; TNF\_family.  
 DR Pfam: PF00229; TNF; 1.  
 DR PRINTS: PR01234; TNECROSISFCT.  
 DR PRODOM: PD002012; TNF\_abc; 1.  
 DR SMART: SM00207; TNF; 1.  
 DR PROSITE: PS00251; TNF\_1; 1.  
 DR PROSITE: PS50049; TNF\_2; 1.  
 KM Cytokine; Cytotoxin; Transmembrane; Phosphorylation; Signal-anchor.  
 FT CHAIN 1 233 TUMOR NECROSIS FACTOR, MEMBRANE FORM.  
 FT CHAIN 77 233 TUMOR NECROSIS FACTOR, SOLUBLE FORM.  
 FT DOMAIN 1 35 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 36 56 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)  
 FT FT  
 FT DOMAIN 57 233 (POTENTIAL).  
 FT SITE 76 77 EXTRACELLULAR (POTENTIAL).  
 FT MOD\_RES 2 2 CLEAVAGE (BY ADAM17) (BY SIMILARITY).  
 FT DISULFID 145 177 PHOSPHORYLATION (BY CK1) (BY SIMILARITY).  
 SO SEQUENCE 233 AA; 25558 MW; 6ABF2C3AB132C217 CRC64;

Query Match 100.0%; Score 81; DB 1; Length 233;  
 Best Local Similarity 100.0%; Pred. No. 4.2e-06;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ORETEGAACKPMY 14  
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 DB 178 ORETEGAACKPMY 191

## RESULT 6

TNFA\_MACMU STANDARD; PRT; 233 AA.  
 AC P48094;  
 DT 01-FEB-1996 (Rel. 33, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor  
 DE ligand superfamily member 2) (Cachectin).  
 GN TNF OR TNFSF2 OR TNFA.  
 OS Macaca mulatta (Rhesus macaque).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
 OC Cercopithecinae; Macaca.  
 NCBI\_TaxID=9544;  
 RX [1]  
 RN SEQUENCE FROM N.A.  
 RP MEDLINE=96003435; PubMed=7561102;  
 RX Villinger F.J., Brar S.S., Mayne A.E., Chikala N., Ansari A.A.;  
 RA "Comparative sequence analysis of cytokine genes from human and  
 RA nonhuman primates."  
 RT J. Immunol. 155:3946-3954(1995).  
 RL -1- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and  
 CC TNFRSF1B/TNFR. It is mainly secreted by macrophages and can  
 CC induce cell death of certain tumor cell lines. It is potent  
 CC pyrogen causing fever by direct action or by stimulation of  
 CC interleukin 1 secretion and is implicated in the induction of  
 CC cachexia, under certain conditions it can stimulate cell  
 CC proliferation and induce cell differentiation.  
 CC -1- SUBUNIT: Homotrimer (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an  
 CC extracellular soluble form (By similarity).  
 CC -1- PTM: The soluble form derives from the membrane form by  
 CC proteolytic processing (By similarity).  
 CC -1- PTM: The membrane form, but not the soluble form, is  
 CC phosphorylated on serine residues. Dephosphorylation of the  
 CC membrane form occurs by binding to soluble TNFRSF1A/TNFR1 (By  
 CC similarity).  
 CC -1- DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF DISEASES, INCLUDING  
 CC CANCER AND INFECTION, AND IS CHARACTERIZED BY GENERAL ILL HEALTH  
 CC AND MALNUTRITION.  
 CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL: U19850; AAA86712.1; -  
 DR HSSP: P01375; 4TSV.  
 DR InterPro: IPR003636; TNF\_abc.  
 DR InterPro: IPR000478; TNF\_family.  
 DR Pfam: PF00229; TNF; 1.

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PRINTS; PR01234; TNECROSISFCT.
Prodom; PD002012; TNF_abc; 1.
SMART; SM00207; TNF_1.
PROSITE; PS00251; TNF_1; 1.
PROSITE; PS50049; TNF_2; 1.
CYTOKINE; Cytokine; Transmembrane; Phosphorylation; Signal-anchor.
CHAIN 1 233
DOMAIN 77 233 TUMOR NECROSIS FACTOR, MEMBRANE FORM.
DOMAIN 1 35 TUMOR NECROSIS FACTOR, SOLUBLE FORM.
TRANSMEM 36 56 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
(POTENTIAL).
DOMAIN 57 233 EXTRACELLULAR (POTENTIAL).
SITE 76 77 CLEAVAGE (BY ADAM17) (BY SIMILARITY).
MOD_RES 2 2 PHOSPHORYLATION (BY CK1) (BY SIMILARITY).
DISULFID 145 177 BY SIMILARITY.
SEQUENCE 233 AA; 25630 MW; 96F6F5050595D59 CRC64;

Query Match 100.0%; Score 81; DB 1; Length 233;
Best Local Similarity 100.0%; Pred. No. 4.2e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 QRETPGAEAKPMY 14
|||||
178 QRETPGAEAKPMY 191

SOUT 7
7A_PAPHU STANDARD; PRT; 233 AA.
077510;
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor
ligand superfamily member 2) (Cachectin).
TNF OR TNFSF2 OR TNFA.
Papio hamadryas ursinus (Chacma baboon).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
Cercopithecidae; Papio.
NCBI_TaxID=36229;
[1]
SEQUENCE FROM N.A.
MEDLINE=98147379; PubMed=9488055;
Haudek S.B., Redl H., Schlag G., Giroir B.P.;
"Complementary DNA (cDNA) sequence of baboon tumor necrosis factor
alpha.";
Mol. Immunol. 34:1041-1042(1997).
-1- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and
TNFRSF1B/TNFR. It is mainly secreted by macrophages and can
induce cell death of certain tumor cell lines. It is potent
pyrogen causing fever by direct action or by stimulation of
interleukin 1 secretion and is implicated in the induction of
cachexia. Under certain conditions it can stimulate cell
proliferation and induce cell differentiation.
-1- SUBUNIT: Homotrimer (By similarity).
-1- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an
extracellular soluble form (By similarity).
-1- PTM: The soluble form derives from the membrane form by
proteolytic processing (By similarity).
-1- PTM: The membrane form, but not the soluble form, is
phosphorylated on serine residues. Dephosphorylation of the
membrane form occurs by binding to soluble TNFRSF1A/TNFR1 (By
similarity).
-1- DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF DISEASES, INCLUDING
CANCER AND INFECTION, AND IS CHARACTERIZED BY GENERAL ILL HEALTH
AND MALNUTRITION.
-1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
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CC
CC EMBL; AF019963; AAC31675.1; -.
CC DR HSSP; P01375; 4TSV.
CC DR InterPro; IPR003636; TNF_abc.
CC DR InterPro; IPR000478; TNF_family.
CC DR Pfam; PF00229; TNF_1.
CC PRINTS; PR01234; TNECROSISFCT.
CC Prodom; PD002012; TNF_abc; 1.
CC DR SMART; SM00207; TNF_1.
CC DR PROSITE; PS00251; TNF_1; 1.
CC DR PROSITE; PS50049; TNF_2; 1.
CC CYTOKINE; Cytokine; Transmembrane; Phosphorylation; Signal-anchor.
CC CHAIN 1 233
CC DOMAIN 77 233 TUMOR NECROSIS FACTOR, MEMBRANE FORM.
CC TRANSMEM 36 56 CYTOPLASMIC (POTENTIAL).
CC SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
CC (POTENTIAL).
CC DOMAIN 57 233 EXTRACELLULAR (POTENTIAL).
CC SITE 76 77 CLEAVAGE (BY ADAM17) (BY SIMILARITY).
CC MOD_RES 2 2 PHOSPHORYLATION (BY CK1) (BY SIMILARITY).
CC DISULFID 145 177 BY SIMILARITY.
CC SEQUENCE 233 AA; 25658 MW; B9403255058D4A03 CRC64;

Query Match 100.0%; Score 81; DB 1; Length 233;
Best Local Similarity 100.0%; Pred. No. 4.2e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRETPGAEAKPMY 14
|||||
DB 178 QRETPGAEAKPMY 191

RESULT 8
TNFA_PAPSP STANDARD; PRT; 233 AA.
AC P33620;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor
ligand superfamily member 2) (Cachectin).
GN TNF OR TNFSF2 OR TNFA.
OS Papio sp. (Baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecidae; Papio.
OX NCBI_TaxID=61183;
RN [1]
RP SEQUENCE FROM N.A.
RL Sanjanvala M., Edwards A.;
RA Submitted (SEP-1991) to the EMBL/Genbank/DDJ databases.
CC -1- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and
CC TNFRSF1B/TNFR. It is mainly secreted by macrophages and can
CC induce cell death of certain tumor cell lines. It is potent
CC pyrogen causing fever by direct action or by stimulation of
CC interleukin 1 secretion and is implicated in the induction of
CC cachexia. Under certain conditions it can stimulate cell
CC proliferation and induce cell differentiation.
CC -1- SUBUNIT: Homotrimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an
CC extracellular soluble form (By similarity).
CC -1- PTM: The soluble form derives from the membrane form by
CC proteolytic processing (By similarity).
CC -1- PTM: The membrane form, but not the soluble form, is
CC phosphorylated on serine residues. Dephosphorylation of the
CC membrane form occurs by binding to soluble TNFRSF1A/TNFR1 (By
CC similarity).
CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
CC -----
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL; X62141; CAA44068.1; -  
 CC PIR; S22052.  
 CC HSP; P01375; 1A8M.  
 CC InterPro: IPR003636; TNF\_abc.  
 CC InterPro: IPR000478; TNF\_family.  
 CC Pfam: PF00229; TNF; 1.  
 CC PRINTS: PR01234; TNCRSISFCT.  
 CC PRODOM: PD002012; TNF\_abc; 1.  
 CC SMART: SM00207; TNF; 1.  
 CC PROSITE: PS00251; TNF\_1; 1.  
 CC PROSITE: PS50049; TNF\_2; 1.  
 CC Cytokine; Cytotoxin; Transmembrane; Phosphorylation; Signal-anchor;  
 CC Myristate.  
 CC CHAIN 1 233 TUMOR NECROSIS FACTOR, MEMBRANE FORM.  
 CC FT 77 233 TUMOR NECROSIS FACTOR, SOLUBLE FORM.  
 CC DOMAIN 1 35 CYTOPLASMIC (POTENTIAL).  
 CC TRANSMEM 36 56 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)  
 CC (POTENTIAL).  
 CC DOMAIN 57 233 EXTRACELLULAR (POTENTIAL).  
 CC SITE 76 77 CLEAVAGE (BY ADAM17) (BY SIMILARITY).  
 CC MOD\_RES 2 2 PHOSPHORYLATION (BY CK1) (BY SIMILARITY).  
 CC FT 19 19 MYRISTATE (BY SIMILARITY).  
 CC FT 20 20 MYRISTATE (BY SIMILARITY).  
 CC FT LIPID 145 177 BY SIMILARITY.  
 CC FT DISULFID 233 AA; 25557 MW; 455360B48DC74173 CRC64;  
 CC SO SEQUENCE

Query Match 100.0%; Score 81; DB 1; Length 233;  
 Best Local Similarity 100.0%; Pred. No. 4.2e-06;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 QRETPGCAKAPWY 14  
 DB 178 QRETPGCAKAPWY 191

RESULT 9  
 TNFA\_TURTR STANDARD; PRT; 233 AA.  
 AC Q9BEAL;  
 DT 15-JUN-2002 (Rel. 41, Created)  
 DT 15-JUN-2002 (Rel. 41, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor  
 DE ligand superfamily member 2) (Cachectin).  
 GN TNF OR TNFSF2 OR TNFA.  
 OS Turistis truncatus (Atlantic bottle-nosed dolphin).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Cetacea; Odontoceti; Delphinidae;  
 OC Turistops.  
 CC Mammalia; Eutheria; Cetartiodactyla; Cetacea; Odontoceti; Delphinidae;  
 CC Turistops.  
 CC NCB1\_TaxID-9739;  
 CC [1]  
 CC SEQUENCE FROM N.A.  
 CC PubMed-11587733;  
 CC Shoji Y., Inoue Y., Sugisawa H., Ito T., Endo T., Sakai T.;  
 CC "Molecular cloning and functional characterization of bottlenose  
 CC RT dolphin (Tursiops truncatus) tumor necrosis factor alpha.";  
 CC Vet. Immunol. Immunopathol. 83:183-192(2001).  
 CC -1- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and  
 CC TNFRSF1B/TNFR2. It is mainly secreted by macrophages and can  
 CC induce cell death of certain tumor cell lines. It is potent  
 CC pyrogen causing fever by direct action or by stimulation of  
 CC interleukin 1 secretion and is implicated in the induction of  
 CC cachexia. Under certain conditions it can stimulate cell  
 CC proliferation and induce cell differentiation (By similarity).  
 CC -1- SUBUNIT: Homotrimer (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an

CC extracellular soluble form (By similarity).  
 CC -1- PTM: The soluble form derives from the membrane form by  
 CC proteolytic processing (By similarity).  
 CC -1- PTM: The membrane form, but not the soluble form, is  
 CC phosphorylated on serine residues. Dephosphorylation of the  
 CC membrane form occurs by binding to soluble TNFRSF1A/TNFR1 (By  
 CC similarity).  
 CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.  
 CC -----  
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 CC -----  
 CC EMBL; AB049358; BAB39855.1; -  
 CC HSP; P01375; 4TSV.  
 CC InterPro: IPR003636; TNF\_abc.  
 CC InterPro: IPR000478; TNF\_family.  
 CC Pfam: PF00229; TNF; 1.  
 CC PRINTS: PR01234; TNCRSISFCT.  
 CC PRODOM: PD002012; TNF\_abc; 1.  
 CC SMART: SM00207; TNF; 1.  
 CC PROSITE: PS00251; TNF\_1; 1.  
 CC PROSITE: PS50049; TNF\_2; 1.  
 CC Cytokine; Cytotoxin; Transmembrane; Glycoprotein; Phosphorylation;  
 CC Signal-anchor.  
 CC CHAIN 1 233 TUMOR NECROSIS FACTOR, MEMBRANE FORM.  
 CC FT 78 233 TUMOR NECROSIS FACTOR, SOLUBLE FORM.  
 CC DOMAIN 1 35 CYTOPLASMIC (POTENTIAL).  
 CC TRANSMEM 36 56 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)  
 CC (POTENTIAL).  
 CC DOMAIN 57 233 EXTRACELLULAR (POTENTIAL).  
 CC SITE 77 78 CLEAVAGE (BY ADAM17) (BY SIMILARITY).  
 CC MOD\_RES 2 2 PHOSPHORYLATION (BY CK1) (BY SIMILARITY).  
 CC FT DISULFID 145 177 BY SIMILARITY.  
 CC FT CARBOHYD 95 95 N-LINKED (GLCNAC...) (POTENTIAL).  
 CC SO SEQUENCE 233 AA; 25404 MW; 71CC39C69CC49D9 CRC64;  
 CC

Query Match 100.0%; Score 81; DB 1; Length 233;  
 Best Local Similarity 100.0%; Pred. No. 4.2e-06;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 QRETPGCAKAPWY 14  
 DB 178 QRETPGCAKAPWY 191

RESULT 10  
 TNFA\_CANFA STANDARD; PRT; 233 AA.  
 AC P51742; Q28339;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor  
 DE ligand superfamily member 2) (Cachectin).  
 GN TNF OR TNFSF2 OR TNFA.  
 OS Canis familiaris (Dog).  
 OC Eukaryota; Metazoa; Chordata; Cranialia; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
 CC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
 CC NCB1\_TaxID-9615;  
 CC [1]  
 CC SEQUENCE FROM N.A.  
 CC Fiers W., Beernaert M.;  
 CC Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.  
 CC [2]  
 CC SEQUENCE FROM N.A.  
 CC Zucker K., Lu P., Fuller L., Ashtana D., Esquenazi V., Miller J.;  
 CC "Cloning and expression of the cDNA for canine tumor necrosis  
 CC factor-alpha in E. coli.";



Lymphokine Res. 13:191-196(1994).

[3]

SEQUENCE OF 74-205 FROM N.A.

STRAIN-Beagle; TISSUE-Blood;

Gilmore W.H., Carter S.D., Bennett M., Barnes A., Kelly D.F.;

Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.

-1- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and

TNFRSF1B/TNFR2. It is mainly secreted by macrophages and can

induce cell death of certain tumor cell lines. It is potent

pyrogen causing fever by direct action or by stimulation of

interleukin 1 secretion and is implicated in the induction of

cachexia. Under certain conditions it can stimulate cell

proliferation and induce cell differentiation.

-1- SUBUNIT: Homotrimer (By similarity).

-1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN

EXTRACELLULAR SOLUBLE FORM (BY SIMILARITY).

-1- PTM: THE SOLUBLE FORM DERIVES FROM THE MEMBRANE FORM BY

PROTEOLYTIC PROCESSING (BY SIMILARITY).

-1- PTM: The membrane form, but not the soluble form, is

phosphorylated on serine residues. Dephosphorylation of the

membrane form occurs by binding to soluble TNFRSF1A/TNFR1 (by

similarity). CACHEXIA ACCOMPANIES A VARIETY OF DISEASES, INCLUDING

CANCER AND INFECTION, AND IS CHARACTERIZED BY GENERAL ILL HEALTH

AND MALNUTRITION.

-1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.

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EMBL; X94932; CAA64403.1; -

EMBL; S74068; AAB32391.1; -

EMBL; Z70046; CAA93908.1; -

HSSP; P01375; ATSV.

InterPro: IPR003636; TNF\_abc.

InterPro: IPR00478; TNF\_family.

Pfam: PF00229; TNF; 1.

PRINTS: PR0134; TNCRSISFCT.

PRODOM: PD002012; TNF\_abc; 1.

SMART: SM00207; TNF; 1.

PROSITE: PS00251; TNF\_1; 1.

PROSITE: PS50049; TNF\_2; 1.

Cytokine; Cytotoxin; Transmembrane; Phosphorylation; Signal-anchor.

CHAIN 1 233 TUMOR NECROSIS FACTOR, MEMBRANE FORM.

DOMAIN 77 233 TUMOR NECROSIS FACTOR, SOLUBLE FORM.

TRANSHEM 36 56 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)

(POTENTIAL).

EXTRACELLULAR (POTENTIAL).

CLEAVAGE (BY ADAMT) (BY SIMILARITY).

PHOSPHORYLATION (BY CK1) (BY SIMILARITY).

BY SIMILARITY.

OR -> PE (IN REF. 2).

G -> C (IN REF. 2).

A -> V (IN REF. 3).

A -> D (IN REF. 2).

G -> D (IN REF. 2).

IT -> DS (IN REF. 2).

SEQUENCE 233 AA; 23447 MW; 785888FBC8B23340 CRC64;

Query Match 95.1%; Score 77; DB 1; Length 233;

Best Local Similarity 92.9%; Pred. No. 1.9e-05;

Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 QRETPGAKAPMY 14

111111 111111

178 QRETPGAKAPMY 191

RESULT 11

TNFA\_CAPHI

ID

TNFA\_CAPHI

STANDARD;

PRT; 234 AA.

AC P13256; Q28320; Q9WY22;

DT 01-JAN-1990 (Rel. 13, Created)

DT 15-JUN-2002 (Rel. 41, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor

ligand superfamily member 2) (Cachectin).

GN TNF OR TNFSF2 OR TNFA.

OS Capra hircus (Goat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

OC Bovidae; Caprinae; Capra.

OX NCBI\_TaxID=9925;

RA [1]

SEQUENCE FROM N.A.

RA TISSUE-Spleenocyte;

RA Takakura H., Mori Y., Tatsumi M.;

RT "Molecular cloning of caprine TNF-alpha cDNA and its expression in

E.coli and insect cells."

RT Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.

RL [2]

SEQUENCE OF 41-234 FROM N.A.

RA Goldstein I.M., Henner D., Talhouk A.;

RA Submitted (MAR-1989) to the EMBL/GenBank/DBJ databases.

RL [3]

SEQUENCE OF 44-234 FROM N.A.

RA TISSUE-Ovarian follicle;

RA Wang B., Zhang Y.;

RT "Goat ovarian TNF alpha cDNA sequence."

RT Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.

RL [4]

SEQUENCE OF 75-234 FROM N.A.

RA TISSUE-Blood;

RA Rimstad E.;

RA Submitted (JAN-1994) to the EMBL/GenBank/DBJ databases.

CC -1- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and

induces cell death of certain tumor cell lines. It is potent

pyrogen causing fever by direct action or by stimulation of

interleukin 1 secretion and is implicated in the induction of

cachexia. Under certain conditions it can stimulate cell

proliferation and induce cell differentiation.

-1- SUBUNIT: Homotrimer (By similarity).

-1- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an

extracellular soluble form (By similarity).

-1- PTM: The soluble form derives from the membrane form by

proteolytic processing (By similarity).

-1- PTM: The membrane form, but not the soluble form, is

phosphorylated on serine residues. Dephosphorylation of the

membrane form occurs by binding to soluble TNFRSF1A/TNFR1 (by

similarity).

-1- DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF DISEASES, INCLUDING

CANCER AND INFECTION, AND IS CHARACTERIZED BY GENERAL ILL HEALTH

AND MALNUTRITION.

-1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.

-1- CAUTION: Ref.2 sequence differs from that shown due to a

frameshift in position 60.

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EMBL; D86587; BAA13130.1; -

DR EMBL; X14828; CAA32937.1; ALT\_FRAME.

DR EMBL; AF276985; AAF87741.1; -

DR EMBL; X77317; CAA54523.1; -

DR PIR: S06192; S06192.  
 DR HSSP: P01375; 4TSV.  
 DR InterPro: IPR003636; TNF\_abc.  
 DR InterPro: IPR000478; TNF\_family.  
 DR Pfam: PF00229; TNF; 1.  
 DR ProDom: PD002012; TNF\_abc; 1.  
 DR SMART: SM00207; TNF; 1.  
 DR PROSITE: PS00251; TNF\_1; 1.  
 DR PROSITE: PS50049; TNF\_2; 1.  
 DR Cytokine: Cytotoxin; Transmembrane; Phosphorylation; Signal-anchor.  
 FT CHAIN 1 234 TUMOR NECROSIS FACTOR, MEMBRANE FORM.  
 FT CHAIN 79 234 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 36 56 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)  
 FT DOMAIN 57 233 (POTENTIAL).  
 FT MOD\_RES 2 2 EXTRACELLULAR (POTENTIAL).  
 FT SITE 78 79 PHOSPHORYLATION (BY CK1) (BY SIMILARITY).  
 FT DISULFID 146 178 CLEAVAGE (BY ADAM17) (BY SIMILARITY).  
 FT CARBOHYD 96 96 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CONFLICT 79 79 R -> S (IN REF. 4).  
 FT CONFLICT 119 119 E -> A (IN REF. 4).  
 FT CONFLICT 129 129 T -> N (IN REF. 4).  
 FT CONFLICT 155 155 H -> Q (IN REF. 4).  
 FT CONFLICT 164 164 Y -> D (IN REF. 4).  
 FT CONFLICT 184 184 E -> EG (IN REF. 4).  
 FT CONFLICT 185 185 MISSING (IN REF. 2).  
 FT CONFLICT 215 215 Q -> L (IN REF. 3 AND 4).  
 FT SEQUENCE 234 AA; 25519 MW; 9768E3BBAB041 CRC64;  
 Query Match 93.8%; Score 76; DB 1; Length 234;  
 Best Local Similarity 100.0%; Pred. No. 2.7e-05;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 REPTEGAERKPMY 14  
 Db 180 REPTEGAERKPMY 192  
 RESULT 12  
 TNFA\_CAVPO STANDARD; PRT; 234 AA.  
 AC P51435;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor  
 DE ligand superfamily member 2) (Cachectin).  
 GN TNF OR TNFSF2 OR TNFA.  
 OS Cavia porcellus (Guinea pig).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Hystriocognathi; Caviidae; Cavia.  
 OX NCBI\_TaxID=10141;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Hartley; TISSUE=Lung;  
 RA Yuan H.T.; Kelly F.J.; Bingle C.D.;  
 RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Dunkin-Hartley;  
 RX MEDLINE=97462215; PubMed=9316485;  
 RA White A.M.; Yoshimura T.; Smith A.W.; Westwick J.; Watson M.L.;  
 RT "Airway inflammation induced by recombinant guinea pig tumor necrosis  
 factor-alpha";  
 RL Am. J. Physiol. 273:1524-1530(1997).  
 CC -1- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and  
 CC TNFRSF1B/TNFR. It is mainly secreted by macrophages and can  
 CC induce cell death of certain tumor cell lines. It is potent  
 CC interleukin 1 secretion and is implicated in the induction of  
 CC cachexia, under certain conditions it can stimulate cell  
 CC proliferation and induce cell differentiation.

CC -1- SUBUNIT: Homotrimer (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an  
 CC extracellular soluble form (By similarity).  
 CC -1- PTM: The soluble form derives from the membrane form by  
 CC proteolytic processing (By similarity).  
 CC -1- PTM: The membrane form, but not the soluble form, is  
 CC phosphorylated on serine residues. Dephosphorylation of the  
 CC membrane form occurs by binding to soluble TNFRSF1A/TNFR1 (By  
 CC similarity).  
 CC -1- DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF DISEASES, INCLUDING  
 CC CANCER AND INFECTION, AND IS CHARACTERIZED BY GENERAL ILL HEALTH  
 CC AND MALNUTRITION.  
 CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.  
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 CC -----  
 CC EMBL: U39839; AB06492.1; -;  
 CC EMBL: U77036; AAB19210.1; -;  
 CC HSSP: P06804; 2TNF.  
 CC InterPro: IPR003636; TNF\_abc.  
 CC InterPro: IPR000478; TNF\_family.  
 CC Pfam: PF00229; TNF; 1.  
 CC PRINTS: PR01234; TNFECROSISFCT.  
 CC ProDom: PD002012; TNF\_abc; 1.  
 CC SMART: SM00207; TNF; 1.  
 CC PROSITE: PS00251; TNF\_1; 1.  
 CC PROSITE: PS50049; TNF\_2; 1.  
 CC Cytokine; Cytotoxin; Transmembrane; Phosphorylation; Signal-anchor.  
 FT CHAIN 1 234 TUMOR NECROSIS FACTOR, MEMBRANE FORM.  
 FT CHAIN 80 234 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 36 56 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)  
 FT TRANSMEM 36 56 (POTENTIAL).  
 FT DOMAIN 57 234 EXTRACELLULAR (POTENTIAL).  
 FT SITE 79 80 CLEAVAGE (BY ADAM17) (BY SIMILARITY).  
 FT MOD\_RES 2 2 PHOSPHORYLATION (BY CK1) (BY SIMILARITY).  
 FT DISULFID 147 178 BY SIMILARITY.  
 FT SEQUENCE 234 AA; 25793 MW; 7272C940393E7E9B CRC64;  
 Query Match 90.1%; Score 73; DB 1; Length 234;  
 Best Local Similarity 85.7%; Pred. No. 8.5e-05;  
 Matches 12; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 QREPTEGAERKPMY 14  
 Db 179 QREPTEGAERKPMY 192  
 RESULT 13  
 TNFA\_CEREL STANDARD; PRT; 229 AA.  
 AC P51745;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor  
 DE ligand superfamily member 2) (Cachectin) (Fragment).  
 GN TNF OR TNFSF2 OR TNFA.  
 OS Cervus elaphus (Red deer).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervidae;  
 OC Cervidae; Cervinae; Cervus.  
 OX NCBI\_TaxID=9860;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC lockhart E.A.;  
 RA Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.

- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and TNFRSF1B/TNFR. It is mainly secreted by macrophages and can induce cell death of certain tumor cell lines. It is potent pyrogen causing fever by direct action or by stimulation of interleukin 1 secretion and is implicated in the induction of cachexia, under certain conditions it can stimulate cell proliferation and induce cell differentiation.

- SUBUNIT: Homotrimer (By similarity).

- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN EXTRACELLULAR SOLUBLE FORM (BY SIMILARITY).

- PTM: THE SOLUBLE FORM DERIVES FROM THE MEMBRANE FORM BY PROTEOLYTIC PROCESSING (BY SIMILARITY).

- DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF DISEASES, INCLUDING CANCER AND INFECTION, AND IS CHARACTERIZED BY GENERAL ILL HEALTH AND MALNUTRITION.

- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.

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EMBL; U14683; AAA50759.1; -  
HSSP; P01375; 4TSV.  
InterPro: IPR0003636; TNF\_abc.  
InterPro: IPR000478; TNF\_family.  
Pfam; PF00229; TNF; 1.  
ProDom; PD002012; TNF\_abc; 1.  
SMART; SM00207; TNF; 1.  
PROSITE; PS00251; TNF\_1; 1.  
PROSITE; PS50049; TNF\_2; 1.  
Cytokine; Cytotoxin; Transmembrane; Signal-anchor.  
NON\_TER 1 1  
CHAIN 1 229  
DOMAIN 74 229  
DOMAIN 41 30  
TRANSMEM 31 51  
DOMAIN 52 229  
SITE 72 73  
SITE 141 173  
SEQUENCE 229 AA; 24987 MW; 16D5E57AA5A7DB35 CRC64;

Query Match 84.0%; Score 68; DB 1; Length 229;  
Best Local Similarity 92.3%; Pred. No. 0.00054;  
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

2 RETPGCAEAKPMY 14  
|||||  
175 RETPEMAEAKPMY 187

SOLT 14  
7A BOVIN  
TNFA BOVIN STANDARD: PRT: 233 AA.  
006599: 018779;  
01-JUN-1994 (Rel. 29, Created)  
01-JUN-1994 (Rel. 29, Last sequence update)  
15-JUN-2002 (Rel. 41, Last annotation update)  
Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor ligand superfamily member 2) (Cachectin).  
TNF OR TNFSF2 OR TNFA.  
Bos taurus (Bovine).  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.  
NCBI\_TaxID=9913;  
[1]  
SEQUENCE FROM N.A.  
MEDLINE=94083525; PubMed=8260599;

RA Cludts I., Cleuter Y., Kettmann R., Burny A., Droogmans L.;  
RT "Cloning and characterization of the tandemly arranged bovine  
RT lymphokine and tumor necrosis factor-alpha genes.";  
RL Cytokine 5:336-341(1993).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN-Boran, and N'Dama;  
RA Iraqi F.;  
RT "Bovine TNF-alpha gene.";  
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE OF 50-233 FROM N.A.  
RC TISSUE-Blood;  
RX MEDLINE=96006582; PubMed=7590981.  
RA Mertens B.E.L.C., Murtiki M., Gaidulis L.;  
RT "Cloning of two members of the TNF-superfamily in cattle: CD40 ligand  
RT and tumor necrosis factor alpha.";  
RL Immunogenetics 42:430-431(1995).  
CC -1- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and  
CC TNFRSF1B/TNFR. It is mainly secreted by macrophages and can  
CC induce cell death of certain tumor cell lines. It is potent  
CC pyrogen causing fever by direct action or by stimulation of  
CC interleukin 1 secretion and is implicated in the induction of  
CC cachexia, under certain conditions it can stimulate cell  
CC proliferation and induce cell differentiation.

CC -1- SUBUNIT: Homotrimer (By similarity).

CC -1- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an  
CC extracellular soluble form (By similarity).

CC -1- PTM: The soluble form derives from the membrane form by  
CC proteolytic processing (By similarity).

CC -1- PTM: The membrane form, but not the soluble form, is  
CC phosphorylated on serine residues. Dephosphorylation of the  
CC membrane form occurs by binding to soluble TNFRSF1A/TNFR1 (By  
CC similarity).

CC -1- DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF DISEASES, INCLUDING  
CC CANCER AND INFECTION, AND IS CHARACTERIZED BY GENERAL ILL HEALTH  
CC AND MALNUTRITION.

CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.

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EMBL; 214137; CAAT8511.1; -  
EMBL; AF011926; AAB84086.1; -  
EMBL; AF011927; AAB84087.1; -  
EMBL; 248808; CA88743.1; -  
PIR; S24642; S24642.  
DR HSSP; P01375; 4TSV.  
DR InterPro: IPR003636; TNF\_abc.  
DR InterPro: IPR000478; TNF\_family.  
DR Pfam: PF00229; TNF; 1.  
DR PRINTS; PR01234; TNENCRSISFCT.  
DR PRODOM; PD002012; TNF\_abc; 1.  
DR SMART; SM00207; TNF; 1.  
DR PROSITE; PS00251; TNF\_1; 1.  
DR PROSITE; PS50049; TNF\_2; 1.  
KW Cytokine; Cytotoxin; Transmembrane; Phosphorylation; Signal-anchor;  
KW Polymorphism.  
FT CHAIN 1 233  
FT DOMAIN 78 233  
FT DOMAIN 1 35  
FT TRANSMEM 36 56  
FT DOMAIN 57 233  
FT SITE 77 78  
FT MOD\_RES 2 2  
FT DISULFID 145 177  
FT VARIANT 48 48  
F -> C (IN STRAIN N'DAMA).

TUMOR NECROSIS FACTOR, MEMBRANE FORM.  
TUMOR NECROSIS FACTOR, SOLUBLE FORM.  
CYTOPLASMIC (POTENTIAL).  
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)  
(POTENTIAL).  
EXTRACELLULAR (POTENTIAL).  
CLEAVAGE (BY ADAM17) (BY SIMILARITY).  
PHOSPHORYLATION (BY CK1) (BY SIMILARITY).  
BY SIMILARITY.

FT CONFLICT 62 62 E -> EQ (IN REF. 3).  
 SO SEQUENCE 233 AA; 25439 MW; 8AF55C02A9763B0 CRC64;  
 Query Match 84.0%; Score 68; DB 1; Length 233;  
 Best Local Similarity 92.3%; Pred. No. 0.00055;  
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 RETPEGAEAKPMY 14  
 ||||| |||||  
 Db 179 RETPEGAEAKPMY 191

RESULT 15  
 ID TNFA\_SHEEP STANDARD; PRT; 234 AA.  
 AC P23383;  
 DT 01-NOV-1991 (Rel. 20, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor  
 ligand superfamily member 2) (cachectin).  
 GN TNF OR TNFSF2 OR TNFA.  
 OS Ovis aries (Sheep).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Caprinae; Ovis.  
 OX NCBI\_TaxID=9940;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Liver;  
 RX MEDLINE=91067496; PubMed=2251151;  
 RA Young A.J., Hay J.B., Chan J.Y.C.;  
 RT "Primary structure of ovine tumor necrosis factor alpha cDNA.";  
 RL Nucleic Acids Res. 18:6723-6723(1990).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Alveolar macrophage;  
 RX MEDLINE=92112044; PubMed=1765267;  
 RA Green I.R., Sargan D.R.;  
 RT "Sequence of the cDNA encoding ovine tumor necrosis factor-alpha:  
 problems with cloning by inverse PCR.";  
 RL Gene 109:203-210(1991).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=92155784; PubMed=1786996;  
 RA Andrews A.E., Nash A.D., Barcham G.J., Brandon M.R.;  
 RT "Molecular cloning, expression and characterization of ovine TNF  
 alpha.";  
 RL Immunol. Cell Biol. 69:273-283(1991).  
 CC -I- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and  
 TNFRSF1B/TNFR. It is mainly secreted by macrophages and can  
 induce cell death of certain tumor cell lines. It is potent  
 pyrogen causing fever by direct action or by stimulation of  
 interleukin 1 secretion and is implicated in the induction of  
 cachexia, under certain conditions it can stimulate cell  
 proliferation and induce cell differentiation.  
 CC -I- SUBUNIT: Homotrimer (By similarity).  
 CC -I- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an  
 extracellular soluble form (By similarity).  
 CC -I- PTM: The soluble form derives from the membrane form by  
 proteolytic processing (By similarity).  
 CC -I- PTM: The membrane form, but not the soluble form, is  
 phosphorylated on serine residues. Dephosphorylation of the  
 membrane form occurs by binding to soluble TNFRSF1A/TNFR1 (By  
 similarity).  
 CC -I- DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF DISEASES, INCLUDING  
 CANCER AND INFECTION, AND IS CHARACTERIZED BY GENERAL ILL HEALTH  
 AND MAINTENANCE.  
 CC -I- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.  
 CC -----  
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 CC -----  
 CC DR EMBL: X55966; CAA39437.1; -  
 CC DR EMBL: X55152; CAA38952.1; -  
 CC DR EMBL: X56756; CAA40076.1; -  
 CC DR EMBL: A19163; CAA01445.1; -  
 CC PIR: S13114; S13114.  
 CC PIR: S20661; S20661.  
 CC PIR: JH0529; JH0529.  
 CC HSSP: P01375; 4TSV.  
 CC DR InterPro: IPR000478; TNF\_family.  
 CC DR Pfam: PF00229; TNF\_1.  
 CC DR PRINTS: PR01234; TNFECROSISFCT.  
 CC DR PRODOM: PD002012; TNF\_abc; 1.  
 CC DR SMART: SM00207; TNF\_1.  
 CC DR PROSITE: PS00251; TNF\_1; 1.  
 CC DR PROSITE: PS00049; TNF\_2; 1.  
 CC KW Cytokine; Cytotoxin; Transmembrane; Glycoprotein; Phosphorylation;  
 KW Signal-anchor.  
 FT CHAIN 1 234 TUMOR NECROSIS FACTOR, MEMBRANE FORM.  
 FT SITE 78 234 TUMOR NECROSIS FACTOR, SOLUBLE FORM.  
 FT DOMAIN 1 35 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 36 56 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)  
 FT DOMAIN 57 234 EXTRACELLULAR (POTENTIAL).  
 FT SITE 77 78 CLEAVAGE (BY ADAM17) (BY SIMILARITY).  
 FT MOD\_RES 2 2 PHOSPHORYLATION (BY CK1) (BY SIMILARITY).  
 FT DISULFID 146 178 BY SIMILARITY.  
 FT CARBOHYD 96 96 N-LINKED (GLCNAC...) (POTENTIAL).  
 FT CONFLICT 63 63 MISSING (IN REF. 1).  
 SO SEQUENCE 234 AA; 25536 MW; 4BCF8CCAB7956B88 CRC64;

OY 2 RETPEGAEAKPMY 14  
 ||||| |||||  
 Db 180 RETPEGAEAKPMY 192

Search completed: April 4, 2003, 08:40:26  
 Job time : 7.64516 secs

GenCore version 5.1.4.p5.4578  
Copyright (c) 1993 - 2003 Compugen Ltd.

# OM protein - protein search, using sw model

Run on: April 4, 2003, 08:37:16 ; Search time 20.3226 seconds  
(without alignments)  
141.944 Million cell updates/sec

Title: US-09-779-703-1  
Perfect score: 81  
Sequence: 1 ORETEGAEAKPMY 14

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

## Database :

SPTREMBL\_21:\*  
1: sp\_bacteria:\*  
2: sp\_fungi:\*  
3: sp\_human:\*  
4: sp\_invertebrate:\*  
5: sp\_mammal:\*  
6: sp\_mhc:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_todent:\*  
12: sp\_virus:\*  
13: sp Vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_virus:\*  
16: sp\_bacteriap:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES.

Result No.	Score	Query Match	Length	DB ID	Description
1	81	100.0	66	4	Q9PIQ2
2	81	100.0	149	6	Q97543
3	81	100.0	217	6	Q9BEF4
4	81	100.0	232	4	Q9UUV3
5	78	96.3	216	6	Q9BEC4
6	76	93.8	157	4	Q43647
7	76	93.8	217	6	Q9BEG0
8	73	90.1	217	6	Q9BEG1
9	72	88.9	215	6	Q9BEC8
10	68	85.2	217	6	Q9BEC5
11	68	84.0	104	6	Q27978
12	65	80.2	156	11	Q912L4
13	65	80.2	217	11	Q9ERG6
14	65	80.2	235	11	Q9J126
15	63	77.8	138	6	Q9TNG7
16	63	77.8	149	6	Q97538

17	63	77.8	149	6	Q9TNG8	Q9TNG8 aotus nigri
18	63	77.8	216	11	Q70332	Q70332 mesocricetu
19	61	75.3	235	11	Q9J127	Q9J127 rattus norv
20	59	72.8	234	6	Q9TRJ3	Q9TRJ3 equus caball
21	55	67.9	216	6	Q9BEC9	Q9BEC9 ochotona pr
22	53	65.4	215	11	Q99ND1	Q99ND1 tamiasciuru
23	47	58.0	711	16	Q9RVE5	Q9RVE5 delinococcus
24	45	55.6	466	3	Q9PEV5	Q9PEV5 neurospora
25	44	54.3	77	13	Q8UM12	Q8UM12 xenopus lae
26	44	54.3	140	3	Q9Y8D2	Q9Y8D2 cochliobolu
27	44	54.3	299	2	Q93A65	Q93A65 uncultured
28	44	54.3	406	2	Q8VPN0	Q8VPN0 micrococcus
29	44	54.3	713	16	Q8U9Z5	Q8U9Z5 agrobacteri
30	44	54.3	1003	4	Q9P2F3	Q9P2F3 homo sapien
31	43.5	53.7	879	5	Q76978	Q76978 sycon rapha
32	43	53.1	157	16	Q8YH06	Q8YH06 bruceella me
33	43	53.1	674	13	Q9P783	Q9P783 xenopus lae
34	43	53.1	674	13	Q9P782	Q9P782 xenopus lae
35	43	53.1	902	4	Q9PR6	Q9PR6 homo sapien
36	43	53.1	1021	16	Q9KSQ8	Q9KSQ8 vibrio chol
37	43	53.1	1236	12	Q9J1K1	Q9J1K1 western equ
38	43	53.1	1677	11	Q70373	Q70373 mus musculu
39	42	51.9	187	17	Q9V0A1	Q9V0A1 pyrococcus
40	42	51.9	187	17	Q8UD06	Q8UD06 mus musculu
41	42	51.9	335	11	Q9JLM9	Q9JLM9 mus musculu
42	42	51.9	350	16	Q8Z375	Q8Z375 salmonella
43	42	51.9	400	17	Q8TXJ7	Q8TXJ7 methanopyru
44	42	51.9	800	11	Q63257	Q63257 rattus norv
45	42	51.9	801	11	Q9WTM8	Q9WTM8 rattus norv

## ALIGNMENTS

RESULT 1  
Q9PIQ2 ID Q9PIQ2 PRELIMINARY: PRT: 66 AA.  
AC Q9PIQ2;  
DT 01-OCR-2000 (TREMblrel. 15, Created)  
DT 01-OCR-2000 (TREMblrel. 15, Last sequence update)  
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)  
DE APCI protein (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=PROSTATE TUMOR;  
RA Shao C., Yan W., Zhu F., Yue W., Chai Y., Zhao Z., Wang C.;  
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF098751; AAF71992.1; -  
DR HSSP: P01375; STSW.  
DR InterPro: IPR003636; TNF\_abc.  
DR InterPro: IPR000478; TNF\_family.  
DR Pfam: PF00229; TNF\_1.  
DR PRINTS: PR01234; TNECROSISFCT.  
DR PRODOM: PD002012; TNF\_abc; 1.  
DR PROSITE: PS00495; TNF\_2; 1.  
FT NON\_TER 66  
SQ SEQUENCE 66 AA: 7300 MW: C58DC35377B6D368 CRC64;

Query Match 100.0%; Score 81; DB 4; Length 66;  
Best Local Similarity 100.0%; Pred. No. 8.5e-06;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ORETEGAEAKPMY 14  
DB 30 ORETEGAEAKPMY 43

RESULT 2  
Q97543

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097543      PRELIMINARY;      PRT;      149 AA.
097543;
01-MAY-1999 (TREMblrel. 10, Created)
01-MAY-1999 (TREMblrel. 10, Last sequence update)
01-OCT-2001 (TREMblrel. 18, Last annotation update)
Tumor necrosis factor alpha (Fragment).
TNF-ALPHA.
Aotus nancymae (Owl monkey).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.
NCBI_TaxID=37293;
[1]
SEQUENCE FROM N.A.
Echeverry S.J., Hernandez E., Moreno A., Patarroyo M.F., Murillo L.A.;
"Identification, cloning and sequencing of different interleukin genes
in 4 Aotus species."; to the EMBL/GenBank/DBJ databases.
Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
EMBL; AF014513; AAD01539.1; -.
HSSP; P01375; 4TSV.
InterPro: IPR003636; TNF_abc.
InterPro: IPR000478; TNF_family.
Pfam: PF00229; TNF; 1.
PRINTS; PR01234; TNECROSISFCT.
ProDom; PD002012; TNF_abc; 1.
SMART; SM00207; TNF; 1.
PROSITE; PS00251; TNF_1; 1.
PROSITE; PS50049; TNF_2; 1.
NON_TER      1
NON_TER      1
SEQUENCE      149 AA; 16466 MW; 3C2A6140778EFA8A CRC64;

Query Match      100.0%; Score 81; DB 6; Length 149;
Best Local Similarity 100.0%; Pred. No. 2e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 QRETEGAEAKPMY 14
|||||
95 QRETEGAEAKPMY 108

SULT 3
3EF4
Q9BEF4      PRELIMINARY;      PRT;      217 AA.
Q9BEF4;
01-JUN-2001 (TREMblrel. 17, Created)
01-JUN-2001 (TREMblrel. 17, Last sequence update)
01-DEC-2001 (TREMblrel. 19, Last annotation update)
Tumor necrosis factor (Fragment).
TNFA.
Cabassous unicinctus (Southern naked-tailed armadillo).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Edentata; Dasypodidae; Cabassous.
NCBI_TaxID=48852;
[1]
SEQUENCE FROM N.A.
van Dijk M.A.M., de Jong W.W.;
"Indels indicate that rodents are monophyletic and lagomorphs are
their sister group."; to the EMBL/GenBank/DBJ databases.
Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
EMBL; AJ286829; CAC28518.1; -.
HSSP; P01375; 4TSV.
InterPro: IPR003636; TNF_abc.
InterPro: IPR000478; TNF_family.
Pfam: PF00229; TNF; 1.
PRINTS; PR01234; TNECROSISFCT.
ProDom; PD002012; TNF_abc; 1.
SMART; SM00207; TNF; 1.
PROSITE; PS00251; TNF_1; 1.
PROSITE; PS50049; TNF_2; 1.
NON_TER      1
NON_TER      1
SEQUENCE      217 AA; 23742 MW; 83C591DD6883FD86 CRC64;

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Query Match      100.0%; Score 81; DB 6; Length 217;
Best Local Similarity 100.0%; Pred. No. 3e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 QRETEGAEAKPMY 14
|||||
Db      170 QRETEGAEAKPMY 183

RESULT 4
Q90IV3      PRELIMINARY;      PRT;      232 AA.
ID Q90IV3;
AC Q90IV3;
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE Tumor necrosis factor.
GN TNF.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OC NCBI_TaxID=9606;
OX [1]
RX SEQUENCE FROM N.A.
RX MEDLINE=93272029; Pubmed=8499947;
RA Iris F., Bougueret L., Prieur S., Caterina D., Primas G., Perrot V.,
RA Jurka J., Rodriguez-Tome P., Clavierie U., Cohen D., Dausset J.,
RA "Dense Alu clustering and a potential new member of the NF-kappa
RA family within a 90 kilobase HLA class III segment.";
RA Nat. Genet. 3:137-145(1993).
RN [2]
RX SEQUENCE FROM N.A.
RX MEDLINE=96215741; Pubmed=8629302;
RA Utans U., Quist W.C., McManus B.M., Wilson J.E., Arcaci R.J.,
RA Wallace A.F., Russell M.E.;
RA "Allograft inflammatory factor-1. A cytokine-responsive macrophage
RA molecule expressed in transplanted human hearts.";
RA Transplantation 61:1387-1392(1996).
RN [3]
RX SEQUENCE FROM N.A.
RX MEDLINE=96006565; Pubmed=7590964;
RA Holzinger I., de Baey A., Messer G., Kick G., Zwielerzina H.,
RA Weiss E.H.;
RA "Cloning and genomic characterization of LST1: a new gene in the human
RA TNF region.";
RA Immunogenetics 42:315-322(1995).
RN [4]
RX SEQUENCE FROM N.A.
RX MEDLINE=93208881; Pubmed=791655;
RA Browning J.L., Ngam-ek A., Lawton P., Demarinis J., Tizard R.,
RA Chow E.P., Hession C., O'Brien-Greco B., Foley S.F., Ware C.F.;
RA "Lymphotoxin-beta: A new member of the TNF family that forms a
RA heteromeric complex with lymphotoxin on the cell surface.";
RA Cell 72:847-856(1993).
RN [5]
RX SEQUENCE FROM N.A.
RX MEDLINE=91086846; Pubmed=1670638;
RA Nedwin G.E., Naylor S.L., Sakaguchi A.Y., Smith D., Jarrett-Nedwin J.,
RA Pennica D., Goeddel D.V., Gray P.W.;
RA "Human lymphotoxin and tumor necrosis factor genes: structure,
RA homology and chromosomal localization.";
RA Nucleic Acids Res. 13:6361-6373(1985).
RN [6]
RX SEQUENCE FROM N.A.
RX MEDLINE=91086846; Pubmed=1670638;
RA Messer G., Spengler U., Jung M.C., Honold G., Bloemer K., Pape G.R.,
RA Riethmuller G., Weiss E.H.;
RA "Polymorphic Structure of the Tumor Necrosis Factor (TNF) Locus: An
RA Ncol Polymorphism in the First Intron of the Human TNF-beta Gene
RA Correlates with A Variant Amino Acid in Position 26 and a Reduced
RA Level of TNF-beta Production.";
RA J. Exp. Med. 173:209-219(1991).
RN [7]

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RP SEQUENCE FROM N.A.
RA MEDLINE-91139175; PubMed-1671667;
RA Abraham L.J., Du D.C., Zahedi K., Dawkins R.L., Whitehead A.S.;
RT "Haplotypic polymorphisms of the TNFB gene.";
RL Immunogenetics 33:50-53(1991).
RN [8]
RN SEQUENCE FROM N.A.
RP MEDLINE-94362679; PubMed-8081366;
RA Albertella M.R., Campbell D.R.;
RT "Characterization of a novel gene in the human major
RT histocompatibility complex that encodes a potential new member of the
RT I kappa B family of proteins.";
RL Hum. Mol. Genet. 3:793-799(1994).
RN [9]
RN SEQUENCE FROM N.A.
RP MEDLINE-95324911; PubMed-7601445;
RA Peelman L., Chaddon P., Nunes M., Renard C., Geffroy C., Vaïman M.,
RA Van zeveren A., Coppieiers W., Van de Weghe A., Bouquet Y., Choy W.,
RA Strominger J., Spies T.;
RT "The BAT1 Gene in the MHC Encodes an Evolutionarily Conserved Putative
RT Nuclear RNA Helicase of the D-E-A-D Family.";
RL Genomics 26:210-218(1995).
RN [10]
RN SEQUENCE FROM N.A.
RP MEDLINE-20132445; PubMed-10668961;
RA Neville M.J., Campbell R.D.;
RT "Alternative splicing of the LST-1 gene located in the major
RT histocompatibility complex on human chromosome 6.";
RL DNA Seq. 8:155-160(1997).
RN [11]
RN SEQUENCE FROM N.A.
RP MEDLINE-98035883; PubMed-9367684;
RA de Baey A., Fellerhoff B., Mater S., Martinozzi S., Weidle U.,
RA Weiss E.H.;
RT "Complex expression pattern of the TNF region gene LST1 through
RT differential regulation, initiation, and alternative splicing.";
RL Genomics 45:591-600(1997).
RN [12]
RN SEQUENCE FROM N.A.
RP MEDLINE-98149985; PubMed-9480751;
RA Shima T., Tamia G., Oka A., Yamagata T., Yamagata N., Kikkawa E.,
RA Goto K., Mizuki N., Watanabe K., Fukuzumi Y., Taguchi S., Sugawara C.,
RA Ono A., Chen L., Yamazaki M., Tashiro H., Ando A., Ikemura T.,
RA Kimura M., Inoko H.;
RT "Nucleotide sequencing analysis of the 146-kilobase segment around the
RT Ikb1 and MICA genes at the centromeric end of the HLA class I
RT region.";
RL Genomics 47:372-382(1998).
RN [13]
RN SEQUENCE FROM N.A.
RP EMBL; Y14768; CA75070.1; -.
RA HSSP; P01375; 4TSV.
DR InterPro: IPR003636; TNF-abc.
DR InterPro: IPR004478; TNF-family.
DR Pfam: PF00229; TNF; 1.
DR PRINTS: PR01234; TNCSRISFCT.
DR ProDom: PD002012; TNF-abc; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS0049; TNF_2; 1.
SQ SEQUENCE 232 AA; 25446 MW; EAD71B9C6AE0D03 CRC64;

Query Match 100.0%; Score 81; DB 4; Length 232;
Best Local Similarity 100.0%; Pred. No. 3.3e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ORETEGAEAKPMY 14
DB 177 ORETEGAEAKPMY 190

RESULT 5
O9BEC4 PRELIMINARY; PRT; 216 AA.
AC O9BEC4;
AC O9BEC4;

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DE 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Tumor necrosis factor (Fragment).
GN TNFA.
OC Talpa europaea (European mole).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Insectivora; Talpidae; Talpa.
OX NCBI_TaxID=9375;
RN [1]
RP van Dijk M.A.M., de Jong W.W.;
RA "Indels indicate that rodents are monophyletic and lagomorphs are
RT their sister group.";
RL Submitted (Feb-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ286831; CAC28539.1; -.
DR HSSP; P01375; 1A8M.
DR InterPro; IPR003636; TNF_abc.
DR InterPro; IPR000478; TNF_family.
DR Pfam; PF00228; TNF; 1.
DR PRINTS; PR01234; TNECROSISFCT.
DR ProDom; PD002012; TNF_abc; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS50049; TNF_2; 1.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 216 AA; 23542 MW; FFFEEBDBBD27836 CRC64;

Query Match 96.3%; Score 78; DB 6; Length 216;
Best Local Similarity 92.9%; Pred. No. 9.2e-05;
Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ORETPGAEAKPMY 14
DB 169 ORETPGAEAKPMY 182
|||||
O43647 PRELIMINARY; PRT; 157 AA.
AC O43647;
DT 01-JUN-1998 (TREMBlrel. 06, Created)
DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Tumor necrosis factor alpha (Fragment).
GN TNFA.
OC Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Jang J.S., Kim B.E.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF043342; AAC03542.1; -.
DR HSSP; P01375; 1A8M.
DR InterPro; IPR003636; TNF_abc.
DR InterPro; IPR000478; TNF_family.
DR Pfam; PF00229; TNF; 1.
DR PRINTS; PR01234; TNECROSISFCT.
DR ProDom; PD002012; TNF_abc; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS50049; TNF_2; 1.
FT NON_TER 1
SQ SEQUENCE 157 AA; 17380 MW; D1344822267E9F20 CRC64;

Query Match 93.8%; Score 76; DB 4; Length 157;
Best Local Similarity 92.9%; Pred. No. 0.00014;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ORETPGAEAKPMY 14

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||||| |||||||  
102 QRETPGGAEPKPY 115

SUITE 7

BEGO Q9BEG0 PRELIMINARY: PRT: 217 AA.

Q9BEG0: 01-JUN-2001 (TREMblrel. 17, Created)  
01-JUN-2001 (TREMblrel. 17, Last sequence update)  
01-DEC-2001 (TREMblrel. 19, Last annotation update)  
Tumor necrosis factor (Fragment).  
TNFA.

Cyclopes didactylus (silky anteater).  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Edentata; Myrmecophagidae; Cyclopes.  
NCBI\_TaxID=84074;

[1]  
SEQUENCE FROM N.A.

van Dijk M.A.M., de Jong W.W.;  
"Indels indicate that rodents are monophyletic and lagomorphs are  
their sister group."  
Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.

EMBL: AJ286828; CAC28514.1; -  
HSSP: P01375; 188M.  
InterPro: IPR003636; TNF\_abc.  
InterPro: IPR000478; TNF\_family.  
Pfam: PF00229; TNF\_1.  
PRINTS: PR01234; TNECROSISFCT.  
PRODOM: PD002012; TNF\_abc; 1.  
SMART: SM00207; TNF\_1.  
PROSITE: PS00251; TNF\_1; 1.  
PROSITE: PS50049; TNF\_2; 1.  
NON\_TER 1  
NON\_TER 1  
SEQUENCE 217 AA; 23753 MW; F760E887F6C29EBB CRC64;

Query Match 93.8%; Score 76; DB 6; Length 217;  
Best Local Similarity 92.9%; Pred. No. 0.00019;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 QRETPGGAEPKPY 14  
||||| |||||||  
170 QRETPGGAEPKPY 183

SUITE 8

BEG1 Q9BEG1 PRELIMINARY: PRT: 217 AA.

Q9BEG1: 01-JUN-2001 (TREMblrel. 17, Created)  
01-JUN-2001 (TREMblrel. 17, Last sequence update)  
01-DEC-2001 (TREMblrel. 19, Last annotation update)  
Tumor necrosis factor (Fragment).  
TNFA.

Bradyus tridactylus (Pale-throated three-toed sloth).  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Edentata; Bradypodidae; Bradypus.  
NCBI\_TaxID=9354;

[1]  
SEQUENCE FROM N.A.

van Dijk M.A.M., de Jong W.W.;  
"Indels indicate that rodents are monophyletic and lagomorphs are  
their sister group."  
Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.

EMBL: AJ286827; CAC28513.1; -  
HSSP: P01375; 188M.  
InterPro: IPR003636; TNF\_abc.  
InterPro: IPR000478; TNF\_family.  
Pfam: PF00229; TNF\_1.  
PRINTS: PR01234; TNECROSISFCT.  
PRODOM: PD002012; TNF\_abc; 1.  
SMART: SM00207; TNF\_1.

DR PROSITE; PS00251; TNF\_1; 1.  
DR PROSITE; PS50049; TNF\_2; 1.  
FT NON\_TER 1  
FT NON\_TER 1  
SQ SEQUENCE 217 AA; 23655 MW; A7056710B6238074 CRC64;

Query Match 90.1%; Score 73; DB 6; Length 217;  
Best Local Similarity 85.7%; Pred. No. 0.00058;  
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QRETPGGAEPKPY 14  
||||| |||||||  
Db 170 QRETPGGAEPKPY 183

RESULT 9  
Q9BEE8 PRELIMINARY: PRT: 215 AA.

Q9BEE8: 01-JUN-2001 (TREMblrel. 17, Created)  
01-JUN-2001 (TREMblrel. 17, Last sequence update)  
01-DEC-2001 (TREMblrel. 19, Last annotation update)  
Tumor necrosis factor (Fragment).  
TNFA.  
Erinaceus europaeus (Western European hedgehog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Insectivora; Erinaceidae; Erinaceinae; Erinaceus.  
NCBI\_TaxID=9365;

[1]  
SEQUENCE FROM N.A.  
van Dijk M.A.M., de Jong W.W.;  
"Indels indicate that rodents are monophyletic and lagomorphs are  
their sister group."  
Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.

EMBL: AJ286830; CAC28522.1; -  
HSSP: P01375; 47SV.  
InterPro: IPR003636; TNF\_abc.  
InterPro: IPR000478; TNF\_family.  
Pfam: PF00229; TNF\_1.  
PRINTS: PR01234; TNECROSISFCT.  
PRODOM: PD002012; TNF\_abc; 1.  
SMART: SM00207; TNF\_1.  
DR PROSITE; PS00251; TNF\_1; 1.  
DR PROSITE; PS50049; TNF\_2; 1.  
FT NON\_TER 1  
FT NON\_TER 1  
SQ SEQUENCE 215 AA; 23696 MW; 3E337E7E65F074EA CRC64;

Query Match 88.9%; Score 72; DB 6; Length 215;  
Best Local Similarity 85.7%; Pred. No. 0.00083;  
Matches 12; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QRETPGGAEPKPY 14  
||||| |||||||  
Db 168 QRETPGGAEPKPY 181

RESULT 10  
Q9BEC5 PRELIMINARY: PRT: 217 AA.

Q9BEC5: 01-JUN-2001 (TREMblrel. 17, Created)  
01-JUN-2001 (TREMblrel. 17, Last sequence update)  
01-DEC-2001 (TREMblrel. 19, Last annotation update)  
Tumor necrosis factor (Fragment).  
TNFA.

Tenrec ecaudatus (tailless tenrec).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Insectivora; Tenrecidae; Tenrec.  
NCBI\_TaxID=94439;  
[1]  
SEQUENCE FROM N.A.  
van Dijk M.A.M., de Jong W.W.;



RT \*Indels indicate that rodents are monophyletic and lagomorphs are

RT their sister group. to the EMBL/GenBank/DBJ databases.

RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AJ286826; CAC28538.1; -

DR HSSP; P01375; 4TSV.

DR InterPro: IPR003636; TNF\_abc.

DR InterPro: IPR000478; TNF\_family.

DR Pfam: PF00229; TNF\_1.

DR PRINTS; PR01234; TNCRSISFCT.

DR PRODOM; PD002012; TNF\_abc; 1.

DR SMART; SM00207; TNF\_1.

DR PROSITE; PS00251; TNF\_1; 1.

DR PROSITE; PS50049; TNF\_2; 1.

FT NON\_TER 1 1

FT NON\_TER 1 1

FT NON\_TER 1 1

FT NON\_TER 1 1

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FT NON\_TER 1 1

DT 01-DEC-2001 (TREMBLrel. 19, Created)

DT 01-DEC-2001 (TREMBLrel. 19, last sequence update)

DT 01-MAR-2002 (TREMBLrel. 20, last annotation update)

DE Tumor necrosis factor alpha (Fragment).

OS Sigmodon hispidus (Hispid cotton rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;

OC Sigmodon.

OC NCBI\_TaxID=42415;

OX NCBI\_TaxID=42415;

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OX NCBI\_TaxID=42415;

DT 01-DEC-2001 (TREMBLrel. 19, Created)

DT 01-DEC-2001 (TREMBLrel. 19, last sequence update)

DT 01-MAR-2002 (TREMBLrel. 20, last annotation update)

DE Tumor necrosis factor alpha (Fragment).

OS Sigmodon hispidus (Hispid cotton rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;

OC Sigmodon.

OC NCBI\_TaxID=42415;

OX NCBI\_TaxID=42415;

OX NCBI\_TaxID=42415;

OX NCBI\_TaxID=42415;

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OX NCBI\_TaxID=42415;

OX NCBI\_TaxID=42415;

OX NCBI\_TaxID=42415;

OX NCBI\_TaxID=42415;

173 KETPEGSELKPMY 185

SUBJ 14

09J126

PRELIMINARY; PRT; 235 AA.

01-OCT-2000 (TREMBlrel. 15, Created)  
01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
TNF-alpha propeptide 3 (Fragment).  
Rattus norvegicus (Rat).  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
NCBI\_TaxID=10116;  
[1]

SEQUENCE FROM N.A.  
STRAIN=DARK AGOUTI;  
Seidel M.F., Junier M.-P., Vetter H.;  
"TNF-alpha polymorphism in rats with collagen-induced arthritis.",  
Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.  
EMBL: AF269160; AAF82568.1; -.  
HSP; P06804; 2TNF.  
InterPro: IPR003636; TNF\_abc.  
InterPro: IPR000478; TNF\_family.  
Pfam: PF00229; TNF; 1.  
PRINTS: PRO1234; TNECROSISRCT.  
PRODOM: PD002012; TNF\_abc; 1.  
SMART: SM00207; TNF; 1.  
PROSITE: PS00251; TNF\_1; 1.  
PROSITE: PS50049; TNF\_2; 1.  
NON\_TER 235  
SEQUENCE 235 AA: 25789 MW; C801B92D049C2F2E CRC64;

Query Match 80.2%; Score 65; DB 11; Length 235;  
Best Local Similarity 76.9%; Pred. No. 0.012;  
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

2 RETPEGAELKPMY 14

181 KOTPEGAELKPMY 193

SUBJ 15

09TGT7

PRELIMINARY; PRT; 138 AA.

01-MAY-2000 (TREMBlrel. 13, Created)  
01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
01-OCT-2001 (TREMBlrel. 18, Last annotation update)  
Tumor necrosis factor alpha (Fragment).  
TNF-ALPHA.  
Aotus lemurinus (Northern gray-necked night monkey).  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.  
NCBI\_TaxID=43147;  
[1]

SEQUENCE FROM N.A.  
Muriillo L.A., Hernandez E., Echeverry S.J., Mendez J.A.,  
Patarroyo M.E.;  
"Aotus lemurinus gene for TNF alpha.",  
Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.  
EMBL: AF097329; AAF21304.1; -.  
HSP; P01375; 4TSV.  
InterPro: IPR003636; TNF\_abc.  
InterPro: IPR000478; TNF\_family.  
Pfam: PF00229; TNF; 1.  
PRINTS: PRO1234; TNECROSISRCT.  
PRODOM: PD002012; TNF\_abc; 1.  
SMART: SM00207; TNF; 1.  
PROSITE: PS00251; TNF\_1; 1.  
PROSITE: PS50049; TNF\_2; 1.  
NON\_TER 1

SO SEQUENCE 138 AA: 15269 MW: 29275EE4F4CD5068 CRC64;

Query Match 77.8%; Score 63; DB 6; Length 138;  
Best Local Similarity 71.4%; Pred. No. 0.014;  
Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 ORETPEGAELKPMY 14  
Db 95 ORETPEGAELKPMY 108

Search completed: April 4, 2003, 08:42:04  
Job time : 22.3226 secs

GenCore version 5.1.4.p5\_4578  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 4, 2003, 08:37:56 ; Search time 9.03226 Seconds  
(Without alignments)  
45.606 Million cell updates/sec

Title: US-09-779-703-1

Perfect score: 81

Sequence: 1 QREPEGAAXPMY 14

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: Issued\_Patents\_AA:\*

2: /cgn2\_6/prodata/1/1aa/5A\_COMB.pep:\*

3: /cgn2\_6/prodata/1/1aa/5B\_COMB.pep:\*

4: /cgn2\_6/prodata/1/1aa/5A\_COMB.pep:\*

5: /cgn2\_6/prodata/1/1aa/5B\_COMB.pep:\*

6: /cgn2\_6/prodata/1/1aa/Backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	81	100.0	17	2	US-08-500-860A-25
2	81	100.0	147	1	US-07-668-517-1
3	81	100.0	148	1	US-07-668-517-2
4	81	100.0	148	1	US-07-668-517-15
5	81	100.0	149	1	US-07-668-517-3
6	81	100.0	149	1	US-07-668-517-16
7	81	100.0	150	1	US-07-668-517-4
8	81	100.0	150	1	US-07-668-517-5
9	81	100.0	150	1	US-07-668-517-6
10	81	100.0	150	1	US-07-668-517-8
11	81	100.0	150	1	US-07-668-517-9
12	81	100.0	150	1	US-07-668-517-10
13	81	100.0	150	1	US-07-668-517-11
14	81	100.0	150	1	US-07-668-517-12
15	81	100.0	150	1	US-07-668-517-13
16	81	100.0	150	1	US-07-668-517-14
17	81	100.0	150	1	US-07-668-517-17
18	81	100.0	150	1	US-07-668-517-17
19	81	100.0	150	1	US-07-668-517-29
20	81	100.0	150	1	US-07-668-517-31
21	81	100.0	150	1	US-07-668-517-35
22	81	100.0	150	1	US-07-668-517-37
23	81	100.0	150	1	US-07-994-469A-6
24	81	100.0	150	1	US-07-994-469A-7
25	81	100.0	150	1	US-07-994-469A-8
26	81	100.0	150	4	US-09-286-529-25
27	81	100.0	151	1	US-07-668-517-7

28	81	100.0	151	1	US-07-668-517-18	Sequence 18, Appl
29	81	100.0	151	1	US-07-668-517-19	Sequence 19, Appl
30	81	100.0	151	1	US-07-668-517-20	Sequence 20, Appl
31	81	100.0	151	1	US-07-668-517-22	Sequence 22, Appl
32	81	100.0	151	1	US-07-668-517-23	Sequence 23, Appl
33	81	100.0	151	1	US-07-668-517-24	Sequence 24, Appl
34	81	100.0	151	1	US-07-668-517-25	Sequence 25, Appl
35	81	100.0	151	1	US-07-668-517-26	Sequence 26, Appl
36	81	100.0	151	1	US-07-668-517-27	Sequence 27, Appl
37	81	100.0	151	1	US-07-668-517-28	Sequence 28, Appl
38	81	100.0	151	1	US-07-668-517-30	Sequence 30, Appl
39	81	100.0	151	1	US-07-668-517-32	Sequence 32, Appl
40	81	100.0	151	1	US-07-668-517-36	Sequence 36, Appl
41	81	100.0	151	1	US-07-668-517-38	Sequence 38, Appl
42	81	100.0	152	1	US-07-763-512-1	Sequence 21, Appl
43	81	100.0	155	1	US-07-994-469A-1	Sequence 1, Appl
44	81	100.0	155	1	US-07-994-469A-3	Sequence 3, Appl
45	81	100.0	155	1	US-07-994-469A-3	

#### ALIGNMENTS

RESULT 1  
US-08-500-860A-25  
Sequence 25, Application US/08500860A  
Patent No. 5891679  
GENERAL INFORMATION:  
APPLICANT: LUCAS, RUDOLPH  
APPLICANT: DE BAETSELIER, PATRICK  
APPLICANT: FRANKEN, LUCIE  
APPLICANT: SABON, ERWIN  
TITLE OF INVENTION: TNF-MOTIFINS, A PROCESS FOR PREPARING THEM AND  
TITLE OF INVENTION: THEIR USE AS ACTIVE SUBSTANCES IN PHARMACEUTICAL COMPOSITIO  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: NIXON & VANDERHAYE P.C.  
STREET: 1100 NORTH GLEBE ROAD  
CITY: ARLINGTON  
STATE: VIRGINIA  
COUNTRY: U.S.A.  
ZIP: 22201-4714  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/500, 860A  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: BYRNE, THOMAS E.  
REGISTRATION NUMBER: 32,205  
REFERENCE/DOCKET NUMBER: 1487-8  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703)816-4000  
TELEFAX: (703)816-4100  
TELEX: 200797 NIXN UR  
INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Binding-site  
LOCATION: 1  
OTHER INFORMATION: /note= "Biotin-Gly-Gly is coupled  
to the N-terminus of the peptide"  
US-08-500-860A-25

Query Match 100.0%; Score 81; DB 2; Length 17;  
Best Local Similarity 100.0%; Pred. No. 2.2e-07;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRETEGAEAKPMY 14  
DB 3 QRETEGAEAKPMY 16

## RESULT 2

US-07-668-517-1  
; Sequence 1, Application US/07668517  
; Patent No. 5262309  
; GENERAL INFORMATION:  
; APPLICANT: Satoshi NAKAMURA et al.  
; TITLE OF INVENTION: No. 5262309el Physiologically Active  
; TITLE OF INVENTION: Polypeptide, Recombinant Plasmid, Recombinant Microorganism  
; TITLE OF INVENTION: Cell, Pharmaceutical Composition and Method of Recovering  
; NUMBER OF SEQUENCES: 50  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Wenderoth, Lind & Ponack  
; STREET: 805 Fifteenth Street, N.W., #700  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 5.25 inch, 500 KB  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: DisplayWrite  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/668.517  
; FILING DATE: 19910322  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Matthew Jacob  
; REGISTRATION NUMBER: 25,154  
; REFERENCE/DOCKET NUMBER:  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-371-8850  
; TELEFAX: 202-371-8856  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 147 amino acids  
; TYPE: AMINO ACID  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; FEATURE:  
; NAME/KEY:  
; LOCATION:  
; IDENTIFICATION METHOD:  
; OTHER INFORMATION:  
US-07-668-517-1  
Query Match 100.0%; Score 81; DB 1; Length 147;  
Best Local Similarity 100.0%; Pred. No. 2.5e-06;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRETEGAEAKPMY 14  
DB 92 QRETEGAEAKPMY 105

## RESULT 3

US-07-668-517-2  
; Sequence 2, Application US/07668517  
; Patent No. 5262309  
; GENERAL INFORMATION:

; APPLICANT: Satoshi NAKAMURA et al.  
; TITLE OF INVENTION: No. 5262309el Physiologically Active  
; TITLE OF INVENTION: Polypeptide, Recombinant Plasmid, Recombinant Microorganism  
; TITLE OF INVENTION: Cell, Pharmaceutical Composition and Method of Recovering  
; NUMBER OF SEQUENCES: 50  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Wenderoth, Lind & Ponack  
; STREET: 805 Fifteenth Street, N.W., #700  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 5.25 inch, 500 KB  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: DisplayWrite  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/668.517  
; FILING DATE: 19910322  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Matthew Jacob  
; REGISTRATION NUMBER: 25,154  
; REFERENCE/DOCKET NUMBER:  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-371-8850  
; TELEFAX: 202-371-8856  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 148 amino acids  
; TYPE: AMINO ACID  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; FEATURE:  
; NAME/KEY:  
; LOCATION:  
; IDENTIFICATION METHOD:  
; OTHER INFORMATION:  
US-07-668-517-2

Query Match 100.0%; Score 81; DB 1; Length 148;  
Best Local Similarity 100.0%; Pred. No. 2.5e-06;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRETEGAEAKPMY 14  
DB 93 QRETEGAEAKPMY 106

## RESULT 4

US-07-668-517-15  
; Sequence 15, Application US/07668517  
; Patent No. 5262309  
; GENERAL INFORMATION:  
; APPLICANT: Satoshi NAKAMURA et al.  
; TITLE OF INVENTION: No. 5262309el Physiologically Active  
; TITLE OF INVENTION: Polypeptide, Recombinant Plasmid, Recombinant Microorganism  
; TITLE OF INVENTION: Cell, Pharmaceutical Composition and Method of Recovering  
; NUMBER OF SEQUENCES: 50  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Wenderoth, Lind & Ponack  
; STREET: 805 Fifteenth Street, N.W., #700  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 5.25 inch, 500 KB

```

COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: DisplayWrite
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/668,517
FILING DATE: 19910322
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Matthew Jacob
REGISTRATION NUMBER: 25,154
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX: 202-371-8856
TELEX:
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 148 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
US-07-668-517-15

Query Match
Best Local Similarity 100.0%; Score 81; DB 1; Length 148;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRETEGAEAKPMY 14
Db 93 QRETEGAEAKPMY 106

RESULT 5
US-07-668-517-3
Sequence 3, Application US/07668517
Patent No. 5262309
GENERAL INFORMATION:
APPLICANT: Satoshi NAKAMURA et al.
TITLE OF INVENTION: No. 5262309el Physiologically Active
TITLE OF INVENTION: Polypeptide, Recombinant Plasmid, Recombinant Microorganism
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSER: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 KB
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: DisplayWrite
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/668,517
FILING DATE: 19910322
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Matthew Jacob
REGISTRATION NUMBER: 25,154
REFERENCE/DOCKET NUMBER:
REFERENCE/DOCKET NUMBER:

```

```

TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX: 202-371-8856
TELEX:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 149 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
US-07-668-517-3

Query Match
Best Local Similarity 100.0%; Score 81; DB 1; Length 149;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRETEGAEAKPMY 14
Db 94 QRETEGAEAKPMY 107

RESULT 6
US-07-668-517-16
Sequence 16, Application US/07668517
Patent No. 5262309
GENERAL INFORMATION:
APPLICANT: Satoshi NAKAMURA et al.
TITLE OF INVENTION: No. 5262309el Physiologically Active
TITLE OF INVENTION: Polypeptide, Recombinant Plasmid, Recombinant Microorganism
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSER: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 KB
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: DisplayWrite
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/668,517
FILING DATE: 19910322
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Matthew Jacob
REGISTRATION NUMBER: 25,154
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX: 202-371-8856
TELEX:
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 149 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:

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OTHER INFORMATION:  
US-07-668-517-16

Query Match 100.0%; Score 81; DB 1; Length 149;

Best Local Similarity 100.0%; Pred. No. 2.5e-06;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;OY 1 ORETEGAEAKPMY 14  
|||||

DB 94 ORETEGAEAKPMY 107

RESULT 7  
US-07-668-517-4; Sequence 4, Application US/07668517  
; Patent No. 5262309

; GENERAL INFORMATION:

; APPLICANT: Satoshi NAKAMURA et al.

; TITLE OF INVENTION: No. 5262309el Physiologically Active

; TITLE OF INVENTION: Polypeptide, Recombinant Plasmid, Recombinant Microorganism

; NUMBER OF SEQUENCES: 50  
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Wenderoth, Lind &amp; Ponack

; STREET: 805 Fifteenth Street, N.W., #700

; CITY: Washington

; STATE: D.C.

; COUNTRY: U.S.A.

; ZIP: 20005

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 5.25 inch, 500 Kb

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: MS-DOS

; SOFTWARE: DisplayWrite

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/668,517

; FILING DATE: 19910322

; CLASSIFICATION: 530

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Matthew Jacob

; REGISTRATION NUMBER: 25,154

; REFERENCE/DOCKET NUMBER:

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 202-371-8850

; TELEFAX: 202-371-8856

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 150 amino acids

; TYPE: AMINO ACID

; STRANDEDNESS: single

; TOPOLOGY: linear

; FEATURE:

; NAME/KEY:

; LOCATION:

; IDENTIFICATION METHOD:

; OTHER INFORMATION:

US-07-668-517-4

Query Match 100.0%; Score 81; DB 1; Length 150;

Best Local Similarity 100.0%; Pred. No. 2.5e-06;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ORETEGAEAKPMY 14  
|||||

DB 95 ORETEGAEAKPMY 108

RESULT 8  
US-07-668-517-5; Sequence 5, Application US/07668517  
; Patent No. 5262309

; GENERAL INFORMATION:

; APPLICANT: Satoshi NAKAMURA et al.

; TITLE OF INVENTION: No. 5262309el Physiologically Active

; TITLE OF INVENTION: Polypeptide, Recombinant Plasmid, Recombinant Microorganism

; NUMBER OF SEQUENCES: 50  
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Wenderoth, Lind &amp; Ponack

; STREET: 805 Fifteenth Street, N.W., #700

; CITY: Washington

; STATE: D.C.

; COUNTRY: U.S.A.

; ZIP: 20005

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 5.25 inch, 500 Kb

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: MS-DOS

; SOFTWARE: DisplayWrite

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/668,517

; FILING DATE: 19910322

; CLASSIFICATION: 530

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Matthew Jacob

; REGISTRATION NUMBER: 25,154

; REFERENCE/DOCKET NUMBER:

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 202-371-8850

; TELEFAX: 202-371-8856

; INFORMATION FOR SEQ ID NO: 5:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 150 amino acids

; TYPE: AMINO ACID

; STRANDEDNESS: single

; TOPOLOGY: linear

; FEATURE:

; NAME/KEY:

; LOCATION:

; IDENTIFICATION METHOD:

; OTHER INFORMATION:

US-07-668-517-5

Query Match 100.0%; Score 81; DB 1; Length 150;

Best Local Similarity 100.0%; Pred. No. 2.5e-06;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ORETEGAEAKPMY 14  
|||||

DB 95 ORETEGAEAKPMY 108

RESULT 9  
US-07-668-517-6; Sequence 6, Application US/07668517  
; Patent No. 5262309

; GENERAL INFORMATION:

; APPLICANT: Satoshi NAKAMURA et al.

; TITLE OF INVENTION: No. 5262309el Physiologically Active

; TITLE OF INVENTION: Polypeptide, Recombinant Plasmid, Recombinant Microorganism

; NUMBER OF SEQUENCES: 50  
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Wenderoth, Lind &amp; Ponack

; STREET: 805 Fifteenth Street, N.W., #700

; CITY: Washington

; STATE: D.C.

; COUNTRY: U.S.A.

ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch, 500 Kb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: DisplayWrite  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/668,517  
FILING DATE: 19910322  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Matthew Jacob  
REGISTRATION NUMBER: 25,154  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-8850  
TELEFAX: 202-371-8856  
TELEX:  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 150 amino acids  
TYPE: AMINO ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY:  
LOCATION:  
IDENTIFICATION METHOD:  
OTHER INFORMATION:  
US-07-668-517-6

Query Match 100.0%; Score 81; DB 1; Length 150;  
Best Local Similarity 100.0%; Pred. No. 2.5e-06;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRETPGAEAKPW 14  
DB 95 QRETPGAEAKPW 108

RESULT 10  
US-07-668-517-8  
Sequence 8, Application US/07668517  
Patent No. 5262309  
GENERAL INFORMATION:  
APPLICANT: Satoshi NAKAMURA et al.  
TITLE OF INVENTION: No. 5262309el Physiologically Active  
TITLE OF INVENTION: Polypeptide, Recombinant Plasmid, Recombinant Microorganism  
TITLE OF INVENTION: Cell, Pharmaceutical Composition and Method of Recovering  
NUMBER OF SEQUENCES: 50  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wenderoth, Lind & Ponack  
STREET: 805 Fifteenth Street, N.W., #700  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch, 500 Kb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: DisplayWrite  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/668,517  
FILING DATE: 19910322  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:

NAME: Matthew Jacob  
REGISTRATION NUMBER: 25,154  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-8850  
TELEFAX: 202-371-8856  
TELEX:  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 150 amino acids  
TYPE: AMINO ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY:  
LOCATION:  
IDENTIFICATION METHOD:  
OTHER INFORMATION:  
US-07-668-517-8

Query Match 100.0%; Score 81; DB 1; Length 150;  
Best Local Similarity 100.0%; Pred. No. 2.5e-06;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRETPGAEAKPW 14  
DB 95 QRETPGAEAKPW 108

RESULT 11  
US-07-668-517-9  
Sequence 9, Application US/07668517  
Patent No. 5262309  
GENERAL INFORMATION:  
APPLICANT: Satoshi NAKAMURA et al.  
TITLE OF INVENTION: No. 5262309el Physiologically Active  
TITLE OF INVENTION: Polypeptide, Recombinant Plasmid, Recombinant Microorganism  
TITLE OF INVENTION: Cell, Pharmaceutical Composition and Method of Recovering  
NUMBER OF SEQUENCES: 50  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wenderoth, Lind & Ponack  
STREET: 805 Fifteenth Street, N.W., #700  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch, 500 Kb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: DisplayWrite  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/668,517  
FILING DATE: 19910322  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Matthew Jacob  
REGISTRATION NUMBER: 25,154  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-8850  
TELEFAX: 202-371-8856  
TELEX:  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 150 amino acids  
TYPE: AMINO ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:

NAME/KEY:  
LOCATION:  
IDENTIFICATION METHOD:  
OTHER INFORMATION:  
US-07-668-517-9

Query Match 100.0%; Score 81; DB 1; Length 150;  
Best Local Similarity 100.0%; Pred. No. 2.5e-06;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRETPGAEAKPMY 14  
|||||

DB 95 QRETPGAEAKPMY 108

## RESULT 12

US-07-668-517-10  
Sequence 10, Application US/07668517  
Patent No. 5262309

GENERAL INFORMATION:

APPLICANT: Satoshi NAKAMURA et al.

TITLE OF INVENTION: No. 5262309el Physiologically Active

TITLE OF INVENTION: Polypeptide, Recombinant Plasmid, Recombinant Microorganism

NUMBER OF SEQUENCES: 50

CORRESPONDENCE ADDRESS:

ADDRESSEE: Wenderoth, Lind & Ponack

STREET: 805 Fifteenth Street, N.W., #700

CITY: Washington

STATE: D.C.

COUNTRY: U.S.A.

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 5.25 inch, 500 Kb

OPERATING SYSTEM: MS-DOS

SOFTWARE: DisplayWrite

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/668,517

FILING DATE: 19910322

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Matthew Jacob

REGISTRATION NUMBER: 25,154

REFERENCE/DOCKET NUMBER:

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-371-8850

TELEFAX: 202-371-8856

TELEX:

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 150 amino acids

TYPE: AMINO ACID

STRANDEDNESS: single

TOPOLOGY: linear

FEATURE:

NAME/KEY:

LOCATION:

IDENTIFICATION METHOD:

OTHER INFORMATION:

US-07-668-517-10

Query Match 100.0%; Score 81; DB 1; Length 150;  
Best Local Similarity 100.0%; Pred. No. 2.5e-06;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRETPGAEAKPMY 14  
|||||

DB 95 QRETPGAEAKPMY 108

## RESULT 13

US-07-668-517-11  
Sequence 11, Application US/07668517  
Patent No. 5262309

GENERAL INFORMATION:

APPLICANT: Satoshi NAKAMURA et al.

TITLE OF INVENTION: No. 5262309el Physiologically Active

TITLE OF INVENTION: Polypeptide, Recombinant Plasmid, Recombinant Microorganism

NUMBER OF SEQUENCES: 50

CORRESPONDENCE ADDRESS:

ADDRESSEE: Wenderoth, Lind & Ponack

STREET: 805 Fifteenth Street, N.W., #700

CITY: Washington

STATE: D.C.

COUNTRY: U.S.A.

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 5.25 inch, 500 Kb

OPERATING SYSTEM: MS-DOS

SOFTWARE: DisplayWrite

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/668,517

FILING DATE: 19910322

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Matthew Jacob

REGISTRATION NUMBER: 25,154

REFERENCE/DOCKET NUMBER:

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-371-8850

TELEFAX: 202-371-8856

TELEX:

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:

LENGTH: 150 amino acids

TYPE: AMINO ACID

STRANDEDNESS: single

TOPOLOGY: linear

FEATURE:

NAME/KEY:

LOCATION:

IDENTIFICATION METHOD:

OTHER INFORMATION:

US-07-668-517-11

Query Match 100.0%; Score 81; DB 1; Length 150;  
Best Local Similarity 100.0%; Pred. No. 2.5e-06;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRETPGAEAKPMY 14  
|||||

DB 95 QRETPGAEAKPMY 108

## RESULT 14

US-07-668-517-12  
Sequence 12, Application US/07668517  
Patent No. 5262309

GENERAL INFORMATION:

APPLICANT: Satoshi NAKAMURA et al.

TITLE OF INVENTION: No. 5262309el Physiologically Active

TITLE OF INVENTION: Polypeptide, Recombinant Plasmid, Recombinant Microorganism

NUMBER OF SEQUENCES: 50

CORRESPONDENCE ADDRESS:

ADDRESSEE: Wenderoth, Lind & Ponack

STREET: 805 Fifteenth Street, N.W., #700



```

: CITY: Washington
: STATE: D.C.
: COUNTRY: U.S.A.
: ZIP: 20005
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette, 5.25 inch, 500 Kb
: COMPUTER: IBM Compatible
: OPERATING SYSTEM: MS-DOS
: SOFTWARE: DisplayWrite
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/07/668,517
: FILING DATE: 19910322
: CLASSIFICATION: 530
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER:
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Matthew Jacob
: REGISTRATION NUMBER: 25,154
: REFERENCE/DOCKET NUMBER:
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 202-371-8850
: TELEFAX: 202-371-8856
: TELEX:
: INFORMATION FOR SEQ ID NO: 12:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 150 amino acids
: TYPE: AMINO ACID
: STRANDEDNESS: single
: TOPOLOGY: linear
: FEATURE:
: NAME/KEY:
: LOCATION:
: IDENTIFICATION METHOD:
: OTHER INFORMATION:
: US-07-668-517-12

Query Match      100.0%; Score 81; DB 1; Length 150;
Best Local Similarity 100.0%; Pred. No. 2.5e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRETPGAEAKPMY 14
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Db 95 QRETPGAEAKPMY 108

RESULT 15
US-07-668-517-13
: Sequence 13, Application US/07668517
: Patent No. 5262309
: GENERAL INFORMATION:
: APPLICANT: Satoshi NAKAMURA et al.
: TITLE OF INVENTION: No. 5262309el Physiologically Active
: TITLE OF INVENTION: Polypeptide, Recombinant Plasmid, Recombinant Microorganism
: TITLE OF INVENTION: Cell, Pharmaceutical Composition and Method of Recovering
: NUMBER OF SEQUENCES: 50
: CORRESPONDENCE ADDRESS:
: ADDRESS: Wenderoth, Lind & Ponack
: STREET: 805 Fifteenth Street, N.W., #700
: CITY: Washington
: STATE: D.C.
: COUNTRY: U.S.A.
: ZIP: 20005
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette, 5.25 inch, 500 Kb
: COMPUTER: IBM Compatible
: OPERATING SYSTEM: MS-DOS
: SOFTWARE: DisplayWrite
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/07/668,517
: FILING DATE: 19910322
: CLASSIFICATION: 530
: PRIOR APPLICATION DATA:

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: APPLICATION NUMBER:
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Matthew Jacob
: REGISTRATION NUMBER: 25,154
: REFERENCE/DOCKET NUMBER:
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 202-371-8850
: TELEFAX: 202-371-8856
: TELEX:
: INFORMATION FOR SEQ ID NO: 13:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 150 amino acids
: TYPE: AMINO ACID
: STRANDEDNESS: single
: TOPOLOGY: linear
: FEATURE:
: NAME/KEY:
: LOCATION:
: IDENTIFICATION METHOD:
: OTHER INFORMATION:
: US-07-668-517-13

Query Match      100.0%; Score 81; DB 1; Length 150;
Best Local Similarity 100.0%; Pred. No. 2.5e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRETPGAEAKPMY 14
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Db 95 QRETPGAEAKPMY 108

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Search completed: April 4, 2003, 08:43:41  
Job time: 10.0323 secs

GenCore version 5.1.4\_p5-4578  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 4, 2003, 08:42:11 ; Search time 8.80645 Seconds  
(without alignments)  
97.191 Million cell updates/sec

Title: US-09-779-703-1  
Perfect score: 81  
Sequence: 1 QRETPGCAKPMY 14

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 248812 seqs, 61136040 residues  
Total number of hits satisfying chosen parameters: 248812

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

- Database :
- 1: Published.Applications\_AA:\*
  - 2: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep:\*
  - 3: /cgn2\_6/ptodata/2/pubpaa/PCR\_NEW\_PUB.pep:\*
  - 4: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep:\*
  - 5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep:\*
  - 6: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep:\*
  - 7: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep:\*
  - 8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep:\*
  - 9: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep:\*
  - 10: /cgn2\_6/ptodata/2/pubpaa/US09\_PUBCOMB.pep:\*
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  - 12: /cgn2\_6/ptodata/2/pubpaa/US10\_PUBCOMB.pep:\*
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  - 14: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	81	100.0	150	US-09-877-156-25	Sequence 25, Appli
2	81	100.0	150	US-10-116-378-28	Sequence 28, Appli
3	81	100.0	152	US-09-779-050A-24	Sequence 24, Appli
4	81	100.0	157	US-09-903-327A-7	Sequence 7, Appli
5	81	100.0	157	US-10-043-432-1	Sequence 1, Appli
6	81	100.0	157	US-09-756-301A-1	Sequence 1, Appli
7	81	100.0	157	US-09-927-703-1	Sequence 19, Appli
8	81	100.0	157	US-09-854-280-19	Sequence 13, Appli
9	81	100.0	157	US-09-934-465-13	Sequence 1, Appli
10	81	100.0	157	US-09-766-535A-1	Sequence 19, Appli
11	81	100.0	157	US-09-854-208-19	Sequence 1, Appli
12	81	100.0	157	US-09-756-161A-1	Sequence 1, Appli
13	81	100.0	157	US-10-010-329-1	Sequence 1, Appli
14	81	100.0	157	US-10-043-450-1	Sequence 1, Appli
15	81	100.0	157	US-10-044-534-1	Sequence 1, Appli
16	81	100.0	164	US-09-798-789-2	Sequence 2, Appli
17	81	100.0	164	US-09-981-289-2	Sequence 2, Appli
18	81	100.0	193	US-10-145-014-3	Sequence 3, Appli
19	81	100.0	193	US-09-982-308-3	Sequence 3, Appli

20	81	100.0	233	8	US-08-971-317A-5	Sequence 5, Appli
21	81	100.0	233	9	US-10-136-511-3	Sequence 3, Appli
22	81	100.0	233	9	US-10-145-014-22	Sequence 22, Appli
23	81	100.0	233	9	US-09-131-237-3	Sequence 3, Appli
24	81	100.0	233	9	US-10-174-654-9	Sequence 9, Appli
25	81	100.0	233	9	US-10-151-882-42	Sequence 42, Appli
26	81	100.0	233	10	US-09-193-663-5	Sequence 5, Appli
27	81	100.0	233	10	US-09-879-919-5	Sequence 5, Appli
28	81	100.0	233	10	US-09-782-980-43	Sequence 43, Appli
29	81	100.0	233	10	US-09-840-707A-14	Sequence 14, Appli
30	81	100.0	233	10	US-09-246-129B-3	Sequence 3, Appli
31	81	100.0	233	10	US-09-345-790-3	Sequence 3, Appli
32	81	100.0	233	10	US-09-929-493-3	Sequence 3, Appli
33	81	100.0	233	10	US-09-899-059-3	Sequence 3, Appli
34	81	100.0	233	12	US-10-082-260-5	Sequence 5, Appli
35	81	100.0	233	12	US-10-012-452-10	Sequence 10, Appli
36	81	100.0	537	9	US-09-903-327A-11	Sequence 11, Appli
37	65	80.2	151	9	US-09-779-050A-40	Sequence 40, Appli
38	65	80.2	235	9	US-10-017-910-8	Sequence 8, Appli
39	65	80.2	268	9	US-10-185-425-6	Sequence 6, Appli
40	54	66.7	104	10	US-09-911-777-5	Sequence 5, Appli
41	49	60.5	235	9	US-09-131-237-7	Sequence 7, Appli
42	49	60.5	235	10	US-09-246-129B-7	Sequence 7, Appli
43	49	60.5	235	10	US-09-899-059-7	Sequence 7, Appli
44	49	60.5	235	12	US-10-012-452-14	Sequence 14, Appli
45	41	50.6	624	12	US-10-062-254-340	Sequence 340, App

ALIGNMENTS

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RESULT 1
US-09-877-156-25
; Sequence 25, Application US/09877156
; Patent No. US20020055625A1
; GENERAL INFORMATION:
; APPLICANT: Catherine Tribouley
; TITLE OF INVENTION: NEW MEMBERS OF TNF AND TNFR FAMILIES
; FILE REFERENCE: 1408.003/200130.439C1
; CURRENT APPLICATION NUMBER: 45/09/877,156
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 09/286,529
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 25
; LENGTH: 150
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-877-156-25

Query Match      100.0%; Score 81; DB 10; Length 150;
Best Local Similarity 100.0%; Pred. No. 6.4e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 QRETPGCAKPMY 14
Db      95 QRETPGCAKPMY 108

RESULT 2
US-10-116-378-28
; Sequence 28, Application US/10116378
; Patent No. US2002015093A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Goddard, Audrey
; APPLICANT: Gurney, Austin
; APPLICANT: Maisters, Scot A.
; APPLICANT: Pittl, Robert M.
; APPLICANT: Wood, William
; TITLE OF INVENTION: NOVEL TUMOR NECROSIS FACTOR RECEPTOR HOMOLOG AND
; TITLE OF INVENTION: NOVEL TUMOR NECROSIS FACTOR RECEPTOR HOMOLOG AND

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; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P1206R1
; CURRENT APPLICATION NUMBER: 2002-04-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/247,225
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/074,087
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-09
; NUMBER OF SEQ ID NOS: 31
; SEQ ID NO 28
; LENGTH: 150
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-116-378-28

Query Match
Best Local Similarity 100.0%; Score 81; DB 12; Length 150;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 QRETEGAEAKPMY 14
Db 95 QRETEGAEAKPMY 108

RESULT 3
US-09-779-050A-24
; Sequence 24, Application US/09779050A
; Patent No. US20020160416A1
; GENERAL INFORMATION:
; APPLICANT: BOYLE, WILLIAM
; APPLICANT: HSU, HAILING
; TITLE OF INVENTION: RECEPTOR FROM TNF FAMILY
; FILE REFERENCE: A-570B
; CURRENT APPLICATION NUMBER: US/09/779,050A
; CURRENT FILING DATE: 2001-02-12
; PRIOR APPLICATION NUMBER: 60/181,800
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 24
; LENGTH: 152
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-779-050A-24

Query Match
Best Local Similarity 100.0%; Score 81; DB 9; Length 152;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 QRETEGAEAKPMY 14
Db 97 QRETEGAEAKPMY 110

RESULT 4
US-09-903-327A-7
; Sequence 7, Application US/09903327A
; Patent No. US20020164333A1
; GENERAL INFORMATION:
; APPLICANT: Nemerow, Glen R.
; APPLICANT: Li, Eryuang
; TITLE OF INVENTION: BIFUNCTIONAL MOLECULES AND VECTORS COMPLEXED THEREWITH FOR TARGET
; TITLE OF INVENTION: GENE
; TITLE OF INVENTION: DELIVERY
; FILE REFERENCE: 22908-1228
; CURRENT APPLICATION NUMBER: US/09/903,327A
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 09/613,017
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 157
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; TYPE: PRT
; ORGANISM: Human
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (0)...(0)
; OTHER INFORMATION: Tumor necrosis factor-alpha (TNF alpha, mature
; OTHER INFORMATION: peptide)
US-09-903-327A-7

Query Match
Best Local Similarity 100.0%; Score 81; DB 9; Length 157;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 QRETEGAEAKPMY 14
Db 102 QRETEGAEAKPMY 115

RESULT 5
US-10-043-432-1
; Sequence 1, Application US/10043432
; Publication No. US20030054004A1
; GENERAL INFORMATION:
; APPLICANT: Vilecek, Jan
; APPLICANT: Daddona, Peter
; APPLICANT: Ghayeb, John
; APPLICANT: Knight, David M.
; APPLICANT: Siegel, Scott
; TITLE OF INVENTION: Anti-TNF Antibodies and Peptides of
; TITLE OF INVENTION: Human Tumor Necrosis Factor
; FILE REFERENCE: 0975.1005-013
; CURRENT APPLICATION NUMBER: US/10/043,432
; CURRENT FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: 09/927,703
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: U.S. 09/756,398
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: U.S. 09/133,119
; PRIOR FILING DATE: 1998-08-12
; PRIOR APPLICATION NUMBER: U.S. 08/570,674
; PRIOR FILING DATE: 1995-12-11
; PRIOR APPLICATION NUMBER: U.S. 08/324,799
; PRIOR FILING DATE: 1994-10-18
; PRIOR APPLICATION NUMBER: U.S. 08/192,102
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/192,861
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/192,093
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/010,406
; PRIOR FILING DATE: 1993-01-29
; PRIOR APPLICATION NUMBER: U.S. 08/013,413
; PRIOR FILING DATE: 1993-02-02
; PRIOR APPLICATION NUMBER: U.S. 07/943,852
; PRIOR FILING DATE: 1992-09-11
; PRIOR APPLICATION NUMBER: U.S. 07/853,606
; PRIOR FILING DATE: 1992-03-18
; PRIOR APPLICATION NUMBER: U.S. 07/670,827
; PRIOR FILING DATE: 1991-03-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 157
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-043-432-1

Query Match
Best Local Similarity 100.0%; Score 81; DB 9; Length 157;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 QRETEGAEAKPMY 14
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Db 102 QRETPGAEAKPMY 115

RESULT 6  
US-09-756-301A-1

Sequence 1, Application US/09756301A  
Patent No. US20010027249A1  
GENERAL INFORMATION:  
APPLICANT: Le, Junming  
APPLICANT: Vilcek, Jan  
APPLICANT: Daddona, Peter  
APPLICANT: Ghayeb, John  
APPLICANT: Knight, David M.  
APPLICANT: Siegel, Scott  
TITLE OF INVENTION: Anti-TNF Antibodies and Peptides of  
FILE REFERENCE: 0975.1005-008  
CURRENT APPLICATION NUMBER: US/09/756,301A  
CURRENT FILING DATE: 2001-01-08  
PRIOR APPLICATION NUMBER: U.S. 09/133,119  
PRIOR FILING DATE: 1998-08-12  
PRIOR APPLICATION NUMBER: U.S. 08/570,674  
PRIOR FILING DATE: 1995-12-11  
PRIOR APPLICATION NUMBER: U.S. 08/324,799  
PRIOR FILING DATE: 1994-10-18  
PRIOR APPLICATION NUMBER: U.S. 08/192,102  
PRIOR FILING DATE: 1994-02-04  
PRIOR APPLICATION NUMBER: U.S. 08/192,861  
PRIOR FILING DATE: 1994-02-04  
PRIOR APPLICATION NUMBER: U.S. 08/192,093  
PRIOR FILING DATE: 1994-02-04  
PRIOR APPLICATION NUMBER: U.S. 08/010,406  
PRIOR FILING DATE: 1993-01-29  
PRIOR APPLICATION NUMBER: U.S. 08/013,413  
PRIOR FILING DATE: 1993-02-02  
PRIOR APPLICATION NUMBER: U.S. 07/943,852  
PRIOR FILING DATE: 1992-09-11  
PRIOR APPLICATION NUMBER: U.S. 07/853,606  
PRIOR FILING DATE: 1992-03-18  
PRIOR APPLICATION NUMBER: U.S. 07/670,827  
PRIOR FILING DATE: 1991-03-18  
NUMBER OF SEQ ID NOS: 19  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 1  
LENGTH: 157  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-756-301A-1

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Best Local Similarity 100.0%; Pred. No. 6.7e-06;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRETPGAEAKPMY 14  
Db 102 QRETPGAEAKPMY 115

RESULT 7  
US-09-927-703-1  
Sequence 1, Application US/09927703  
Patent No. US20020022720A1  
GENERAL INFORMATION:  
APPLICANT: Le, Junming  
APPLICANT: Vilcek, Jan  
APPLICANT: Daddona, Peter  
APPLICANT: Ghayeb, John  
APPLICANT: Knight, David M.  
APPLICANT: Siegel, Scott  
TITLE OF INVENTION: Anti-TNF Antibodies and Peptides of  
FILE REFERENCE: 0975.1005-013

CURRENT APPLICATION NUMBER: US/09/927,703  
CURRENT FILING DATE: 2001-08-10  
PRIOR APPLICATION NUMBER: U.S. 09/756,398  
PRIOR FILING DATE: 2001-01-08  
PRIOR APPLICATION NUMBER: U.S. 09/133,119  
PRIOR FILING DATE: 1998-08-12  
PRIOR APPLICATION NUMBER: U.S. 08/570,674  
PRIOR FILING DATE: 1995-12-11  
PRIOR APPLICATION NUMBER: U.S. 08/324,799  
PRIOR FILING DATE: 1994-10-18  
PRIOR APPLICATION NUMBER: U.S. 08/192,102  
PRIOR FILING DATE: 1994-02-04  
PRIOR APPLICATION NUMBER: U.S. 08/192,861  
PRIOR FILING DATE: 1994-02-04  
PRIOR APPLICATION NUMBER: U.S. 08/192,093  
PRIOR FILING DATE: 1994-02-04  
PRIOR APPLICATION NUMBER: U.S. 08/010,406  
PRIOR FILING DATE: 1993-01-29  
PRIOR APPLICATION NUMBER: U.S. 08/013,413  
PRIOR FILING DATE: 1993-02-02  
PRIOR APPLICATION NUMBER: U.S. 07/943,852  
PRIOR FILING DATE: 1992-09-11  
PRIOR APPLICATION NUMBER: U.S. 07/853,606  
PRIOR FILING DATE: 1992-03-18  
PRIOR APPLICATION NUMBER: U.S. 07/670,827  
PRIOR FILING DATE: 1991-03-18  
NUMBER OF SEQ ID NOS: 19  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 1  
LENGTH: 157  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-927-703-1

Query Match 100.0%; Score 81; DB 10; Length 157;  
Best Local Similarity 100.0%; Pred. No. 6.7e-06;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRETPGAEAKPMY 14  
Db 102 QRETPGAEAKPMY 115

RESULT 8  
US-09-854-280-19  
Sequence 19, Application US/09854280  
Patent No. US20020052027A1  
GENERAL INFORMATION:  
APPLICANT: Chen, Jian  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Goddard, Audrey  
APPLICANT: Gurney, Austin  
APPLICANT: Li, Hanzhong  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF  
FILE REFERENCE: P1381R1C2  
CURRENT APPLICATION NUMBER: US/09/854,280  
CURRENT FILING DATE: 2001-05-10  
PRIOR APPLICATION NUMBER: US 09/311,832  
PRIOR FILING DATE: 1999-05-14  
PRIOR APPLICATION NUMBER: US 60/085,579  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: US 60/113,621  
PRIOR FILING DATE: 1998-12-23  
NUMBER OF SEQ ID NOS: 26  
SEQ ID NO 19  
LENGTH: 157  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-854-280-19

Query Match 100.0%; Score 81; DB 10; Length 157;  
Best Local Similarity 100.0%; Pred. No. 6.7e-06;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRETPGAEAKPMY 14  
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Db 102 QRETPGAEAKPMY 115

RESULT 9  
US-09-934-465-13  
; Sequence 13, Application US/09934465  
; Patent No. US20020102233A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; TITLE OF INVENTION: APO-2 LIGAND  
; FILE REFERENCE: 11669.22US03  
; CURRENT APPLICATION NUMBER: US/09/934,465  
; CURRENT FILING DATE: 2001-08-21  
; PRIOR APPLICATION NUMBER: 08/584,031  
; PRIOR FILING DATE: 1996-01-09  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 13  
; LENGTH: 157  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-934-465-13

Query Match 100.0%; Score 81; DB 10; Length 157;  
Best Local Similarity 100.0%; Pred. No. 6.7e-06;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRETPGAEAKPMY 14  
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Db 102 QRETPGAEAKPMY 115

RESULT 10  
US-09-766-535A-1  
; Sequence 1, Application US/09766535A  
; Patent No. US20020106372A1  
; GENERAL INFORMATION:  
; APPLICANT: Le, Junming  
; APPLICANT: Vilcek, Jan  
; APPLICANT: Daddona, Peter  
; APPLICANT: Ghrayeb, John  
; APPLICANT: Knight, David M.  
; APPLICANT: Siegel, Scott  
; TITLE OF INVENTION: Anti-TNF Antibodies and Peptides of  
; FILE REFERENCE: 0975.1005-010  
; CURRENT APPLICATION NUMBER: US/09/766,535A  
; CURRENT FILING DATE: 2001-01-18  
; PRIOR APPLICATION NUMBER: U.S. 09/133,119  
; PRIOR FILING DATE: 1998-08-12  
; PRIOR APPLICATION NUMBER: U.S. 08/570,674  
; PRIOR FILING DATE: 1995-12-11  
; PRIOR APPLICATION NUMBER: U.S. 08/324,799  
; PRIOR FILING DATE: 1994-10-18  
; PRIOR APPLICATION NUMBER: U.S. 08/192,102  
; PRIOR FILING DATE: 1994-02-04  
; PRIOR APPLICATION NUMBER: U.S. 08/192,861  
; PRIOR FILING DATE: 1994-02-04  
; PRIOR APPLICATION NUMBER: U.S. 08/192,093  
; PRIOR FILING DATE: 1994-02-04  
; PRIOR APPLICATION NUMBER: U.S. 08/010,406  
; PRIOR FILING DATE: 1993-01-29  
; PRIOR APPLICATION NUMBER: U.S. 08/013,413  
; PRIOR FILING DATE: 1993-02-02  
; PRIOR APPLICATION NUMBER: U.S. 07/943,852  
; PRIOR FILING DATE: 1992-09-11  
; PRIOR APPLICATION NUMBER: U.S. 07/853,606  
; PRIOR FILING DATE: 1992-03-18  
; PRIOR APPLICATION NUMBER: U.S. 07/670,827

; PRIOR FILING DATE: 1991-03-18  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 157  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-766-535A-1

Query Match 100.0%; Score 81; DB 10; Length 157;  
Best Local Similarity 100.0%; Pred. No. 6.7e-06;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRETPGAEAKPMY 14  
|||||

Db 102 QRETPGAEAKPMY 115

RESULT 11  
US-09-854-208-19  
; Sequence 19, Application US/09854208  
; Patent No. US20020106743A1  
; GENERAL INFORMATION:  
; APPLICANT: Chen, Jian  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Gunney, Austin  
; APPLICANT: Li, Hanzhong  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES  
; FILE REFERENCE: P1381-R1  
; CURRENT APPLICATION NUMBER: US/09/854,208  
; CURRENT FILING DATE: 2001-05-10  
; PRIOR APPLICATION NUMBER: US/09/311,832  
; PRIOR FILING DATE: 1999-05-14  
; PRIOR APPLICATION NUMBER: US 60/085,579  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: US 60/113,621  
; PRIOR FILING DATE: 1998-12-23  
; NUMBER OF SEQ ID NOS: 26  
; SEQ ID NO 19  
; LENGTH: 157  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-854-208-19

Query Match 100.0%; Score 81; DB 10; Length 157;  
Best Local Similarity 100.0%; Pred. No. 6.7e-06;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRETPGAEAKPMY 14  
|||||

Db 102 QRETPGAEAKPMY 115

RESULT 12  
US-09-756-161A-1  
; Sequence 1, Application US/09756161A  
; Patent No. US20020132307A1  
; GENERAL INFORMATION:  
; APPLICANT: Le, Junming  
; APPLICANT: Vilcek, Jan  
; APPLICANT: Daddona, Peter  
; APPLICANT: Ghrayeb, John  
; APPLICANT: Knight, David M.  
; APPLICANT: Siegel, Scott  
; TITLE OF INVENTION: Anti-TNF Antibodies and Peptides of  
; FILE REFERENCE: 0975.1005-007  
; CURRENT APPLICATION NUMBER: US/09/756,161A  
; CURRENT FILING DATE: 2001-01-08  
; PRIOR APPLICATION NUMBER: U.S. 09/133,119

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; PRIOR FILING DATE: 1998-08-12
; PRIOR APPLICATION NUMBER: U.S. 08/570,674
; PRIOR FILING DATE: 1995-12-11
; PRIOR APPLICATION NUMBER: U.S. 08/324,799
; PRIOR FILING DATE: 1994-10-18
; PRIOR APPLICATION NUMBER: U.S. 08/192,102
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/192,861
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/192,093
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/010,406
; PRIOR FILING DATE: 1993-01-29
; PRIOR APPLICATION NUMBER: U.S. 08/013,413
; PRIOR FILING DATE: 1993-02-02
; PRIOR APPLICATION NUMBER: U.S. 07/943,852
; PRIOR FILING DATE: 1992-09-11
; PRIOR APPLICATION NUMBER: U.S. 07/853,606
; PRIOR FILING DATE: 1992-03-18
; PRIOR APPLICATION NUMBER: U.S. 07/670,827
; PRIOR FILING DATE: 1991-03-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 157
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-756-161A-1
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Query Match 100.0%; Score 81; DB 10; Length 157;
Best Local Similarity 100.0%; Pred. No. 6.7e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 QRETPGAGAKPMY 14
Db 102 QRETPGAGAKPMY 115
```

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RESULT 13
US-10-010-229-1
; Sequence 1, Application US/10010229
; Patent No. US20020114805A1
; GENERAL INFORMATION:
; APPLICANT: Le, Junming
; APPLICANT: Vilcek, Jan
; APPLICANT: Daddona, Peter
; APPLICANT: Ghayeb, John
; APPLICANT: Knight, David M.
; APPLICANT: Siegel, Scott
; TITLE OF INVENTION: Anti-TNF Antibodies and Peptides of
; FILE REFERENCE: 0975.1005-013
; CURRENT APPLICATION NUMBER: US/10/010,229
; PRIOR FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: US/09/927,703
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 157
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-010-229-1
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```

Query Match 100.0%; Score 81; DB 12; Length 157;
Best Local Similarity 100.0%; Pred. No. 6.7e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 QRETPGAGAKPMY 14
Db 102 QRETPGAGAKPMY 115
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RESULT 14
US-10-043-450-1
; Sequence 1, Application US/10043450
; Patent No. US20020141996A1
; GENERAL INFORMATION:
; APPLICANT: Le, Junming
; APPLICANT: Vilcek, Jan
; APPLICANT: Daddona, Peter
; APPLICANT: Ghayeb, John
; APPLICANT: Knight, David M.
; APPLICANT: Siegel, Scott
; TITLE OF INVENTION: Anti-TNF Antibodies and Peptides of
; FILE REFERENCE: 0975.1005-013
; CURRENT APPLICATION NUMBER: US/10/043,450
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: 09/927,703
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: U.S. 09/756,398
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: U.S. 09/133,119
; PRIOR FILING DATE: 1998-08-12
; PRIOR APPLICATION NUMBER: U.S. 08/570,674
; PRIOR FILING DATE: 1995-12-11
; PRIOR APPLICATION NUMBER: U.S. 08/324,799
; PRIOR FILING DATE: 1994-10-18
; PRIOR APPLICATION NUMBER: U.S. 08/192,102
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/192,861
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/192,093
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/010,406
; PRIOR FILING DATE: 1993-01-29
; PRIOR APPLICATION NUMBER: U.S. 08/013,413
; PRIOR FILING DATE: 1993-02-02
; PRIOR APPLICATION NUMBER: U.S. 07/943,852
; PRIOR FILING DATE: 1992-09-11
; PRIOR APPLICATION NUMBER: U.S. 07/853,606
; PRIOR FILING DATE: 1992-03-18
; PRIOR APPLICATION NUMBER: U.S. 07/670,827
; PRIOR FILING DATE: 1991-03-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 157
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-043-450-1
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Query Match 100.0%; Score 81; DB 12; Length 157;
Best Local Similarity 100.0%; Pred. No. 6.7e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 QRETPGAGAKPMY 14
Db 102 QRETPGAGAKPMY 115
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RESULT 15
US-10-044-534-1
; Sequence 1, Application US/10044534
; Patent No. US20020146419A1
; GENERAL INFORMATION:
; APPLICANT: Le, Junming
; APPLICANT: Vilcek, Jan
; APPLICANT: Daddona, Peter
; APPLICANT: Ghayeb, John
; APPLICANT: Knight, David M.
; APPLICANT: Siegel, Scott
; TITLE OF INVENTION: Anti-TNF Antibodies and Peptides of
; FILE REFERENCE: 0975.1005-013
```

```

CURRENT APPLICATION NUMBER: US/10/044,534
CURRENT FILING DATE: 2002-01-10
PRIOR APPLICATION NUMBER: 09/927,703
PRIOR FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: U.S. 09/756,398
PRIOR FILING DATE: 2001-01-08
PRIOR APPLICATION NUMBER: U.S. 09/133,119
PRIOR FILING DATE: 1998-08-12
PRIOR APPLICATION NUMBER: U.S. 08/570,674
PRIOR FILING DATE: 1995-12-11
PRIOR APPLICATION NUMBER: U.S. 08/324,799
PRIOR FILING DATE: 1994-10-18
PRIOR APPLICATION NUMBER: U.S. 08/192,102
PRIOR FILING DATE: 1994-02-04
PRIOR APPLICATION NUMBER: U.S. 08/192,861
PRIOR FILING DATE: 1994-02-04
PRIOR APPLICATION NUMBER: U.S. 08/192,093
PRIOR FILING DATE: 1994-02-04
PRIOR APPLICATION NUMBER: U.S. 08/010,406
PRIOR FILING DATE: 1993-01-29
PRIOR APPLICATION NUMBER: U.S. 08/013,413
PRIOR FILING DATE: 1993-02-02
PRIOR APPLICATION NUMBER: U.S. 07/943,852
PRIOR FILING DATE: 1992-09-11
PRIOR APPLICATION NUMBER: U.S. 07/853,606
PRIOR FILING DATE: 1992-03-18
PRIOR APPLICATION NUMBER: U.S. 07/670,827
PRIOR FILING DATE: 1991-03-18
NUMBER OF SEQ ID NOS: 19
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 157
TYPE: PRT
ORGANISM: Homo sapiens
US-10-044-534-1

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Query Match      100.0%; Score 81; DB 12; Length 157;
Best Local Similarity 100.0%; Pred. No. 6,7e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 ORETEGAAKPMY 14
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Db      102 ORETEGAAKPMY 115

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 Job time : 11.8065 secs

GenCore version 5.1.4.p5.4578  
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OM protein - protein search, using sw model

Run on: April 4, 2003, 08:36:10 ; Search time 25.9677 Seconds  
(without alignments)  
71.839 Million cell updates/sec

Title: US-09-779-703-2  
Perfect score: 84  
Sequence: 1 PKDTPGAEUKPMY 14

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	84	100.0	14	21	AAy82195	Tumour necrosis fa
2	84	100.0	17	15	AAy82197	mtNF-alpha tip. S
3	84	100.0	17	21	AAy82197	Tumour necrosis fa
4	84	100.0	19	21	AAy82198	Murine TNF derived
5	84	100.0	154	8	AAp70557	Tumour necrosis fac
6	84	100.0	156	7	AAp60526	Sequence of tumour
7	84	100.0	156	14	AAr41861	Rat TNF-alpha mute
8	84	100.0	156	14	AAr41862	Murine TNF-alpha m
9	84	100.0	156	15	AAp60244	Mouse-alpha. Mus
10	84	100.0	157	7	AAp60527	Sequence of tumour

11	84	100.0	157	14	AAr38077	Non-human TNF-alpha
12	84	100.0	170	8	AAp70558	Tumour necrosis fac
13	84	100.0	233	10	AAp90424	Human tumour necro
14	84	100.0	235	7	AAp60530	Sequence of tumour
15	84	100.0	235	11	AAr05328	Rat tumour necrosi
16	84	100.0	235	11	AAr05396	Rat tumour necrosi
17	84	100.0	235	17	AAr88589	Mouse tumour necro
18	84	100.0	235	21	AAr88596	Murine tumour necr
19	84	100.0	235	23	AAU10546	Rat tumour necrosi
20	84	100.0	268	22	AAr86310	Fusion construct T
21	72	85.7	155	21	AAr08283	Amino acid sequenc
22	69	82.1	157	10	AAp91633	Polypeptide derive
23	67	79.8	19	21	AAy82199	Murine TNF derived
24	65	77.4	14	21	AAy82194	Tumour necrosis fa
25	65	77.4	17	11	AAr05469	Tumour necrosis fa
26	65	77.4	17	15	AAr60233	hTNF-alpha tip. S
27	65	77.4	17	21	AAr82196	Tumour necrosis fa
28	65	77.4	25	11	AAr05513	Tumour necrosis fa
29	65	77.4	140	16	AAr72456	Tumour necrosis fa
30	65	77.4	145	9	AAp82043	Sequence of new tu
31	65	77.4	147	9	AAr81953	Sequence of modifi
32	65	77.4	147	22	AAr67245	Human tumour necro
33	65	77.4	147	22	AAr71982	C-terminal region
34	65	77.4	149	10	AAp91635	Polypeptide derive
35	65	77.4	149	11	AAr05612	Antitumour peptide
36	65	77.4	150	8	AAp70528	Synthetic tumour n
37	65	77.4	150	8	AAp71245	TNF-derived polype
38	65	77.4	150	9	AAr81236	Modified tumour ne
39	65	77.4	150	9	AAp82190	TNF analogue. AA
40	65	77.4	150	9	AAp82303	Sequence of new ph
41	65	77.4	150	9	AAp81066	Sequence of new ph
42	65	77.4	150	10	AAr81068	Anti-tumour active
43	65	77.4	150	10	AAp95660	New polypeptide wi
44	65	77.4	150	11	AAr05286	Polypeptide with a
45	65	77.4	150	11	AAr08151	

## ALIGNMENTS

RESULT 1  
AAy82195  
ID AAY82195 standard; peptide; 14 AA.  
XX  
AC AAY82195;  
XX  
DT 08-JUN-2000 (first entry)  
XX  
DE Tumour necrosis factor alpha derived peptide #2.  
XX  
DE Tumour necrosis factor alpha; TNF-alpha; human; mouse; oedema;  
KW proinflammatory; pulmonary oedema.  
XX  
OS Mus sp.  
XX  
PN WO200009149-A1.  
XX  
PD 24-FEB-2000.  
XX  
PF 10-AUG-1999; 99WO-EP05806.  
XX  
PR 14-AUG-1998; 98EP-0870180.  
XX  
PR 18-SEP-1998; 98EP-0870198.  
XX  
PR 21-OCT-1998; 98EP-0870222.  
XX  
PA (INNO-) INNOGENETICS NV.  
XX  
PI Lucas R, De Baetselier P, Pugin J, Bloc A, Fransen L;  
XX  
XX WPI, 2000-282855/24.  
XX  
XX use of peptides derived from human or mouse tissue necrosis  
XX factor-alpha (TNF-alpha), and comprising 7-17 contiguous amino acids,



PT for preventing or treating oedema  
 XX  
 PS Claim 5; Page 16; 26pp; English.  
 XX  
 CC The present invention describes the use of peptides comprising a chain  
 CC of 7-17 contiguous amino acids derived from the Ser100-Glu116 region  
 CC of human tumour necrosis factor-alpha (TNF-alpha), or Ser99-Glu115  
 CC region of mouse TNF-alpha, for treating oedema. The peptides form  
 CC pharmaceutical compositions for treating oedema, especially pulmonary  
 CC oedema. The peptides are non-toxic, whilst retaining the oedema  
 CC resorption-inducing capacity as TNF. The present sequence represents  
 CC a specifically claimed TNF-alpha peptide from the present invention.  
 XX  
 SQ Sequence 14 AA:  
 Query Match 100.0%; Score 84; DB 21; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-06;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 PKDTPGAEELKPMY 14  
 Db 1 PKDTPGAEELKPMY 14  
 RESULT 2  
 ID AAR60232 standard; peptide; 17 AA.  
 XX AAR60232:  
 XX 16-MAR-1995 (first entry)  
 XX  
 DE mTNF-alpha tip.  
 XX  
 KM TNF-alpha; tumor necrosis factor-alpha; tip peptide; mutin; cancer;  
 KM sepsis; inflammation; cytokine; metastasis; lectin; adhesion;  
 KM mutagenesis; trypanoside.  
 XX  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT MISC-difference 1 /note= "N-terminal biotin gly-gly"  
 FT  
 XX WC9418325-A.  
 XX  
 PD 18-AUG-1994.  
 XX  
 PF 02-FEB-1994; 94WO-EP00286.  
 XX  
 PR 03-FEB-1993; 93EP-0400262.  
 XX  
 PA (INNO-) INNOGENETICS NV SA.  
 XX  
 PI De Baetselier P, Franssen L, Lucas R, Sablon E;  
 DR WPI; 1994-279746/34.  
 XX  
 PT New tumour necrosis factor -alpha muteins, antibodies and  
 PT antisense peptide(s) - used in the treatment of diseases and  
 PT conditions associated with the in vivo activities of TNF-A eg  
 XX cancer, sepsis, inflammation, etc  
 XX  
 PS Disclosure; Page 61; 132pp; English.  
 XX  
 CC The TNF-alpha tip peptides given in AAR60232-42 were modified with  
 CC N-terminal biotin-gly-gly moieties and were used to demonstrate  
 CC that the tip region of mouse and human TNF-alpha contains the  
 CC trypanosomal and lectin-like activities of the molecule and is  
 CC is involved in TNF-induced lethal shock.  
 XX  
 SQ Sequence 17 AA:

Query Match 100.0%; Score 84; DB 15; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-06;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 PKDTPGAEELKPMY 14  
 Db 3 PKDTPGAEELKPMY 16  
 RESULT 3  
 ID AAY82197 standard; peptide; 17 AA.  
 XX AAY82197:  
 AC AAY82197;  
 DT 08-JUN-2000 (first entry)  
 XX  
 DE Tumour necrosis factor alpha derived circularised peptide #2.  
 XX  
 KM Tumour necrosis factor alpha; TNF-alpha; human; mouse; oedema;  
 KM proinflammatory; pulmonary oedema; cyclic.  
 XX  
 OS Mus sp.  
 XX  
 FH Key Location/Qualifiers  
 FT Disulfide-bond 1..17  
 FT  
 XX WO200009149-A1.  
 XX  
 PD 24-FEB-2000.  
 XX  
 PF 10-AUG-1999; 99WO-EP05806.  
 XX  
 PR 14-AUG-1998; 98EP-0870180.  
 PR 18-SEP-1998; 98EP-0870198.  
 PR 21-OCT-1998; 98EP-0870222.  
 XX  
 PA (INNO-) INNOGENETICS NV.  
 XX  
 PI Lucas R, De Baetselier P, Pugin J, Bloc A, Franssen L;  
 DR WPI; 2000-282855/24.  
 XX  
 PT Use of peptides derived from human or mouse tissue necrosis  
 PT factor-alpha (TNF-alpha), and comprising 7-17 contiguous amino acids,  
 PT for preventing or treating oedema  
 XX  
 PS Claim 8; Page 16; 26pp; English.  
 XX  
 CC The present invention describes the use of peptides comprising a chain  
 CC of 7-17 contiguous amino acids derived from the Ser100-Glu116 region  
 CC of human tumour necrosis factor-alpha (TNF-alpha), or Ser99-Glu115  
 CC region of mouse TNF-alpha, for treating oedema. The peptides form  
 CC pharmaceutical compositions for treating oedema, especially pulmonary  
 CC oedema. The peptides are non-toxic, whilst retaining the oedema  
 CC resorption-inducing capacity as TNF. The present sequence represents  
 CC a specifically claimed TNF-alpha circularised peptide from the present  
 CC invention.  
 XX  
 SQ Sequence 17 AA:  
 Query Match 100.0%; Score 84; DB 21; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-06;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 PKDTPGAEELKPMY 14  
 Db 3 PKDTPGAEELKPMY 16  
 RESULT 4  
 ID AAY82198 standard; peptide; 19 AA.

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XX AA82198;
AC
XX
DT 08-JUN-2000 (first entry)
XX
DE Murine TNF derived peptide long lip peptide 99-115 (Lrip).
XX
KW Tumour necrosis factor alpha; TNF-alpha; human; mouse; oedema;
XX proinflammatory; pulmonary oedema.
XX
OS Mus sp.
XX
PN WO200009149-A1.
XX
PD 24-FEB-2000.
XX
PF 10-AUG-1999; 99WO-EP05806.
XX
PR 14-AUG-1998; 98EP-0870180.
XX 18-SEP-1998; 98EP-0870198.
XX 21-OCT-1998; 98EP-0870222.
XX (INNO-) INNOGENETICS NV.
XX
PI Lucas R, De Baetseller P, Pugin J, Bloc A, Fransen L;
XX
DR WPI: 2000-28285/24.
XX
PT Use of peptides derived from human or mouse tissue necrosis
XX factor-alpha (TNF-alpha), and comprising 7-17 contiguous amino acids,
XX for preventing or treating oedema.
XX
PS Example 1; Page 7; 26pp; English.
XX
CC The present invention describes the use of peptides comprising a chain
XX of 7-17 contiguous amino acids derived from the Ser100-Glu116 region
XX of human tumour necrosis factor-alpha (TNF-alpha), or Ser99-Glu115
XX region of mouse TNF-alpha, for treating oedema. The peptides form
XX pharmaceutical compositions for treating oedema, especially pulmonary
XX oedema. The peptides are non-toxic, whilst retaining the oedema
XX resorption-inducing capacity as TNF. The present sequence represents
XX a murine TNF derived peptide used in an example from the present
XX invention.
XX
SQ Sequence 19 AA;
XX
Query Match 100.0%; Score 84; DB 21; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.6e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 PKDTPEGALKPWY 14
DB 5 PKDTPEGALKPWY 18
XX
RESULT 5
AAP70557
ID AAP70557 standard; protein; 154 AA.
XX
AC AAP70557;
XX
DT 26-FEB-1991 (first entry)
XX
DE Tumour necrosis factor.
XX
KW TNF; antitumor.
XX
PN Jp62135493-A.
XX
PD 18-JUN-1987.
XX
PF 06-DEC-1985; 85JP-0275392.
XX

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```

PR 06-DEC-1985; 85JP-0275392.
XX
XX (TANA) TANABE SEIYAKU KK.
XX
DR WPI: 1987-209318/30.
XX
PT Anticancer factor - expressed by specified amino acid sequence.
XX
PS Disclosure; Page 12; 12pp; Japanese.
XX
XX The sequence encodes tumor necrosis factor which is an antitumor
XX agent and a lymphokine. The sequence may optionally have up to 16
XX additional AA as the N-terminal.
XX
SQ Sequence 154 AA;
XX
Query Match 100.0%; Score 84; DB 8; Length 154;
Best Local Similarity 100.0%; Pred. No. 1.4e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 PKDTPEGALKPWY 14
DB 99 PKDTPEGALKPWY 112
XX
RESULT 6
AAP60526
ID AAP60526 standard; protein; 156 AA.
XX
AC AAP60526;
XX
DT 07-AUG-1991 (first entry)
XX
DE Sequence of tumour necrosis factor (TNF).
XX
KW Anticancer agent; antitumor; antimalarial; tumour necrosis factor.
XX
PN WO8603751-A.
XX
PD 03-JUL-1986.
XX
PF 19-DEC-1985; 85WO-EP00721.
XX
PR 09-OCT-1985; 85US-0785847.
XX 21-DEC-1984; 84US-0684595.
XX 09-OCT-1986; 86WO-US02133.
XX
PA (BIOJ) BIOGEN NV.
XX (FIER/) FIER W C.
XX (ALLE/) ALLET B.
XX (BIOG-) BIOGEN INC.
XX
PI Piers WC, Fransen LM, Tavernier JHL, Marmenout ALM;
XX VanderHeyden J, Allet B, Washima EH;
XX
DR WPI: 1986-182891/28.
XX
DR N-PSDB; AAN60440.
XX
PT Mammalian tumour necrosis factors - produced by culturing
XX pro-karyotic hosts transformed with recombinant DNA
XX
PS claim 12; Page 66-67; 93pp; English.
XX
CC TNF-like polypeptides and comps. are produced by the fermentation
XX of host cells transformed with at least one DNA sequence which codes
XX for a mammalian TNF-like polypeptide operatively linked to an
XX expression control sequence in the transformed host.
XX
SQ Sequence 156 AA;
XX
Query Match 100.0%; Score 84; DB 7; Length 156;
Best Local Similarity 100.0%; Pred. No. 1.4e-05;

```

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PKDPEGAEKPMY 14  
 ||||||||||||  
 DB 101 PKDPEGAEKPMY 114

RESULT 7  
 AAR41861  
 ID AAR41861 standard; protein; 156 AA.

XX AAR41861;

AC 29-MAR-1994 (first entry)

XX Rat TNF-alpha mutein with modified channel-forming activity.

DE Tumour Necrosis Factor alpha; TNF-a; target membrane permeability;  
 XX TNF trimer; 10n channel; mutein.

OS Rattus rattus.

XX Key Location/Qualifiers

FT Misc-difference 11 /label= Glu, Arg, Cys, Asp, Gln, Asn, Ser, Thr  
 FT or His

FT Misc-difference 57 /note= "wild-type channel residue is Lys"

FT /label= Trp, Ser, Thr, Ala, Met, Cys, Phe or Tyr  
 FT /note= "wild-type channel residue is Leu"

FT Misc-difference 59 /label= Trp, Ser, Thr, Ala, Met, Cys or Phe  
 FT /note= "wild-type channel residue is Tyr"

FT Misc-difference 97 /label= Arg, Cys, Glu, Asp, Gln, Asn, Ser, Thr  
 FT or His

FT /note= "wild-type channel residue is Lys"

FT Misc-difference 111 /label= Arg, Cys, Asp, Gln, Asn, Ser, Thr, Glu  
 FT or His

FT /note= "wild-type channel residue is Lys"

FT Misc-difference 115 /label= Lys, Arg, Cys, Asp, Gln, Asn, Ser, His  
 FT or Thr

FT /note= "wild-type channel residue is Glu"

FT Misc-difference 118 /label= Trp, Phe, Ser, Thr, Ala, Met or Cys  
 FT /note= "wild-type channel residue is Tyr"

FT Misc-difference 120 /label= Ala, Val, Ser or Thr  
 FT /note= "wild-type channel residue is Gly"

FT Misc-difference 154 /label= Trp, Ser, Thr, Ala, Met, Cys, Phe or Tyr  
 FT /note= "wild-type channel residue is Ile"

FT Misc-difference 156 /label= Trp, Ser, Thr, Ala, Cys or Tyr  
 FT /note= "wild-type channel residue is Leu"

XX W09318148-A.

XX 16-SEP-1993.

XX 12-MAR-1993; 93WO-US02475.

XX 12-MAR-1992; 92US-0852625.

XX (WISN/) WISNIESKI B J.

XX Wisniewski BJ;

XX WPI; 1993-303462/38.

XX Producing modified tumour necrosis factor alpha - useful for

PM regulating tumour necrosis factor channel activity e.g.  
 PT increasing permeability

XX Claim 6; Page 37-38 and 51-53; 72pp; English.

XX The sequence of rat TNF-alpha disclosed in Agric.Biol.Chem 53:

CC 1733-1736 (1989) is given in the specification. A modified version

CC of this sequence is claimed in which at least one of the channel

CC residues is substituted (see Features Table). The resulting

CC TNF-alpha mutein has modified channel activity compared to wild-type.

XX Sequence 156 AA;

SO Query Match. 100.0%; Score 84; DB 14; Length 156;

Best Local Similarity 100.0%; Pred. No. 1.4e-05; Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PKDPEGAEKPMY 14  
 ||||||||||||  
 DB 101 PKDPEGAEKPMY 114

RESULT 8  
 AAR41862  
 ID AAR41862 standard; protein; 156 AA.

XX AAR41862;

XX 29-MAR-1994 (first entry)

DE Murine TNF-alpha mutein with modified channel-forming activity.

KW Tumour Necrosis Factor alpha; TNF-a; target membrane permeability;

XX TNF trimer; 10n channel; mutein.

XX Mus musculus.

XX Key Location/Qualifiers

FT Misc-difference 11 /label= Glu, Arg, Cys, Asp, Gln, Asn, Ser, Thr  
 FT or His

FT /note= "wild-type channel residue is Lys"

FT Misc-difference 57 /label= Trp, Ser, Thr, Ala, Met, Cys, Phe or Tyr  
 FT /note= "wild-type channel residue is Leu"

FT Misc-difference 59 /label= Trp, Ser, Thr, Ala, Met, Cys or Phe  
 FT /note= "wild-type channel residue is Tyr"

FT Misc-difference 97 /label= Arg, Cys, Glu, Asp, Gln, Asn, Ser, Thr  
 FT or His

FT /note= "wild-type channel residue is Lys"

FT Misc-difference 112 /label= Arg, Cys, Asp, Gln, Asn, Ser, Thr, Glu  
 FT or His

FT /note= "wild-type channel residue is Lys"

FT Misc-difference 115 /label= Lys, Arg, Cys, Asp, Gln, Asn, Ser, His  
 FT or Thr

FT /note= "wild-type channel residue is Glu"

FT Misc-difference 118 /label= Trp, Phe, Ser, Thr, Ala, Met or Cys  
 FT /note= "wild-type channel residue is Tyr"

FT Misc-difference 120 /label= Ala, Val, Ser or Thr  
 FT /note= "wild-type channel residue is Gly"

FT Misc-difference 154 /label= Trp, Ser, Thr, Ala, Met, Cys, Phe or Tyr  
 FT /note= "wild-type channel residue is Ile"

FT Misc-difference 156 /label= Trp, Ser, Thr, Ala, Cys or Tyr  
 FT /note= "wild-type channel residue is Leu"

XX Producing modified tumour necrosis factor alpha - useful for

PN M09318148-A.  
 XX 16-SEP-1993.  
 PD  
 XX 12-MAR-1993; 93WO-US02475.  
 PF  
 XX 12-MAR-1992; 92US-0852625.  
 PR  
 XX (WISN/) WISNIESKI B J.  
 PA  
 XX WISNIESKI BJ.  
 PI  
 XX WPI: 1993-303462/38.  
 DR  
 XX Producing modified tumour necrosis factor alpha - useful for  
 PT regulating tumour necrosis factor channel activity e.g.  
 PT increasing permeability  
 XX  
 PS Claim 6; Page 39 and 51-53; 72pp; English.  
 CC The sequence of murine TNF-alpha disclosed in PNAS USA 83:1670-1674  
 CC (1986) is given in the specification. A modified version of this  
 CC sequence is claimed in which at least one of the channel residues is  
 CC substituted (see Features Table). The resulting TNF-alpha mutein has  
 CC modified channel activity compared to wild-type.  
 CC  
 SQ Sequence 156 AA:  
 Query Match 100.0%; Score 84; DB 14; Length 156;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-05;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 PKDTPEGAELEKPMY 14  
 DB 101 PKDTPEGAELEKPMY 114  
 RESULT 9  
 AAR60244  
 ID AAR60244 standard; peptide; 156 AA.  
 XX  
 AC AAR60244;  
 XX  
 DT 16-MAR-1995 (first entry)  
 XX  
 DE Mouse-alpha.  
 XX  
 XX TNF-alpha; tumor necrosis factor-alpha; tip peptide; mutein; cancer;  
 KW sepsis; inflammation; cytokine; metastasis; lectin; adhesion;  
 KW mutagenesis.  
 XX  
 OS Mus sp.  
 XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 1.8 "in TNF muteins, residues 1-8 are replaced  
 FT by a peptide within the region spanning  
 FT aa 5-30 of laminin"  
 FT  
 FT Misc-difference 100  
 FT /note= "in TNF muteins, residue 100 is Ser"  
 FT  
 FT Misc-difference 101  
 FT /note= "in TNF muteins, residue 101 is Arg or  
 FT deleted"  
 FT  
 FT Misc-difference 102  
 FT /note= "in TNF muteins, residue 102 is Trp"  
 FT  
 FT Misc-difference 104  
 FT /note= "in TNF muteins, residue 104 is Pro or Ile  
 FT or residue 104 is Ile and residue 44 is Cys"  
 FT  
 FT Misc-difference 105  
 FT /note= "in TNF muteins, residue 105 is Ser, or  
 FT residue 105 is Ser and residue 130 is Cys"  
 FT  
 FT Misc-difference 107  
 FT /note= "in TNF muteins, residue 107 is Phe"

FT Misc-difference 109  
 FT /note= "in TNF muteins, residue 109 is Lys"  
 FT  
 FT Misc-difference 110..111  
 FT /note= "in TNF muteins, residues 110-111 are  
 FT deleted, or residue 110 is deleted  
 FT or Met, or residue 110 is deleted and  
 FT residue 108 is Gln and residue 119 is His"  
 FT  
 FT Misc-difference 114  
 FT /note= "in TNF muteins, residue 114 is Ile or Cys"  
 FT  
 FT Misc-difference 115  
 FT /note= "in TNF muteins, residue 115 is Lys, His or  
 FT Val"  
 FT  
 FT Misc-difference 114..115  
 FT /note= "in TNF muteins, residues 114-115 are  
 FT Ile-Lys"  
 FT  
 FT  
 FT W09418325-A.  
 PD  
 XX 18-AUG-1994.  
 PD  
 XX  
 PD 02-FEB-1994; 94WO-EP00286.  
 PE  
 XX 03-FEB-1993; 93EP-0400262.  
 PR  
 XX (INNO-) INNOGENETICS NV SA.  
 PA  
 XX  
 XX De Baetselier P, Franssen L, Lucas R, Sablon E;  
 PI  
 XX WPI: 1994-279746/34.  
 DR  
 XX New tumour necrosis factor -alpha muteins, antibodies and  
 PT antisense peptide(s) - used in the treatment of diseases and  
 PT conditions associated with the in vivo activities of TNF-A eg  
 PT cancer, sepsis, inflammation, etc  
 XX  
 XX Disclosure; Page 10; 132pp; English.  
 PS  
 XX  
 XX TNF-alpha muteins were constructed in the tip region (given in  
 CC AAR60231) of mouse TNF-alpha. The mutations resulted in:  
 CC modulation of lectin-like activity; reduced toxic activity;  
 CC induction capacity; reduced metastasis promoting activity; and/or  
 CC increased half-life. Muteins of the human TNF (given in AAR60243)  
 CC were also produced.  
 CC  
 XX  
 SQ Sequence 156 AA:  
 Query Match 100.0%; Score 84; DB 15; Length 156;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-05;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 PKDTPEGAELEKPMY 14  
 DB 101 PKDTPEGAELEKPMY 114  
 RESULT 10  
 AAP60527  
 ID AAP60527 standard; Protein; 157 AA.  
 XX  
 AC AAP60527;  
 XX  
 DT 07-AUG-1991 (first entry)  
 XX  
 DE Sequence of tumour necrosis factor (TNF).  
 XX  
 XX Anticancer agent; antitumour; antimalarial; tumour necrosis factor.  
 KW  
 XX W08603751-A.  
 PN  
 XX 03-JUL-1986.  
 PD  
 XX 19-DEC-1985; 85WO-EP00721.

```

XX 09-OCT-1985; 85US-0785847.
PR 21-DEC-1984; 84US-0684595.
PR 09-OCT-1986; 86WO-US02133.
XX
PA (BIOJ ) BIOGEN NV.
PA (FIER/) FIERIS W C.
PA (ALLE/) ALLET B.
PA (BIOG-) BIOGEN INC.
XX
PI Fiers MC, Franssen LM, Tavernier JHL, Marmenout ALM;
PI Vanderheyden J, Allet B, Washima EH;
XX
DR WPI: 1986-182891/28.
DR N-PSDB: AAN60439.
XX
PT Mammalian tumour necrosis factors - produced by culturing
PT pro-karyotic hosts transformed with recombinant DNA
XX
PS Claim 12; Page 67; 93pp; English.
XX
CC TNF-like polypeptides and compsns. are produced by the fermentation
CC of host cells transformed with at least one DNA sequence which codes
CC for a mammalian TNF-like polypeptide operatively linked to an
CC expression control sequence in the transformed host.
XX
SQ Sequence 157 AA:

Query Match 100.0%; Score 84; DB 7; Length 157;
Best Local Similarity 100.0%; Pred. No. 1.4e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKDTPGAGELKPMY 14
DB 102 PKDTPGAGELKPMY 115

RESULT 11
AAR38077
ID AAR38077 standard; protein; 157 AA.
XX
AC AAR38077;
XX
DT 14-OCT-1993 (first entry)
XX
DE Non-human TNF-alpha.
XX
KW Withdrawal symptom; tumour necrosis factor; narcotic; nicotine;
KW morphine; thymosin; alcohol.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 73 /note="residue not labelled in specification"
XX
PN JP05117161-A.
XX
PD 14-MAY-1993.
XX
PE 23-OCT-1991; 91JP-0337489.
XX
PR 23-OCT-1991; 91JP-0337489.
XX
PA (MIZU/) MIZUNO D.
PA (SOMA/) SOMA G.
XX
DR WPI: 1993-191442/24.
XX
PT Drugs for treating alcohol, morphine narcotics or nicotine
PT withdrawal symptoms - contg. tumour necrosis factor-alpha,
PT thymosin tumour necrosis factor fused cpd. or murine tumour
PT necrosis factor-alpha prepd. from macrophage of human or animal

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XX XX
PS Disclosure; Page 2-3; 5pp; Japanese.
XX
CC Drugs acting on withdrawal symptoms contain TNF, esp. TNF-alpha
CC (AAR38069 and AAR38077), TNF-S-AM1 (AAR38070), TNF-S-AM2 (AAR38071),
CC thymosin-beta4-TNF fused cpd. (AAR38072-76).
CC The drugs are effective in treatment of withdrawal symptoms caused
CC by habitual use of alcohol, morphine narcotics or nicotine in humans
CC or animals (e.g. swine, dog, cat, chicken). The drugs may be
CC administered as TNF at a dose of 10ng-10mg orally or 5ng-1mg i.v.
CC or 50ng-50mg percutaneously a day for a human adult. In animals,
CC the drugs may be administered according to the human dosage (1/60
CC per kg body wt.).
XX
SQ Sequence 157 AA:

Query Match 100.0%; Score 84; DB 14; Length 157;
Best Local Similarity 100.0%; Pred. No. 1.4e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKDTPGAGELKPMY 14
DB 102 PKDTPGAGELKPMY 115

RESULT 12
AAP70558
ID AAP70558 standard; protein; 170 AA.
XX
AC AAP70558;
XX
DT 26-FEB-1991 (first entry)
XX
DE Tumour necrosis factor.
XX
KW TNF; antitumor.
XX
KM JP62135493-A.
XX
PN 18-JUN-1987.
XX
PD 06-DEC-1985; 85JP-0275392.
XX
PE 06-DEC-1985; 85JP-0275392.
XX
PR 06-DEC-1985; 85JP-0275392.
XX
PA (TANA ) TANABE SEIYAKU KK.
XX
DR WPI: 1987-209318/30.
DR N-PSDB: AAN70891.
XX
PT Anticancer factor - expressed by specified amino acid sequence.
XX
PS Disclosure; Page 12; 12pp; Japanese.
XX
CC The sequence encodes tumor necrosis factor which is an antitumor
CC agent and a lymphokine. This sequence is the same as that in
CC AAP70557 but has 16 extra amino acids at the N-terminal.
XX
SQ Sequence 170 AA:

Query Match 100.0%; Score 84; DB 8; Length 170;
Best Local Similarity 100.0%; Pred. No. 1.5e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKDTPGAGELKPMY 14
DB 115 PKDTPGAGELKPMY 128

RESULT 13
AAP90424
ID AAP90424 standard; protein; 233 AA.
XX

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AC AAP90424;
XX
DT 01-NOV-1989 (first entry)
XX
DE Human tumour necrosis factor.
XX
KW Tumour necrosis factor; mouse; DNA; exons; introns;
XX carcinostatic mechanism; expression vector.
XX
OS Murine (Mouse).
XX
PN JP01137976-A.
XX
PD 24-MAY-1989.
XX
PF 20-NOV-1987; 87JP-0291841.
XX
PR 20-NOV-1987; 87JP-0291841.
XX
PA (ASAH ) ASAH1 CHEMICAL IND KK.
XX
DR WPI; 1989-198221/27.
XX
DR N-PSDB; AAN90229.
XX
PT DNA fragment contg. mouse TNF-coding chromosomal gene
PT - contains exon and intron and about 800 bases in the
PT 5'-terminal adjacent to the exon.
XX
PS Claim 1; fig 2; 8bp; Japanese.
XX
CC Tumour necrosis factor of mouse, obtd. after
CC intron splicing (see AAN90229). Used to study carcinostatic
CC mechanism of TNF, and the promoter can be used in an expression
CC vector.
XX
SQ Sequence 233 AA;

Query Match 100.0%; Score 84; DB 10; Length 233;
Best Local Similarity 100.0%; Pred. No. 2.1e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PKDTPGAEELKPMY 14
   .|||||
Db 178 PKDTPGAEELKPMY 191

RESULT 14
AAP60530
ID AAP60530 standard; protein; 235 AA.
XX
AC AAP60530;
XX
DT 07-AUG-1991 (first entry)
XX
DE Sequence of tumour necrosis factor (TNF).
XX
KW Anticancer agent; antitumour; antimalarial; tumour necrosis factor.
XX
OS Mus musculus.
XX
PN W08603751-A.
XX
PD 03-JUL-1986.
XX
PF 19-DEC-1985; 85WO-EP00721.
XX
PR 09-OCT-1985; 85US-0785847.
PR 21-DEC-1984; 84US-0684595.
PR 09-OCT-1986; 86WO-US02133.
XX
PA (BIOJ ) BIOGEN NV.
PA (FIER/) FIERIS W C.
PA (ALLE/) ALLET B.

```

```

PA (BIOC-) BIOGEN INC.
XX
PI Fiers WC, Franssen LM, Tavernier JHL, Marmenout ALM;
XX VanderHeyden J, Allet B, Washima EH;
XX
DR WPI; 1986-182891/28.
XX
DR N-PSDB; AAN60445.
XX
PT Mammalian tumour necrosis factors - produced by culturing
PT pro-karyotic hosts transformed with recombinant DNA
XX
PS Example; Fig 7; 93pp; English.
XX
CC TNF-like polypeptides and compns. are produced by the fermentation
CC of host cells transformed with at least one DNA sequence which codes
CC for a mammalian TNF-like polypeptide operatively linked to an
CC expression control sequence in the transformed host.
XX
SQ Sequence 235 AA;

Query Match 100.0%; Score 84; DB 7; Length 235;
Best Local Similarity 100.0%; Pred. No. 2.1e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PKDTPGAEELKPMY 14
   .|||||
Db 180 PKDTPGAEELKPMY 193

RESULT 15
AAR05328
ID AAR05328 standard; protein; 235 AA.
XX
AC AAR05328;
XX
DT 03-DEC-1990 (first entry)
XX
DE Rat tumour necrosis factor (TNF) gene product.
XX
KW Tumour necrosis factor; TNF; antineoplastic; cancer; ds.
XX
OS Rattus sp.
XX
PN JP02157295-A.
XX
PD 18-JUN-1990.
XX
PF 07-DEC-1988; 88JP-0307751.
XX
PR 07-DEC-1988; 88JP-0307751.
XX
PA (ASAH ) ASAH1 CHEMICAL IND KK.
XX
DR WPI; 1990-228715/30.
DR N-PSDB; AAO05328.
XX
PT Novel anti-oncotic polypeptide - prepd. by culturing microbe
PT contg. DNA.
XX
PS Disclosure; ; Japanese.
XX
CC Fragment of gene product (AAs 80-235) is claimed as an antineoplastic
CC peptide, produced from a transformed microorganism expression
CC system.
XX
SQ Sequence 235 AA;

Query Match 100.0%; Score 84; DB 11; Length 235;
Best Local Similarity 100.0%; Pred. No. 2.1e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PKDTPGAEELKPMY 14
   .|||||

```

DB 180 PKDTPEGALIKPMY 193

Search completed: April 4, 2003, 08:39:55  
Job time : 26.9677 secs

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GenCore version 5.1.4-p5\_4578  
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OM protein - protein search, using sw model

Run on: April 4, 2003, 08:37:36 ; Search time 10.1613 seconds  
(Without alignments) 132.452 Million cell updates/sec

Title: US-09-779-703-2

Perfect score: 84

Sequence: 1 PKDREGARLKPMY 14

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	84	100.0	235	1 QWMSN	tumor necrosis fac
2	84	100.0	235	2 JUV0029	tumor necrosis fac
3	77	91.7	235	1 I34490	tumor necrosis fac
4	65	77.4	232	1 S12606	tumor necrosis fac
5	65	77.4	233	1 QMHUN	tumor necrosis fac
6	65	77.4	233	1 S22052	tumor necrosis fac
7	65	77.4	233	2 S11688	tumor necrosis fac
8	57	67.9	185	2 S52715	tumor necrosis fac
9	57	67.9	233	1 S24642	tumor necrosis fac
10	55	65.5	234	1 JH0529	tumor necrosis fac
11	51	60.7	234	1 J01344	tumor necrosis fac
12	50	59.5	289	2 AH0060	tumor necrosis fac
13	48.5	57.7	193	2 S06192	bis(5'-nucleosyl)-
14	48	57.1	1649	2 S06192	tumor necrosis fac
15	47	56.0	1236	2 C86822	hypothetical prote
16	47	56.0	1239	1 VHWVEE	structural polype
17	47	56.0	1240	1 VHWVEE	structural polype
18	47	56.0	1241	2 S26373	genome polype
19	47	56.0	1242	2 S27350	structural polype
20	47	56.0	1242	2 A56605	structural polype
21	46.5	55.4	543	2 G96570	hypothetical prote
22	46	54.8	711	2 F75440	methylnalonyl-CoA
23	45	53.6	258	2 S75950	hypothetical prote
24	45	53.6	469	2 T48783	related to SGT1 pr
25	45	53.6	684	1 TVHUSN	transforming prote
26	45	53.6	713	2 G98286	methylnalonyl-CoA
27	45	53.6	713	2 AB2997	methylnalonyl-CoA
28	43	51.2	259	1 B42379	bis(5'-nucleosyl)-
29	43	51.2	748	1 S08680	methylnalonyl-CoA

30	43	51.2	750	1 A59145	methylnalonyl-CoA
31	42.5	50.6	1166	2 T27075	hypothetical prote
32	42	50.0	157	2 C75326	hypothetical prote
33	42	50.0	641	2 A71163	hypothetical prote
34	42	50.0	712	2 A96023	probable methylnal
35	42	50.0	730	2 A13351	methylnalonyl-CoA
36	42	50.0	739	2 H75001	methylnalonyl-CoA
37	42	50.0	739	2 F71161	probable chemotaxi
38	41	48.8	142	2 A47159	membrane-bound mul
39	41	48.8	234	1 A25451	tumor necrosis fac
40	41	48.8	244	1 S33819	secretory prote
41	41	48.8	253	2 S33820	secretory prote
42	41	48.8	455	2 S39663	aminopeptidase hom
43	41	48.8	566	2 T46219	hypothetical prote
44	41	48.8	604	2 T45627	replication factor
45	41	48.8	630	2 T03582	probable replicati

#### ALIGNMENTS

##### RESULT 1

QWMSN  
tumor necrosis factor alpha precursor - mouse

N:Alternate names: cachectin; TNF alpha  
C:Species: Mus musculus (house mouse)

C>Date: 31-Mar-1988 #sequence-revision 31-Mar-1988 #text-change 04-Feb-2000  
C/Accession: A22908; S03791; A27303; A25164; A23127; A34251; I59058; A36696

R:Shirai, T.; Shimizu, N.; Shiojiri, S.; Horiguchi, S.; Ito, H.  
DNA 7, 193-201, 1988

A:Title: Cloning and expression in Escherichia coli of the gene for mouse tumor necro  
A:Reference number: A22908; MUID:88224564; PMID:2836146

A:Accession: A22908  
A:Molecule type: DNA

A:Residues: 1-235 <SH1>  
A:Cross-references: GB:M20155

R:Shakhov, A.N.; Nedospasov, S.A.  
Bioorg. Khim. 13, 701-705, 1987

A:Title: Molecular cloning of the genes coding for tumor necrosis factors: complete n  
A:Reference number: S03791; MUID:87298639; PMID:3040015

A:Accession: S03791  
A:Molecule type: DNA

A:Residues: 1-235 <SHA>  
A:Cross-references: GB:M38296; NID:g202086; PIDN:AAA0459.1; PID:g202087

A:Note: article in Russian with English abstract  
R:Semon, D.; Kawashima, E.; Jongeneel, C.V.; Shakhov, A.N.; Nedospasov, S.A.  
Nucleic Acids Res. 15, 9083-9084, 1987

A:Title: Nucleotide sequence of the murine TNF locus, including the TNF-alpha (tumor  
A:Reference number: A93679; MUID:88067722; PMID:3684584

A:Accession: A27303  
A:Molecule type: DNA

A:Residues: 1-235 <SEM>  
A:Cross-references: GB:Y00467; NID:g54830; PIDN:CAA68530.1; PID:g54832

R:Pennica, D.; Hayflick, J.S.; Brindman, T.S.; Palladino, M.A.; Goeddel, D.V.  
Proc. Natl. Acad. Sci. U.S.A. 82, 6060-6064, 1985

A:Title: Cloning and expression in Escherichia coli of the cDNA for murine tumor necr  
A:Reference number: A25164; MUID:85298296; PMID:3898078

A:Accession: A25164  
A:Molecule type: mRNA

A:Residues: 1-235 <PEN>  
A:Cross-references: GB:M11731; NID:g202084; PIDN:AAA0458.1; PID:g202085

R:Fransen, L.; Muller, R.; Marmenout, A.; Tavernier, J.; van der Heyden, J.; Kawashim  
Nucleic Acids Res. 13, 4417-4429, 1985

A:Title: Molecular cloning of mouse tumour necrosis factor cDNA and its eukaryotic ex  
A:Reference number: A23127; MUID:85242112; PMID:2969794

A:Accession: A23127  
A:Molecule type: mRNA

A:Residues: 1-235 <FRA>  
A:Cross-references: GB:X02611; NID:g54844; PIDN:CAA26457.1; PID:g54845

R:Geis, K.; Beutler, B.  
J. Biol. Chem. 264, 16256-16260, 1989

A:Title: Alternative cleavage of the cachectin/tumor necrosis factor propeptide resul  
A:Reference number: A34251; MUID:89380231; PMID:2777790



A:Accession: A34251  
 A:Molecule type: protein  
 A:Residues: 70-87 <CSE>  
 R:Capit, D.; Beutler, B.; Hartog, K.; Thayer, R.; Brown-Shiner, S.L.; Cerami, A.  
 Proc. Natl. Acad. Sci. U.S.A. 83, 1670-1674, 1986  
 A>Title: Identification of a common nucleotide sequence in the 3'-untranslated region of  
 A:Reference number: 159058; MUID:86149365; PMID:2419912  
 A:Accession: 159058  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-230, 'R', 232-235 <RES>  
 A:Cross-references: GB:M13049; NID:9202082; PIDN:AAA40457.1; PID:g202083  
 R:Sherry, B.; Jue, D.M.; Zentella, A.; Cerami, A.  
 Biochem. Biophys. Res. Commun. 173, 1072-1078, 1990  
 A>Title: Characterization of high molecular weight glycosylated forms of murine tumor ne  
 A:Reference number: A36696; MUID:91097531; PMID:2268312  
 A:Accession: A36696  
 A:Molecule type: protein  
 A:Residues: 80-85, 'X', 87-99 <SHE>  
 C:Genetics:  
 A:Note: the first intron occurs in the 5'-untranslated region  
 C:Superfamily: tumor necrosis factor  
 C:Keywords: cytokine; cytotoxin; glycoprotein; lipoprotein; lymphokine; macrophage; mem  
 F:80-235/Product: tumor necrosis factor #status experimental <MAT>  
 F:20/Binding site: myristate (Lys) (covalent) #status predicted  
 F:84/Binding site: carbohydrate (Ser) (covalent) #status predicted  
 F:86/Binding site: carbohydrate (Asn) (covalent) #status predicted  
 F:148-179/Disulfide bonds: #status predicted

Query Match 100.0%; Score 84; DB 1; Length 235;  
 Best Local Similarity 100.0%; Pred. No. 4, 8e-06;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PKDTPGAELEKPMY 14  
 |||||  
 Db 180 PKDTPGAELEKPMY 193

RESULT 2  
 J00029  
 tumor necrosis factor alpha precursor - rat  
 N:Alternate names: cachectin; TNF alpha  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 07-Jun-1990 #sequence, revision 07-Jun-1990 #text\_change 04-Feb-2000  
 C:Accession: J00029; JN0868; S21674  
 R:Shirai, T.; Shimizu, N.; Horiguchi, S.; Ito, H.  
 Agric. Biol. Chem. 53, 1733-1736, 1989  
 A>Title: Cloning and expression in Escherichia coli of the gene for rat tumor necrosis f  
 A:Reference number: J00029  
 A:Accession: J00029  
 A:Molecule type: DNA  
 A:Residues: 1-235 <SHI>  
 R:Kwon, J.; Chung, I.Y.; Benveniste, E.N.  
 Gene 132, 227-236, 1993  
 A>Title: Cloning and sequence analysis of the rat tumor necrosis factor-encoding genes.  
 A:Reference number: JN0868; MUID:94040766; PMID:8224868  
 A:Accession: JN0868  
 A:Molecule type: DNA  
 A:Residues: 1-235 <KMO>  
 A:Cross-references: GB:I00981; NID:9205253; PIDN:AAA16275.1; PID:g205254  
 R:Estler, H.C.; Grove, M.; Gaussling, R.; Pavlovic, M.; Decker, K.  
 Biol. Chem. Hoppe-Seyler 373, 271-281, 1992  
 A>Title: Rat tumor necrosis factor-alpha. Transcription in rat Kupffer cells and in vit  
 A:Reference number: S21674; MUID:92329007; PMID:1627266  
 A:Accession: S21674  
 A:Molecule type: mRNA  
 A:Residues: 1-38, 'P', 40-162, 'T', 164-201, 'S', 203-235 <EST>  
 A:Cross-references: GB:X6553; GB:S40199; NID:9395366; PIDN:CAA47146.1; PID:g395370  
 C:Comment: Tumor necrosis factor is secreted by macrophages in response to endotoxin and  
 A:Gene: TNF-alpha  
 A:Introns: 62/3; 81/1; 97/1

C:Superfamily: tumor necrosis factor  
 C:Keywords: cytokine; cytotoxin; glycoprotein; lipoprotein; lymphokine; macrophage; m  
 F:80-235/Product: tumor necrosis factor #status predicted <MAT>  
 F:19-20/Binding site: myristate (Lys) (covalent) #status predicted  
 F:84/Binding site: carbohydrate (Ser) (covalent) #status predicted  
 F:86/Binding site: carbohydrate (Asn) (covalent) #status predicted  
 F:148-179/Disulfide bonds: #status predicted

Query Match 100.0%; Score 84; DB 2; Length 235;  
 Best Local Similarity 100.0%; Pred. No. 4, 8e-06;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PKDTPGAELEKPMY 14  
 |||||  
 Db 180 PKDTPGAELEKPMY 193

RESULT 3  
 I54490  
 tumor necrosis factor alpha precursor - white-footed mouse  
 C:Species: Peromyscus leucopus (white-footed mouse)  
 C:Date: 02-Aug-1996 #sequence, revision 02-Aug-1996 #text\_change 04-Feb-2000  
 C:Accession: I54490  
 R:Crew, M.D.; Filipowsky, M.E.  
 Immunogenetics 35, 351-353, 1992  
 A>Title: Sequence of the tumor necrosis factor/cachectin (TNF) gene from Peromyscus 1  
 A:Reference number: I54490; MUID:92218012; PMID:1348497  
 A:Accession: I54490  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-235 <RES>  
 A:Cross-references: GB:M59233; NID:9202506; PIDN:AAA40596.1; PID:g202507  
 C:Genetics:  
 A:Gene: P1NF  
 A:Introns: 62/3; 81/1; 97/1  
 C:Superfamily: tumor necrosis factor  
 C:Keywords: glycoprotein; lipoprotein; myristylation  
 F:19-20/Binding site: myristate (Lys) (covalent) #status predicted  
 F:84/Binding site: carbohydrate (Ser) (covalent) #status predicted

Query Match 91.7%; Score 77; DB 2; Length 235;  
 Best Local Similarity 85.7%; Pred. No. 6, 5e-05;  
 Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 PKDTPGAELEKPMY 14  
 |||||  
 Db 180 PKDTPGAELEKPMY 193

RESULT 4  
 S12606  
 tumor necrosis factor alpha precursor - pig  
 C:Species: Sus scrofa domestica (domestic pig)  
 C:Date: 10-Sep-1999 #sequence, revision 10-Sep-1999 #text\_change 04-Feb-2000  
 C:Accession: S12606; S17290; S18965; I46659  
 R:Dress, R.T.; Coffee, B.W.; Prestwood, A.K.; McGraw, R.A.  
 Nucleic Acids Res. 18, 5564, 1990  
 A>Title: Gene sequence of porcine tumor necrosis factor alpha.  
 A:Reference number: S12606; MUID:91016861; PMID:2216741  
 A:Accession: S12606  
 A:Molecule type: DNA  
 A:Residues: 1-232 <RES>  
 A:Cross-references: EMBL:X54001; NID:92135; PIDN:CAA37949.1; PID:g2136  
 R:Kuhmert, P.; Wietrich, C.; Peterhans, E.; Pauli, U.  
 Gene 102, 171-178, 1991  
 A>Title: The porcine tumor necrosis factor-encoding genes: sequence and comparative a  
 A:Reference number: S17290; MUID:91340150; PMID:1874444  
 A:Accession: S17290  
 A:Molecule type: DNA  
 A:Residues: 1-232 <RUH>  
 A:Cross-references: EMBL:X54859; NID:92132; PIDN:CAA38639.1; PID:g2134  
 A:Note: the authors translated the codon GAG for residue 202 as Gly  
 R:Choi, C.S.; Mollitor, T.W.; Lin, G.F.; Murtough, M.P.

## Submitted to the EMBL Data Library, January 1991

A:Description: Complete nucleotide sequence of a cDNA encoding porcine tumor necrosis factor  
 A:Reference number: S18965  
 A:Accession: S18965  
 A:Molecule type: mRNA  
 A:Residues: 1-232 <CHO>  
 A:Cross-references: EMBL:X57321; NID:g2137; PIDN:CAA0591.1; PID:g2138  
 R:Pauli, U.; Beutler, B.; Peterhans, E.  
 Gene 81, 185-191, 1989  
 A:Title: Porcine tumor necrosis factor alpha: Cloning with the polymerase chain reaction  
 A:Reference number: 146659; MUID:90034181; PMID:2478420  
 A:Accession: 146659  
 A:Status: Preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 44-232 <PNU>  
 A:Cross-references: GB:M29079; NID:g146494; PIDN:AAA31128.1; PID:g146495  
 C:Genetics:  
 A:Introns: 62/3; 78/1; 93/1  
 C:Superfamily: tumor necrosis factor  
 C:Keywords: cytokine; cytotoxin; glycoprotein; lipoprotein; lymphokine; macrophage; myel  
 F:1-77/Domain: propeptide #status predicted <PRO>  
 F:78-232/Product: tumor necrosis factor alpha #status predicted <MAT>  
 F:19,20/Binding site: myristate (lys) (covalent) #status predicted  
 F:81/Binding site: carbonyl (Ser) (covalent) #status predicted  
 F:144-176/Disulfide bonds: #status predicted

Query Match 77.4%; Score 65; DB 1; Length 232;  
 Best Local Similarity 76.9%; Pred. No. 0.0056; Mismatches 1; Indels 0; Gaps 0;  
 Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 2 KDTPEGAELKPMY 14  
 Db 178 RETPEGAELKPMY 190  
 ::|||||  
 OY 2 KDTPEGAELKPMY 14  
 Db 178 RETPEGAELKPMY 190

RESULT 5  
 OMHUN  
 tumor necrosis factor alpha precursor [validated] - human  
 N:Alternate names: cachectin; TNFA  
 C:Species: Homo sapiens (man)  
 C:Date: 28-Aug-1985 #sequence\_revision 28-Aug-1985 #text\_change 08-Dec-2000  
 C:Accession: A93585; S36153; A93351; A44189; B61478; I53311; S62610; I54522; A01646; B23  
 R:Nedwin, G.E.; Naylor, S.L.; Sakaguchi, A.Y.; Smith, D.; Jarrett-Nedwin, J.; Pennica, D.  
 Nucleic Acids Res. 13, 6361-6373, 1985  
 A:Title: Human lymphokinin and tumor necrosis factor genes: structure, homology and chro  
 A:Reference number: A93585; MUID:86016093; PMID:2959527  
 A:Accession: A93585  
 A:Molecule type: DNA  
 A:Residues: 1-233 <NED>  
 A:Cross-references: GB:X02910; GB:X02159; NID:g37209; PIDN:CAA26669.1; PID:g37210  
 R:Rits, F.J.M.; Bougueret, L.; Prieur, S.; Caterina, D.; Primas, G.; Petro, V.; Jurka  
 Nature Genet. 3, 137-145, 1993  
 A:Title: Dense Alu clustering and a potential new member of the NFkappaB family within a  
 A:Reference number: S36153; MUID:93272029; PMID:849947  
 A:Accession: S36153  
 A:Status: nucleic acid sequence not shown; translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-233 <IRI>  
 A:Cross-references: EMBL:Z15026; NID:g37211; PIDN:CAA78745.1; PID:g37212  
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1992  
 R:Pennica, D.; Nedwin, G.E.; Hayflick, J.S.; Seeburg, P.H.; Derynck, R.; Palladino, M.A.  
 Nature 312, 724-729, 1984  
 A:Title: Human tumor necrosis factor: precursor structure, expression and homology to I  
 A:Reference number: A93351; MUID:85086244; PMID:6392892  
 A:Accession: A93351  
 A:Molecule type: mRNA  
 A:Residues: 1-233 <PEN>  
 A:Cross-references: GB:X02910; GB:X02159; NID:g37209; PIDN:CAA26669.1; PID:g37210  
 A:Note: this protein was isolated from the monocyte-like cell line HL-60 from a promyeloc  
 R:Wang, A.M.; Cresssey, A.A.; Lahner, M.B.; Lin, L.S.; Strickler, J.; Van Arsdell, J.N.;  
 Science 228, 149-154, 1985  
 A:Title: Molecular cloning of the complementary DNA for human tumor necrosis factor.  
 A:Reference number: A44189; MUID:85142190; PMID:3856324

A:Accession: A44189  
 A:Molecule type: mRNA  
 A:Residues: 1-62, 'S', 64-233 <MAN>  
 A:Cross-references: GB:M10968; NID:g339737; PIDN:AAA61198.1; PID:g339738  
 R:Fukuda, S.; Ando, S.; Sanou, O.; Tanai, M.; Fujii, M.; Masaki, N.; Nakamura, K.I.;  
 Lymphokine Res. 7, 175-185, 1988  
 A:Title: Simultaneous production of natural human tumor necrosis factor-alpha, -beta  
 A:Reference number: A61478; MUID:88301617; PMID:2841543  
 A:Accession: B61478  
 A:Molecule type: protein  
 A:Residues: 83-102;109-119;121-128, 'X', 130-131;142-144, 'X', 146, 'XXX', 150-152;159-174;  
 R:Marmenout, A.; Fransen, L.; Taverrier, J.; Van Der Heyden, J.; Tizard, R.; Kawashim  
 Eur. J. Biochem. 152, 515-522, 1985  
 A:Title: Molecular cloning and expression of human tumor necrosis factor and comparis  
 A:Reference number: I53311; MUID:86030296; PMID:3393069  
 A:Accession: I53311  
 A:Status: translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-233 <MAR>  
 A:Cross-references: GB:M26331; NID:g339763; PIDN:AAA36758.1; PID:g339764  
 A:Experimental source: U-937 cells  
 R:Takakura-Yamamoto, R.; Yamamoto, S.; Fukuda, S.; Kurimoto, M.  
 Eur. J. Biochem. 235, 431-437, 1996  
 A:Title: O-Glycosylated species of natural human tumor necrosis factor-alpha.  
 A:Reference number: S62610; MUID:96202967; PMID:8631363  
 A:Accession: S62610  
 A:Molecule type: protein  
 A:Residues: 77-99 <TRAK>  
 R:D'Alfonso, S.; Richiardi, P.M.  
 Immunogenetics 39, 150-154, 1994  
 A:Title: A polymorphic variation in a putative regulation box of the TNFA promoter re  
 A:Reference number: I54522; MUID:94102809; PMID:7903959  
 A:Accession: I54522  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-8 <DAD>  
 A:Cross-references: GB:S68530; NID:g544751  
 R:Stevenson, F.T.; Bursten, S.L.; Locksley, R.M.; Lovett, D.H.  
 J. Exp. Med. 176, 1053-1062, 1992  
 A:Title: Myristyl acylation of the tumor necrosis factor alpha precursor on specific  
 A:Reference number: A59163; MUID:93018820; PMID:1402651  
 A:Contents: annotation; identification of myristylated lysines  
 R:Aggarwal, B.B.; Kohr, M.J.; Hass, P.E.; Moffat, B.; Spencer, S.A.; Henzel, W.J.; Br  
 J. Biol. Chem. 260, 2345-2354, 1985  
 A:Title: Human tumor necrosis factor. Production, purification, and characterization.  
 A:Reference number: A92511; MUID:85130974; PMID:3871770  
 A:Contents: annotation; disulfide bond  
 C:Comment: Secreted from mitogen-activated macrophages within 4-24 hours after induc  
 out detriment to normal cells. It can also act synergistically with interferon gamma  
 C:Comment: TNF-alpha and -beta (lymphotoxin) are the products of different genes clos  
 ut are produced by different cell types and have different induction kinetics.  
 C:Genetics:  
 A:Gene: GDB:TNF; TNFA  
 A:Cross-references: GDB:120441; OMIM:191160  
 A:Map position: 6p21.3-6p21.3  
 A:Introns: 62/3; 78/1; 94/1  
 C:Complex: homotrimer  
 C:Superfamily: tumor necrosis factor  
 C:Keywords: cytokine; cytotoxin; glycoprotein; homotrimer; lipoprotein; lymphokine; m  
 F:1-76/Domain: propeptide #status predicted <PRO>  
 F:77-233/Product: tumor necrosis factor #status experimental <MAT>  
 F:19,20/Binding site: myristate (lys) (covalent) #status experimental  
 F:81/Binding site: carbonyl (Ser) (covalent) (partial) #status experimental  
 F:145-177/Disulfide bonds: #status experimental

Query Match 77.4%; Score 65; DB 1; Length 233;  
 Best Local Similarity 76.9%; Pred. No. 0.0056; Mismatches 1; Indels 0; Gaps 0;  
 Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 2 KDTPEGAELKPMY 14  
 Db 179 RETPEGAELKPMY 191  
 ::|||||  
 OY 2 KDTPEGAELKPMY 14  
 Db 179 RETPEGAELKPMY 191

## RESULT 6

S22052

tumor necrosis factor alpha precursor - baboon

C:Species: Papio sp. (baboon)

C&gt;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 04-Feb-2000

C:Accession: S22052

C:Sanjwal, M.; Edwards, A.

submitted to the EMBL Data Library, September 1991

A:Description: Baboon Tumor Necrosis Factor Derived from Sequences of Genomic DNA.

A:Reference number: S22052

A:Accession: S22052

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-233 &lt;SAS&gt;

A:Cross-references: EMBL:X62141; NID:g38159; PIDN:CAA44068.1; PID:g38160

C:Genetics:

A:Introns: 62/3; 78/1; 94/1

C:Superfamily: tumor necrosis factor

C:Keywords: glycoprotein; lipoprotein; myristylation; transmembrane protein

F:19,20/Binding site: myristate (Lys) (covalent) #status predicted

F:81/Binding site: carbohydrate (Ser) (covalent) #status predicted

F:145-177/Disulfide bonds: #status predicted

F:145-177/Disulfide bonds: #status predicted

F:145-177/Disulfide bonds: #status predicted

F:145-177/Disulfide bonds: #status predicted

F:145-177/Disulfide bonds: #status predicted

F:145-177/Disulfide bonds: #status predicted

F:145-177/Disulfide bonds: #status predicted

F:145-177/Disulfide bonds: #status predicted

F:145-177/Disulfide bonds: #status predicted

F:145-177/Disulfide bonds: #status predicted

F:145-177/Disulfide bonds: #status predicted

F:145-177/Disulfide bonds: #status predicted

F:145-177/Disulfide bonds: #status predicted

F:145-177/Disulfide bonds: #status predicted

F:145-177/Disulfide bonds: #status predicted

F:145-177/Disulfide bonds: #status predicted

F:145-177/Disulfide bonds: #status predicted

F:145-177/Disulfide bonds: #status predicted

F:145-177/Disulfide bonds: #status predicted

F:145-177/Disulfide bonds: #status predicted

F:145-177/Disulfide bonds: #status predicted

F:145-177/Disulfide bonds: #status predicted

F:145-177/Disulfide bonds: #status predicted

F:145-177/Disulfide bonds: #status predicted

F:145-177/Disulfide bonds: #status predicted

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F:145-177/Disulfide bonds: #status predicted

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F:145-177/Disulfide bonds: #status predicted

F:145-177/Disulfide bonds: #status predicted

F:145-177/Disulfide bonds: #status predicted

F:145-177/Disulfide bonds: #status predicted

F:145-177/Disulfide bonds: #status predicted

F:145-177/Disulfide bonds: #status predicted

F:145-177/Disulfide bonds: #status predicted

F:145-177/Disulfide bonds: #status predicted

F:145-177/Disulfide bonds: #status predicted

A:Description: Cloning and sequence analysis of cDNAs encoding bovine CD40 ligand and

A:Reference number: S52715

A:Accession: S52715

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-185 &lt;MER&gt;

A:Cross-references: EMBL:Z48808; NID:g755701; PIDN:CAA88743.1; PID:g755702

C:Superfamily: tumor necrosis factor

C:Keywords: glycoprotein

F:33/Binding site: carbohydrate (Ser) (covalent) #status predicted

F:97-129/Disulfide bonds: #status predicted

F:97-129/Disulfide bonds: #status predicted

F:97-129/Disulfide bonds: #status predicted

F:97-129/Disulfide bonds: #status predicted

F:97-129/Disulfide bonds: #status predicted

F:97-129/Disulfide bonds: #status predicted

F:97-129/Disulfide bonds: #status predicted

F:97-129/Disulfide bonds: #status predicted

F:97-129/Disulfide bonds: #status predicted

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F:97-129/Disulfide bonds: #status predicted

F:97-129/Disulfide bonds: #status predicted

F:97-129/Disulfide bonds: #status predicted

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F:97-129/Disulfide bonds: #status predicted

F:97-129/Disulfide bonds: #status predicted

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F:97-129/Disulfide bonds: #status predicted

F:97-129/Disulfide bonds: #status predicted

F:97-129/Disulfide bonds: #status predicted

F:97-129/Disulfide bonds: #status predicted

F:97-129/Disulfide bonds: #status predicted

F:97-129/Disulfide bonds: #status predicted

F:97-129/Disulfide bonds: #status predicted

F:97-129/Disulfide bonds: #status predicted

F:97-129/Disulfide bonds: #status predicted

F:97-129/Disulfide bonds: #status predicted

F:97-129/Disulfide bonds: #status predicted

F:97-129/Disulfide bonds: #status predicted

A:Description: Cloning and sequence analysis of cDNAs encoding bovine CD40 ligand and

A:Reference number: S52715

A:Accession: S52715

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-185 &lt;MER&gt;

A:Cross-references: EMBL:Z48808; NID:g755701; PIDN:CAA88743.1; PID:g755702

C:Superfamily: tumor necrosis factor

C:Keywords: glycoprotein

F:33/Binding site: carbohydrate (Ser) (covalent) #status predicted

F:97-129/Disulfide bonds: #status predicted

F:97-129/Disulfide bonds: #status predicted

F:97-129/Disulfide bonds: #status predicted

F:97-129/Disulfide bonds: #status predicted

F:97-129/Disulfide bonds: #status predicted

F:97-129/Disulfide bonds: #status predicted

F:97-129/Disulfide bonds: #status predicted

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F:97-129/Disulfide bonds: #status predicted

F:97-129/Disulfide bonds: #status predicted

F:97-129/Disulfide bonds: #status predicted

A:Reference number: S48118; MUID:92155784; PMID:1786996  
 A:Accession: S48118  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-234 <M>  
 A:Cross-references: EMBL:X56756; NID:g297806; PIDN:CAA40076.1; PID:g297807  
 R:Young, A.J.; Hay, J.B.; Chan, J.Y.C.  
 Nucleic Acids Res. 18, 6723, 1990  
 A:Title: Primary structure of ovine tumor necrosis factor alpha cDNA.  
 A:Reference number: S13114; MUID:91067496; PMID:2251151  
 A:Accession: S13114  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-62,64-234 <Y>  
 A:Cross-references: EMBL:X55966; NID:g1403; PIDN:CA93437.1; PID:g1404  
 A:Note: Comparison with the introns of homologous sequences suggest that this is probably  
 C:Superfamily: tumor necrosis factor  
 C:Keywords: alternative splicing; cytokine; cytotoxin; glycoprotein; lipoprotein; lymph  
 F:1-77/Domain: propeptide #status predicted <PRO>  
 F:78-234/Product: tumor necrosis factor alpha #status predicted <TNF>  
 F:20/Binding site: myristate (Lys) (covalent) #status predicted  
 F:82/Binding site: carboxylate (Ser) (covalent) #status predicted  
 F:96/Binding site: carboxylate (Asn) (covalent) #status predicted  
 F:146-178/Disulfide bonds: #status predicted

Query Match 65.5%; Score 55; DB 1; Length 234;  
 Best Local Similarity 69.2%; Pred. No. 0.23;  
 Matches 9; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 2 KDTEGAEKLPWY 14  
 DB 180 RELEGAERKPMW 192  
 ::||| |||||

RESULT 11  
 JQ1344  
 tumor necrosis factor alpha precursor - horse  
 N:Alternate names: cachectin; TNF alpha  
 C:Species: Equus caballus (domestic horse)  
 C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 04-Feb-2000  
 C:Accession: JQ1344  
 R:Su, X.; Morris, D.D.; McGraw, R.A.  
 Gene 107, 319-321, 1991  
 A:Title: Cloning and characterization of gene TNF alpha encoding equine tumor necrosis f  
 A:Reference number: JQ1344; MUID:92084125; PMID:1748301  
 A:Accession: JQ1344  
 A:Molecule type: DNA  
 A:Residues: 1-234 <SD>  
 A:Cross-references: GB:M64087; NID:g164244; PIDN:AAA30959.1; PID:g164245  
 C:Comment: This protein is an important proximal mediator of endotoxemia.  
 C:Genetics:  
 A:Gene: TNF-alpha  
 A:Introns: 62/3; 79/1; 95/1  
 C:Superfamily: tumor necrosis factor  
 C:Keywords: cytokine; cytotoxin; glycoprotein; lipoprotein; lymphokine; macrophage; mem  
 F:78-234/Product: tumor necrosis factor alpha #status predicted <TNF>  
 F:19-20/Binding site: myristate (Lys) (covalent) #status predicted  
 F:82/Binding site: carboxylate (Ser) (covalent) #status predicted  
 F:146-178/Disulfide bonds: #status predicted

Query Match 60.7%; Score 51; DB 1; Length 234;  
 Best Local Similarity 66.7%; Pred. No. 1;  
 Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 3 DTEGAEKLPWY 14  
 DB 181 ESPQOAEKPMW 192  
 ::||| |||||

RESULT 12  
 AH0060  
 bis(5'-nucleosyl)-tetraphosphatase (symmetrical) (EC 3.6.1.41) [Imported] - Yersinia pest  
 C:Species: Yersinia pestis

C:Date: 02-Nov-2001 #sequence\_revision 02-Nov-2001 #text\_change 11-Jan-2002  
 C:Accession: AH0060  
 R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Tibball, R.W.; Holden, M.T.G.; Prentice, M  
 deno-Tarrage, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G  
 11, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrel  
 Nature 413, 523-527, 2001  
 A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.  
 A:Reference number: AB0001; MUID:21470413; PMID:11586360  
 A:Accession: AB0001  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-289 <KUR>  
 A:Cross-references: GB:A1590842; PIDN:CA689347.1; PID:g15978584; GSPDB:GN00175  
 C:Genetics:  
 A:Gene: apaf  
 C:Superfamily: bis(5'-nucleosyl)-tetraphosphatase (symmetrical); phosphoesterase core  
 C:Keywords: hydrolase

Query Match 59.5%; Score 50; DB 2; Length 289;  
 Best Local Similarity 66.7%; Pred. No. 1.9;  
 Matches 10; Conservative 1; Mismatches 2; Indels 2; Gaps 1;

OY 2 KDTEGAEKLPWY 14  
 DB 197 KDTEGAEKLPWY 211  
 ::||| |||||

RESULT 13  
 S06192  
 tumor necrosis factor alpha precursor - goat (fragment)  
 N:Alternate names: cachectin; TNF alpha  
 C:Species: Capra aegagrus hircus (domestic goat)  
 C:Date: 28-Feb-1990 #sequence\_revision 28-Feb-1990 #text\_change 31-Jan-2000  
 C:Accession: S06192; S41867  
 R:Goldstein, I.M.; Henner, D.; Talhouk, A.  
 submitted to the EMBL Data Library, March 1989  
 A:Reference number: S06192  
 A:Accession: S06192  
 A:Molecule type: mRNA  
 A:Residues: 1-193 <GOL>  
 A:Cross-references: EMBL:X14828; NID:g992; PIDN:CAA32937.1; PID:g993  
 R:Rimstad, E.  
 submitted to the EMBL Data Library, January 1994  
 A:Reference number: S41867  
 A:Accession: S41867  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 36-38, 'S', '40-78, 'A', '80-88, 'N', '90-114, 'O', '116-123, 'D', '125-144, 'G', '145-173,  
 A:Cross-references: EMBL:X77317; NID:g452607; PIDN:CAA54523.1; PID:g452608  
 C:Superfamily: tumor necrosis factor  
 C:Keywords: cytokine; cytotoxin; glycoprotein; lymphokine; macrophage; membrane prote  
 F:42/Binding site: carboxylate (Ser) (covalent) #status predicted  
 F:106-138/Disulfide bonds: #status predicted

Query Match 57.7%; Score 48.5; DB 2; Length 193;  
 Best Local Similarity 69.2%; Pred. No. 2.1;  
 Matches 9; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

OY 2 KDTEGAEKLPWY 14  
 DB 140 RETPEAEKPMW 151  
 ::||| |||||

RESULT 14  
 C86822  
 hypothetical protein ydpk [Imported] - Lactococcus lactis subsp. lactis (strain IL140  
 C:Species: Lactococcus lactis subsp. lactis  
 C:Date: 23-Mar-2001 #sequence\_revision 23-Mar-2001 #text\_change 03-Aug-2001  
 C:Accession: C86822  
 R:Bolet, A.; Winkler, P.; Manger, S.; Jallion, O.; Malarne, K.; Weissenbach, J.; Eh  
 Genome Res. 11, 731-753, 2001  
 A:Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis  
 A:Reference number: AB6625; MUID:2125186; PMID:11337471

A:Accession: C86822  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-1649 <SNO>  
 A:Cross-references: GB:AE005176; PID:g12724583; PIDN:AAK05677.1; GSPDB:GN00146  
 A:Experimental source: strain IL1403  
 C:Genetics:  
 A:Gene: ygbK

Query Match 57.1%; Score 48; DB 2; Length 1649;  
 Best Local Similarity 66.7%; Pred. No. 25;  
 Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 DTPEGAEKPMY 14  
 |||:|||||  
 Db 1545 DTRCGSAKPMY 1556

## RESULT 15

VHWVME

structural polypeptide - western equine encephalomyelitis virus (strain BFS1703)  
 N:Contains: 6K protein; coat protein C; membrane glycoprotein E1; membrane glycoprotein  
 C;Species: western equine encephalomyelitis virus  
 C>Date: 31-Mar-1991 #sequence\_revision 31-Mar-1991 #text\_change 16-Jul-1999  
 C:Accession: A35587  
 R:Hahn, C.S.; Lustig, S.; Strauss, E.G.; Strauss, J.H.  
 Proc. Natl. Acad. Sci. U.S.A. 85, 5997-6001, 1988  
 A:Title: Western equine encephalitis virus is a recombinant virus.  
 A:Reference number: A35587; MUID:88320369; PMID:3413072  
 A:Accession: A35587  
 A:Molecule type: genomic RNA  
 A:Residues: 1-1236 <NAH>  
 A:Cross-references: GB:J03854; NID:g323728; PIDN:AAA42999.1; PID:g323730  
 C:Superfamily: togavirus structural polypeptide  
 C:Keywords: coat protein; glycoprotein; polypeptide; transmembrane protein  
 F:1-259/Product: coat protein C #status predicted <CPC>  
 F:260-319/Product: membrane glycoprotein E3 #status predicted <MG3>  
 F:320-742/Product: membrane glycoprotein E2 #status predicted <MG2>  
 F:684-702/Domain: transmembrane #status predicted <TN1>  
 F:719-737/Domain: transmembrane #status predicted <TN2>  
 F:743-797/Product: 6K protein #status predicted <K6P>  
 F:758-775/Domain: transmembrane #status predicted <TN3>  
 F:777-793/Domain: transmembrane #status predicted <TN4>  
 F:798-1236/Product: membrane glycoprotein E1 #status predicted <MG1>  
 F:1206-1227/Domain: transmembrane #status predicted <TN5>  
 F:50,270,515,637,724,936,1042/binding site: carboxylate (Asn) (covalent) #status predic

Query Match 56.0%; Score 47; DB 1; Length 1236;  
 Best Local Similarity 75.0%; Pred. No. 26;  
 Matches 9; Conservative 1; Mismatches 0; Indels 2; Gaps 1;

QY 2 KDTPGAEKPMY 13  
 |||||:|  
 Db 250 KDTPGSE--PW 259

Search completed: April 4, 2003, 08:42:57  
 Job time : 11.1613 secs

GenCore version 5.1.4-p5\_4578  
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OM protein - protein search, using sw model

Run on: April 4, 2003, 08:36:51 ; Search time 5.64516 Seconds  
(without alignments)  
102.861 Million cell updates/sec

Title: US-09-779-703-2

Sequence: 1 PKDTPGAEIKRPWY 14

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: SwissProt\_40.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	84	100.0	235	1	TNFA_MOUSE
2	84	100.0	235	1	TNFA_MOUSE
3	77	91.7	235	1	TNFA_MOUSE
4	67	79.8	234	1	TNFA_MOUSE
5	65	77.4	232	1	TNFA_MOUSE
6	65	77.4	233	1	TNFA_MOUSE
7	65	77.4	233	1	TNFA_MOUSE
8	65	77.4	233	1	TNFA_MOUSE
9	65	77.4	233	1	TNFA_MOUSE
10	65	77.4	233	1	TNFA_MOUSE
11	65	77.4	233	1	TNFA_MOUSE
12	65	77.4	233	1	TNFA_MOUSE
13	65	77.4	233	1	TNFA_MOUSE
14	65	77.4	233	1	TNFA_MOUSE
15	62	73.8	233	1	TNFA_MOUSE
16	61	72.6	233	1	TNFA_MOUSE
17	57	67.9	229	1	TNFA_MOUSE
18	57	67.9	229	1	TNFA_MOUSE
19	55	65.5	233	1	TNFA_MOUSE
20	51	60.7	234	1	TNFA_MOUSE
21	50	59.5	289	1	APAH_MOUSE
22	48	57.1	629	1	SKIL_MOUSE
23	47	56.0	1336	1	POLS_MOUSE
24	47	56.0	1336	1	POLS_MOUSE
25	46	54.8	951	1	POLS_MOUSE
26	45	53.6	684	1	SKIL_MOUSE
27	45	53.6	684	1	SKIL_MOUSE
28	43	51.2	259	1	APAH_MOUSE
29	43	51.2	748	1	MUTR_MOUSE
30	43	51.2	750	1	MUTR_MOUSE
31	43	51.2	750	1	MUTR_MOUSE
32	42	50.0	702	1	PC16_MOUSE
33	42	50.0	712	1	MUTR_MOUSE

## ALIGNMENTS

RESULT 1	ID	TNFA_MOUSE	STANDARD:	PRT:	235 AA.
AC	P06804	062326; 035853;			
DT	01-JAN-1988	(Rel. 06, Created)			
DT	01-MAR-1989	(Rel. 10, Last sequence update)			
DT	15-JUN-2002	(Rel. 41, Last annotation update)			
DE	Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor ligand superfamily member 2) (Cachectin).				
GN	TNF OR TNFSF2 OR TNFA.				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
OX	NCBI_TaxID=10090;				
RN	[1]	SEQUENCE FROM N.A.			
RP	MEDLINE=88224564; PubMed=2836146;				
RX	Shirai T., Shimizu N., Shiojiri S., Horiguchi S., Ito H.;				
RA	"Cloning and expression in Escherichia coli of the gene for mouse tumor necrosis factor.";				
RT	tumor necrosis factor.";				
RL	DNA 7:193-201(1988).				
RN	[2]	SEQUENCE FROM N.A.			
RP	MEDLINE=85298296; PubMed=3898078;				
RX	Pennica D., Hayflick J.S., Bringham T.S., Palladino M.A.,				
RA	Goeddel D.V.;				
RT	"Cloning and expression in Escherichia coli of the cDNA for murine tumor necrosis factor.";				
RL	Proc. Natl. Acad. Sci. U.S.A. 82:6060-6064(1985).				
RN	[3]	SEQUENCE FROM N.A.			
RP	MEDLINE=86149365; PubMed=2419912;				
RX	Caput D., Beutler B., Hartog K., Thayer R., Brown-Shimer S.,				
RA	Cerami A.;				
RT	"Identification of a common nucleotide sequence in the 3'-untranslated region of mRNA molecules specifying inflammatory mediators.";				
RL	Proc. Natl. Acad. Sci. U.S.A. 83:1670-1674(1986).				
RN	[4]	SEQUENCE FROM N.A.			
RP	MEDLINE=85242112; PubMed=2989794;				
RX	Fransen L., Mueller R., Marmenout A., Tavernier J., van der Heyden J.,				
RA	Kawashima E., Chollet A., Tizard R., van Heuverswyn H., van Vliet A.,				
RT	Ruysschaert M.-R., Fiers W.;				
RL	"Molecular cloning of mouse tumour necrosis factor cDNA and its eukaryotic expression.";				
RN	Nucleic Acids Res. 13:4417-4429(1985).				
RP	[5]	SEQUENCE FROM N.A.			
RX	MEDLINE=87298639; PubMed=3040015;				
RA	Shakhov A.N., Nedospasov S.A.;				
RT	"Molecular cloning of genes coding for tumor necrosis factor. Complete nucleotide sequence of the genome copy of TNF-alpha in mice.";				
RL	Bioorg. Khim. 13:701-705(1987).				
RN	[6]				

34	41	48.8	142	1	YFCC_CHRYI	006536 Chromatium
35	41	48.8	235	1	TNFA_MOUSE	P04924 cryptotagus
36	41	48.8	244	1	S40A_CHITE	005018 chironomus
37	41	48.8	253	1	S40B_CHITE	005019 chironomus
38	41	48.8	455	1	YWAD_BACSV	P25152 bacillus su
39	41	48.8	733	1	MUTR_MOUSE	005065 streptomyce
40	41	48.8	744	1	MUTR_MOUSE	023381 caenorhabdi
41	41	48.8	782	1	DP02_ECOLI	P21189 escherichia
42	41	48.8	1073	1	RAGL_ONCMY	091187 oncorhynchu
43	40	47.6	275	1	APAH_HAETN	P44751 haemophilus
44	40	47.6	280	1	APAH_ECOLI	P05637 escherichia
45	40	47.6	282	1	APAH_ECO57	08xals escherichia

RP SEQUENCE FROM N.A.  
 RA MEDLINE=88067722; PubMed=3684584;  
 RX Semon D., Kawashima E., Jongeneel C.V., Shakhov A.N., Nedospasov S.A.;  
 RT "Nucleotide sequence of the murine TNF locus, including the TNF-alpha  
 RL (tumor necrosis factor) and TNF-beta (lymphotoxin) genes."; Nucleic Acids Res. 15:9083-9084(1987).  
 RN (17)  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-CTS, and NOD;  
 RX MEDLINE=96013654; PubMed=7560085;  
 RA Ikegami H., Makino S., Yamato E., Kawaguchi Y., Ueda H., Sakamoto T.,  
 RT Takekawa K., Ogihara T.;  
 RL "Identification of a new susceptibility locus for insulin-dependent  
 RT diabetes mellitus by ancestral haplotype congenic mapping."; J. Clin. Invest. 96:1936-1942(1995).  
 RN (8)  
 RP SEQUENCE FROM N.A., AND VARIANTS THR-7 AND ALA-77.  
 RC STRAIN-A/J, BALB/c, and C57BL/6;  
 RX MEDLINE=97246744; PubMed=9089109;  
 RA Irigoi F., Teale A.;  
 RT "Cloning and sequencing of the Tnfa genes of three inbred mouse  
 RL strains."; Immunogenetics 45:459-461(1997).  
 RN (9)  
 RP SEQUENCE FROM N.A.  
 RA Rowen L., Qin S., Madan A., Abbasi N., James R., Dickhoff R.,  
 RX Shaffer T., Ratcliffe A., Loretz C., Lasky S., Hood L.;  
 RT "Sequence of the mouse major histocompatibility class III region."; Submitted (Oct-1999) to the EMBL/GenBank/DBJ databases.  
 RN (10)  
 RP SEQUENCE OF 70-87.  
 RX MEDLINE=89380231; PubMed=2777790;  
 RA Cseh K., Beutler B.;  
 RT "Alternative cleavage of the cachectin/tumor necrosis factor  
 RL propeptide results in a larger, inactive form of secreted protein."; J. Biol. Chem. 264:16256-16260(1989).  
 RN (11)  
 RP SEQUENCE OF 80-99.  
 RX MEDLINE=91097531; PubMed=2268312;  
 RA Sherry B., Juc D.-M., Zentella A., Cerami A.;  
 RT "Characterization of high molecular weight glycosylated forms of  
 RL murine tumor necrosis factor."; Biochem. Biophys. Res. Commun. 173:1072-1078(1990).  
 RN (12)  
 RP IDENTIFICATION OF MEMBRANE-BOUND FORM.  
 RX MEDLINE=88165056; PubMed=3349526;  
 RA Krieglner M., Perez X., Defay K., Albert I., Lu S.D.;  
 RT "A novel form of TNF/cachectin is a cell surface cytotoxic  
 RL transmembrane protein: ramifications for the complex physiology of  
 TNF."; Cell 53:45-53(1988).  
 RN (13)  
 RP X-RAY CRYSTALLOGRAPHY (1.4 ANGSTROMS) OF 80-235.  
 RX MEDLINE=99190964; PubMed=10089307;  
 RA Baeyens K.J., De Bondt H.L., Raeymaekers A., Fiers W., De Rantier C.J.;  
 RT "The structure of mouse tumour-necrosis factor at 1.4 A resolution:  
 RL towards modulation of its selectivity and trimerization."; Acta Crystallogr. D 55:772-778(1999).  
 CC -1- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and  
 CC TNFRSF1B/TNFR. It is mainly secreted by macrophages and can  
 CC induce cell death of certain tumor cell lines. It is potent  
 CC pyrogen causing fever by direct action or by stimulation of  
 CC interleukin 1 secretion and is implicated in the induction of  
 CC cachexia, under certain conditions it can stimulate cell  
 CC proliferation and induce cell differentiation.  
 CC -1- SUBUNIT: Homotrimer.  
 CC -1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN  
 CC EXTRACELLULAR SOLUBLE FORM.  
 CC -1- PTM: THE SOLUBLE FORM DERIVES FROM THE MEMBRANE FORM BY  
 CC PROTEOLYTIC PROCESSING.  
 CC -1- PM: The membrane form, but not the soluble form, is  
 CC phosphorylated on serine residues. Dephosphorylation of the  
 CC membrane form occurs by binding to soluble TNFRSF1A/TNFR1 (by

CC similarity).  
 CC -1- DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF DISEASES, INCLUDING  
 CC CANCER AND INFECTION, AND IS CHARACTERIZED BY GENERAL ILL HEALTH  
 CC AND MALNUTRITION.  
 CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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 CC -----  
 CC EMBL; M20155; AAA40462.1; ALT-SEQ.  
 CC EMBL; M11731; AAA40458.1; -  
 CC EMBL; M13049; AAA40457.1; -  
 CC EMBL; X02611; CAA26457.1; -  
 CC EMBL; M38296; AAA40459.1; -  
 CC EMBL; Y00467; CAA68530.1; -  
 CC EMBL; Y06950; AAA18594.1; -  
 CC EMBL; D84196; BAA19512.1; -  
 CC EMBL; D84194; BAA19512.1; JOINED.  
 CC EMBL; D84195; BAA19512.1; JOINED.  
 CC EMBL; D84197; BAA19513.1; -  
 CC EMBL; D84198; BAA19513.1; JOINED.  
 CC EMBL; U68414; AAB65593.1; -  
 CC EMBL; AF109719; AAC82484.1; -  
 CC PIR; A23127; OMMSN.  
 CC PIR; A22908; A22908.  
 CC PIR; A23164; A23164.  
 CC PIR; A27303; A27303.  
 CC PIR; A34251; A34251.  
 CC PIR; S03791; S03791.  
 CC PDB; 2TNF; 12-OCT-99.  
 CC MGD; MGI:104798; Tnf.  
 CC InterPro; IPR003636; Tnf-abc.  
 CC InterPro; IPR000478; Tnf-family.  
 CC Pfam; PF00229; Tnf; 1.  
 CC PRINTS; PR01234; TNECROSISFCT.  
 CC ProDom; PD002012; Tnf-abc; 1.  
 CC SMART; SM00207; Tnf; 1.  
 CC PROSITE; PS00251; Tnf-1; 1.  
 CC PROSITE; PS0049; Tnf-2; 1.  
 CC KW Cytokine; Cytotoxin; Transmembrane; Glycoprotein; Phosphorylation;  
 CC Signal-anchor; Polymorphism; 3D-structure.  
 CC CHAIN 1 235  
 CC DOMAIN 80 235  
 CC TRANSMEM 36 56  
 CC FT DOMAIN 57 235  
 CC FT SITE 79 80  
 CC FT MOD\_RES 2 2  
 CC FT DISULFID 148 179  
 CC FT CARBOHYD 86 86  
 CC FT VARIANT 7 7  
 CC FT VARIANT 77 77  
 CC FT CONFLICT 79 81  
 CC FT CONFLICT 231 231  
 CC SO SEQUENCE 235 AA; 25895 MW; 16DD2A9676D68C5D CRC64;  
 CC  
 CC Query Match 100.0%; Score 84; DB 1; Length 235;  
 CC Best Local Similarity 100.0%; Pred. No. 2; Ie-06;  
 CC Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 CC  
 CC QY 1 PKDTPEGALPKPWY 14  
 CC ||||||||||||  
 CC DB 180 PKDTPEGALPKPWY 193  
 CC  
 CC RESULT 2



ID	TNFA_RAT	STANDARD	PRT	235 AA.
AC	TNFA_RAT P16599.			
DT	01-AUG-1990 (Rel. 15, Created)			
DT	01-AUG-1990 (Rel. 15, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor ligand superfamily member 2) (Cachectin).			
GN	TNF OR TNFSF2 OR TNFA.			
OS	Rattus norvegicus (Rat).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			
OX	NCBI_TaxID=10116;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-Sprague-Dawley; TISSUE-Testis;			
RX	MEDLINE=94040766; PubMed=8224868;			
RA	*Kwon J., Chung I.Y., Benveniste E.N.;			
RT	*Cloning and sequence analysis of the rat tumor necrosis factor-encoding genes.;			
RL	Gene 132:227-236(1993).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RA	Shirai T., Shimizu N., Horiguchi S., Ito H.;			
RT	*Cloning and expression in Escherichia coli of the gene for rat tumor necrosis factor.;			
RL	Agric. Biol. Chem. 53:1733-1736(1989).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=92329007; PubMed=1621266;			
RA	Estler H.C., Grawe M., Gaussling R., Pavlovic M., Decker K.;			
RT	*Rat tumor necrosis factor-alpha. Transcription in rat Kupffer cells and in vitro posttranslational processing based on a PCR-derived cDNA.;			
RL	Biol. Chem. Hoppe-Seyler 373:271-281(1992).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-Various;			
RX	MEDLINE=21369712; PubMed=11474749;			
RA	Fuuya T., Joe B., Salstrom J.L., Hashimoto A., Dobbins D.E.,			
RT	Wilder R.L., Remmers E.F.;			
RL	*Polymorphisms of the tumor necrosis factor alpha locus among autoimmune disease susceptible and resistant inbred rat strains.;			
RN	Genes Immun. 2:229-232(2001).			
RP	[5]			
RP	SEQUENCE FROM N.A.			
RA	Decker K.F.;			
RL	Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.			
RN	[6]			
RP	SEQUENCE OF 1-231 FROM N.A.			
RC	TISSUE-Tail;			
RA	Kistakis M.J., Yardimon D., Kunz H.W., Gail T.J. III;			
RL	Submitted (JUN-1993) to the EMBL/GenBank/DBJ databases.			
CC	-1- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and TNFRSF1B/TNFR. It is mainly secreted by macrophages and can induce cell death of certain tumor cell lines. It is potent pyrogen causing fever by direct action or by stimulation of interleukin 1 secretion and is implicated in the induction of cachexia. Under certain conditions it can stimulate cell proliferation and induce cell differentiation.			
CC	-1- SUBUNIT: Homotrimer (By similarity).			
CC	-1- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an extracellular soluble form (By similarity).			
CC	-1- PTM: The soluble form derives from the membrane form by proteolytic processing (By similarity).			
CC	-1- PPM: The membrane form, but not the soluble form, is phosphorylated on serine residues. Dephosphorylation of the membrane form occurs by binding to soluble TNFRSF1A/TNFR1 (By similarity).			
CC	-1- DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF DISEASES, INCLUDING CANCER AND INFECTION, AND IS CHARACTERIZED BY GENERAL, ILL HEALTH AND MALNUTRITION.			
CC	-1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.			

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DR EMBL; X65639; CAA47146.1; -.  
DR EMBL; L00981; AAA16275.1; -.  
DR EMBL; D00475; BAA00367.1; -.  
DR EMBL; AJ002278; CAA05290.1; -.  
DR EMBL; U19123; AAA42255.1; -.  
DR EMBL; AF329982; AAK53568.1; -.  
DR EMBL; AF329983; AAK53569.1; -.  
DR EMBL; AF329984; AAK53570.1; -.  
DR EMBL; AF329985; AAK53571.1; -.  
DR EMBL; AF329986; AAK53572.1; -.  
DR EMBL; AF329987; AAK53573.1; -.  
DR PIR; J00029; JU00029.  
DR PIR; S21674; S21674.  
DR PIR; J00868; J00868.  
DR HSSP; P06804; 2TNF.  
DR InterPro; IPR003636; TNF_abc.  
DR InterPro; IPR000478; TNF_family.  
DR Pfam; PF00229; TNF; 1.  
DR PRINTS; PR01234; TNECROSISCT.  
DR ProDom; PD002012; TNF_abc; 1.  
DR SMART; SM00207; TNF; 1.  
DR PROSITE; PS00251; TNF_1; 1.  
DR PROSITE; PS0049; TNF_2; 1.  
KW Cyclokinin; Cytotoxin; Transmembrane; Glycoprotein; Phosphorylation;  
KV Signal-anchor.  
FT CHAIN 1 235  
FT CHAIN 80 235  
FT DOMAIN 1 35  
FT TRANSMEM 36 56  
  
FT DOMAIN 57 235  
FT SITE 79 80  
FT MOD_RES 2 2  
FT DISULFD 148 179  
FT CARBOHD 86 86  
FT CONFLICT 39 39  
FT CONFLICT 163 163  
FT CONFLICT 202 202  
SQ SEQUENCE 235 AA; 25806 MW; B808EC6D049C2F3B CRC64;  
  
Query Match 100.0%; Score 84; DB 1; Length 235;  
Best Local Similarity 100.0%; Pred. No. 1e+06;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Oy 1 PKDTPEGAELKPWY 14  
Db 180 PKDTPEGAELKPWY 193  
|||||  
|||  
  
RESULT 3  
ID ID_TNFA_PERLE STANDARD; PTR; 235 AA.  
AC P36939;  
DT 01-JUN-1994 (Rel. 29, Created)  
DT 01-JUN-1994 (Rel. 29, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor  
ligand superfamily member 2) (Cachectin).  
GN TNF OR TNFSF2 OR TNFA.  
OS Peromyscus leucopus (White-footed mouse).  
OC Eukaryota; Metazoa; Chordata; Cranialia; Vertebrata; Euteleostomi;  
CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;  
Peromyscus.  
NCBI Taxid=10041;
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RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-92218012; PubMed-1348497;
RA "Crew M.D., Filipowsky M.E.;"
RT "Sequence of the tumor necrosis factor/cachectin (TNF) gene from
RL Peromyscus leucopus (family Cricetidae).";
CC Immunogenetics 35:351-353(1992).
CC -1- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and
CC TNFRSF1B/TNFR. It is mainly secreted by macrophages and can
CC induce cell death of certain tumor cell lines. It is potent
CC pyrogen causing fever by direct action or by stimulation of
CC interleukin 1 secretion and is implicated in the induction of
CC cachexia. Under certain conditions it can stimulate cell
CC proliferation and induce cell differentiation.
CC -1- SUBUNIT: Homotrimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an
CC extracellular soluble form (By similarity).
CC -1- PTM: The soluble form derives from the membrane form by
CC proteolytic processing (By similarity).
CC -1- PTM: The membrane form, but not the soluble form, is
CC phosphorylated on serine residues. Dephosphorylation of the
CC membrane form occurs by binding to soluble TNFRSF1A/TNFR1 (By
CC similarity).
CC -1- DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF DISEASES, INCLUDING
CC CANCER AND INFECTION, AND IS CHARACTERIZED BY GENERAL ILL HEALTH
CC AND MALNUTRITION.
CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M59233; AAA40596.1; -
DR HSSP; P06804; 2TNF.
DR InterPro; IPR003636; TNF_abc.
DR InterPro; IPR000478; TNF_family.
DR Pfam; PF00229; TNF_1.
DR PRINTS; PR01234; TNECROSISFCT.
DR PRODOM; PD002012; TNF_abc; 1.
DR SMART; SM00207; TNF_1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS50049; TNF_2; 1.
DR Cytokine; Cytotoxin; Transmembrane; Glycoprotein; Phosphorylation;
KW Signal-anchor.
FT CHAIN 1 235 TUMOR NECROSIS FACTOR, MEMBRANE FORM.
FT CHAIN 80 235 TUMOR NECROSIS FACTOR, SOLUBLE FORM.
FT DOMAIN 1 35 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 36 56 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT (POTENTIAL).
FT DOMAIN 57 235 EXTRACELLULAR (POTENTIAL).
FT SITE 79 80 CLEAVAGE (BY ADAM17) (BY SIMILARITY).
FT MOD_RES 2 2 PHOSPHORYLATION (BY CK1) (BY SIMILARITY).
FT DISULFID 148 179 BY SIMILARITY.
FT CARBOHYD 86 86 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 235 AA; 25822 MW; 235A5CF9F9AC624 CRC64;

Query Match 91.7%; Score 77; DB 1; Length 235;
Best Local Similarity 85.7%; Pred. No. 2.8e-05;
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DE 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor
DE ligand superfamily member 2) (Cachectin).
DE TNF OR TNFSF2 OR TNFA.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystriognathi; Cavidae; Cavia.
OX NCBI_Taxid=10141;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-Dunkin-Hartley; TISSUE-Lung;
RA Yuan H.T., Kelly F.J., Bingle C.D.;
RL Submitted (NOV-1995) to the EMBL/Genbank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-Dunkin-Hartley;
RX MEDLINE-97462215; PubMed-9316485;
RA White A.M., Yoshimura T., Smith A.W., Westwick J., Watson M.L.;
RT "Airway inflammation induced by recombinant guinea pig tumor necrosis
RT factor-alpha.";
RL Am. J. Physiol. 273:L524-L530(1997).
CC -1- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and
CC TNFRSF1B/TNFR. It is mainly secreted by macrophages and can
CC induce cell death of certain tumor cell lines. It is potent
CC pyrogen causing fever by direct action or by stimulation of
CC interleukin 1 secretion and is implicated in the induction of
CC cachexia. Under certain conditions it can stimulate cell
CC proliferation and induce cell differentiation.
CC -1- SUBUNIT: Homotrimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an
CC extracellular soluble form (By similarity).
CC -1- PTM: The soluble form derives from the membrane form by
CC proteolytic processing (By similarity).
CC -1- PTM: The membrane form, but not the soluble form, is
CC phosphorylated on serine residues. Dephosphorylation of the
CC membrane form occurs by binding to soluble TNFRSF1A/TNFR1 (By
CC similarity).
CC -1- DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF DISEASES, INCLUDING
CC CANCER AND INFECTION, AND IS CHARACTERIZED BY GENERAL ILL HEALTH
CC AND MALNUTRITION.
CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
CC -----
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CC -----
DR EMBL; U39839; AAB06492.1; -
DR EMBL; U77036; AAB19210.1; -
DR HSSP; P06804; 2TNF.
DR InterPro; IPR003636; TNF_abc.
DR InterPro; IPR000478; TNF_family.
DR Pfam; PF00229; TNF_1.
DR PRINTS; PR01234; TNECROSISFCT.
DR PRODOM; PD002012; TNF_abc; 1.
DR SMART; SM00207; TNF_1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS50049; TNF_2; 1.
DR Cytokine; Cytotoxin; Transmembrane; Phosphorylation; Signal-anchor.
KW CHAIN 1 234 TUMOR NECROSIS FACTOR, MEMBRANE FORM.
FT CHAIN 80 234 TUMOR NECROSIS FACTOR, MEMBRANE FORM.
FT DOMAIN 1 35 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 36 56 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT (POTENTIAL).
FT DOMAIN 57 234 EXTRACELLULAR (POTENTIAL).
FT SITE 79 80 CLEAVAGE (BY ADAM17) (BY SIMILARITY).
FT MOD_RES 2 2 PHOSPHORYLATION (BY CK1) (BY SIMILARITY).
FT DISULFID 147 178 BY SIMILARITY.

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SQ SEQUENCE 234 AA; 25793 MW; 7272C940393E7EBB CRC64;  
 Query Match 79.8%; Score 67; DB 1; Length 234;  
 Best Local Similarity 84.6%; Pred. No. 0.0011;  
 Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 2 KDPPEGAELKPMY 14  
 :|||||  
 DB 180 KETPEGAERKPMY 192

RESULT 5  
 ID TNFA\_PIG STANDARD; PRT; 232 AA.  
 AC P23563;  
 DT 01-NOV-1991 (Rel. 20, Created)  
 DT 15-JUN-2002 (Rel. 41, Last sequence update)  
 DE Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor  
 ligand superfamily member 2) (cachectin).  
 GN TNF OR TNFSF2 OR TNFA.  
 OS Sus scrofa (Pig).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
 OX NCBI\_TaxId=9823;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=91016861; PubMed=2216741;  
 RA Drews R.T., Coffee B.W., Prestwood A.K., McGraw R.A.;  
 RT "Gene sequence of porcine tumor necrosis factor alpha";  
 RL Nucleic Acids Res. 18:5564-5564(1990).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX TISSUE=LIVER;  
 RA MEDLINE=91340150; PubMed=1874444;  
 RA Kuhnert P., Wethlich C., Peterhans E., Pauli U.;  
 RT "The porcine tumor necrosis factor-encoding genes: sequence and  
 comparative analysis";  
 RL Gene 102:171-178(1991).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX TISSUE=Macrophage;  
 RA Choi C.S., Molitor T.W., Lin G.F., Murtaugh M.P.;  
 RT "Complete nucleotide sequence of a cDNA encoding porcine tumor  
 necrosis factor-alpha";  
 RL Anal. Biochem. 2:97-105(1991).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RX STRAIN=Large white; TISSUE=Fibroblast;  
 RA MEDLINE=21108615; PubMed=11169259;  
 RA Chardon P., Rogel-Gallard C., Catolico L., Duprat S., Vaiman M.,  
 Renaud C.;  
 RT "Sequence of the swine major histocompatibility complex region  
 containing all non-classical class I genes";  
 RL Tissue Antigens 57:55-65(2001).  
 RN [5]  
 RP SEQUENCE OF 44-232 FROM N.A.  
 RX MEDLINE=90034181; PubMed=2478420;  
 RA Pauli U., Beutler B., Peterhans E.;  
 RT "Porcine tumor necrosis factor alpha: cloning with the polymerase  
 chain reaction and determination of the nucleotide sequence";  
 RL Gene 81:185-191(1989).  
 CC -1- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and  
 TNFRSF1B/TNFR. It is mainly secreted by macrophages and can  
 induce cell death of certain tumor cell lines. It is potent  
 pyrogen causing fever by direct action or by stimulation of  
 interleukin 1 secretion and is implicated in the induction of  
 cachexia. Under certain conditions it can stimulate cell  
 proliferation and induce cell differentiation.  
 CC -1- SUBUNIT: Homotrimer (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an  
 extracellular soluble form (By similarity).  
 CC -1- PTM: The soluble form derives from the membrane form by

CC proteolytic processing (By similarity).  
 CC -1- PTM: The membrane form, but not the soluble form, is  
 CC phosphorylated on serine residues. Dephosphorylation of the  
 CC membrane form occurs by binding to soluble TNFRSF1A/TNFR1 (By  
 CC similarity).  
 CC -1- DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF DISEASES, INCLUDING  
 CC CANCER AND INFECTION, AND IS CHARACTERIZED BY GENERAL ILL HEALTH  
 CC AND MALNUTRITION.  
 CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.  
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 CC  
 DR EMBL: X54001; CA37949.1; -  
 DR EMBL: X54859; CA38639.1; -  
 DR EMBL: X57321; CA40591.1; -  
 DR EMBL: AJ251914; CAB63852.1; -  
 DR EMBL: M29079; AAA31128.1; -  
 DR PIR: S12606; S12606.  
 DR PIR: S17290; S17290.  
 DR PIR: S18965; S18965.  
 DR HSP; P01375; 4TSV.  
 DR InterPro: IPR003636; TNF\_abC.  
 DR InterPro: IPR00478; TNF\_family.  
 DR Pfam: PF00229; TNF\_1.  
 DR PRINTS; PR01234; TNECROSISFC.  
 DR ProDom; PD002012; TNF\_abC; 1.  
 DR SMART; SM00207; TNF\_1.  
 DR PROSITE; PS00251; TNF\_1; 1.  
 DR PROSITE; PS50049; TNF\_2; 1.  
 KM Cytokine, Cytotoxin; Transmembrane; Phosphorylation; Signal-anchor.  
 FT CHAIN 1 232 TUMOR NECROSIS FACTOR, MEMBRANE FORM.  
 FT CHAIN 77 232 TUMOR NECROSIS FACTOR, SOLUBLE FORM.  
 FT DOMAIN 1 35 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 36 56 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)  
 FT (POTENTIAL).  
 FT DOMAIN 57 232 EXTRACELLULAR (POTENTIAL).  
 FT SITE 76 77 CLEAVAGE (BY ADAM17) (BY SIMILARITY).  
 FT MOD\_RES 2 2 PHOSPHORYLATION (BY CK1) (BY SIMILARITY).  
 FT DISULFID 144 176 BY SIMILARITY.  
 SQ SEQUENCE 232 AA; 25254 MW; 65B28F702D99C8BE CRC64;  
 Query Match 77.4%; Score 65; DB 1; Length 232;  
 Best Local Similarity 76.9%; Pred. No. 0.0024; Indels 0; Gaps 0;  
 Matches 10; Conservative 2; Mismatches 1;  
 QY 2 KDPPEGAELKPMY 14  
 :|||||  
 DB 178 KETPEGAERKPMY 190

RESULT 6  
 ID TNFA\_DELLE STANDARD; PRT; 233 AA.  
 AC O8WNRI;  
 DT 15-JUN-2002 (Rel. 41, Created)  
 DT 15-JUN-2002 (Rel. 41, Last sequence update)  
 DE Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor  
 ligand superfamily member 2) (cachectin).  
 GN TNF OR TNFSF2 OR TNFA.  
 OS Delphinapterus leucas (Beluga whale).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Cetacea; Odontoceti;  
 OC Monodontidae; Delphinapterus.  
 OX NCBI\_TaxId=9749;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RX PubMed-11768130;  
 RA Denis F., Archambault D.;  
 RT "Molecular cloning and characterization of beluga whale  
 RT (Delphinapterus leucas) Interleukin-1beta and tumor necrosis  
 RT factor-alpha.";  
 RL Can. J. Vet. Res. 65:233-240(2001).  
 CC -1- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and  
 CC TNFRSF1B/TNFR. It is mainly secreted by macrophages and can  
 CC induce cell death of certain tumor cell lines. It is potent  
 CC pyrogen causing fever by direct action or by stimulation of  
 CC Interleukin 1 secretion and is implicated in the induction of  
 CC cachexia, under certain conditions it can stimulate cell  
 CC proliferation and induce cell differentiation (By similarity).  
 CC -1- SUBUNIT: Homotrimer (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an  
 CC extracellular soluble form (By similarity).  
 CC -1- PPM: The soluble form derives from the membrane form by  
 CC proteolytic processing (By similarity).  
 CC -1- PPM: The membrane form, but not the soluble form, is  
 CC phosphorylated on serine residues. Dephosphorylation of the  
 CC membrane form occurs by binding to soluble TNFRSF1A/TNFR1 (By  
 CC similarity).  
 CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL: AF320323; AAL56946.1; -  
 DR InterPro: IPR003636; TNF\_abc.  
 DR InterPro: IPR000478; TNF\_family.  
 DR Pfam: PF00229; TNF\_1.  
 DR PRINTS: PRO1234; TNECROSISFCT.  
 DR PRODOM: PD002012; TNF\_abc; 1.  
 DR SMART: SM00207; TNF\_1.  
 DR SMART: SM00251; TNF\_1; 1.  
 DR PROSITE: PS00251; TNF\_1; 1.  
 DR PROSITE: PS50049; TNF\_2; 1.  
 KM Cytokine; Cytotoxin; Transmembrane; Glycoprotein; Phosphorylation;  
 KM Signal-anchor.  
 FT CHAIN 1 233  
 FT CHAIN 78 233  
 FT DOMAIN 1 35  
 FT TRANSMEM 36 56  
 FT DOMAIN 57 233  
 FT SITE 77 78  
 FT MOD\_RES 2 2  
 FT DISULFID 145 177  
 FT CARBOHYD 95 95  
 SQ SEQUENCE 233 AA; 25420 MW; 2DF37DCB8C9E961 CAC64;  
 Query Match 77.4%; Score 65; DB 1; Length 233;  
 Best Local Similarity 76.9%; Pred. No. 0.0024;  
 Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

GN TNF OR TNFSE2 OR TNFA.  
 OS Felis silvestris catus (Cat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.  
 OX NCBI\_TaxID=9685;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Blood;  
 RX MEDLINE-91016860; PubMed-2216740;  
 RA McGraw R.A., Coffee B.W., Otto C.M., Drews R.T., Rawlings C.A.;  
 RT "Gene sequence of feline tumor necrosis factor alpha.";  
 RL Nucleic Acids Res. 18:5563-5563(1990).  
 CC [2]  
 CC SEQUENCE FROM N.A.  
 CC TISSUE=Bone marrow;  
 RA Daniel S.L., Brenner C.A., Legendre A.M., Solomon A., Rouse B.T.;  
 RL Submitted (xxx-1993) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and  
 CC TNFRSF1B/TNFR. It is mainly secreted by macrophages and can  
 CC induce cell death of certain tumor cell lines. It is potent  
 CC pyrogen causing fever by direct action or by stimulation of  
 CC Interleukin 1 secretion and is implicated in the induction of  
 CC cachexia, under certain conditions it can stimulate cell  
 CC proliferation and induce cell differentiation.  
 CC -1- SUBUNIT: Homotrimer (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an  
 CC extracellular soluble form (By similarity).  
 CC -1- PPM: The soluble form derives from the membrane form by  
 CC proteolytic processing (By similarity).  
 CC -1- PPM: The membrane form, but not the soluble form, is  
 CC phosphorylated on serine residues. Dephosphorylation of the  
 CC membrane form occurs by binding to soluble TNFRSF1A/TNFR1 (By  
 CC similarity).  
 CC -1- DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF DISEASES, INCLUDING  
 CC CANCER AND INFECTION, AND IS CHARACTERIZED BY GENERAL ILL HEALTH  
 CC AND MALNUTRITION.  
 CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL: X54000; CA37948.1; -  
 DR EMBL: M92061; AAA30818.1; -  
 DR PIR: S11688; S11688.  
 DR HSSP: P01375; 4TSV.  
 DR InterPro: IPR003636; TNF\_abc.  
 DR InterPro: IPR000478; TNF\_family.  
 DR Pfam: PF00229; TNF\_1.  
 DR PRINTS: PRO1234; TNECROSISFCT.  
 DR PRODOM: PD002012; TNF\_abc; 1.  
 DR SMART: SM00207; TNF\_1.  
 DR PROSITE: PS00251; TNF\_1; 1.  
 DR PROSITE: PS50049; TNF\_2; 1.  
 KM Cytokine; Cytotoxin; Transmembrane; Phosphorylation; Signal-anchor.  
 FT CHAIN 1 233  
 FT CHAIN 77 233  
 FT DOMAIN 1 35  
 FT TRANSMEM 36 56  
 FT DOMAIN 57 233  
 FT SITE 76 77  
 FT MOD\_RES 2 2  
 FT DISULFID 145 177  
 FT CONFLICT 28 28  
 FT CONFLICT 104 104  
 FT CONFLICT 151 151  
 FT CONFLICT 155 155  
 FT CONFLICT 210 210  
 FT CONFLICT 210 210  
 FT A -> T (IN REF. 2).  
 FT T -> A (IN REF. 2).

50 SEQUENCE 233 AA: 25322 MW: 434D239567862506 CRC64;

Query Match 77.4%; Score 65; DB 1; Length 233;

Best Local Similarity 76.9%; Pred. No. 0.0024; Mismatches 1; Indels 0; Gaps 0;

0Y 2 KDTPEGAEKPMW 14

DB 179 RETPEGAEKPMW 191

RESULT 8

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ID TNFA\_HUMAN STANDARD; PRT; 233 AA.  
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DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor  
ligand superfamily member 2) (cachectin).  
GN TNF OR TNFSF2 OR TNFA.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_Taxid=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA MEDLINE-87217060; PubMed-3555974;  
RA MEDOSPASOV S.A., Shakov A.N., Turetskaya R.L., Mett V.A.,  
RA Azizov M.M., Georgiev G.P., Korobko V.G., Dobrynya V.N.,  
RA Filippov S.A., Bystryy N.S., Boldyreva E.F., Chupillo S.A.,  
RA Chumakov A.M., Shingarova L.N., Ovchinnikov Y.A.;  
RT "Tandem arrangement of genes coding for tumor necrosis factor (TNF-  
alpha) and lymphotoxin (TNF-beta) in the human genome.";  
RT Cold Spring Harb. Symp. Quant. Biol. 51:611-624(1986).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA MEDLINE-85086244; PubMed-6392892;  
RA Pennica D., Nedwin G.E., Hayflick J.S., Seedburg P.H., Derynck R.,  
RA Palladino M.A., Kohr W.J., Aggarwal B.B., Goeddel D.V.;  
RT "Human tumor necrosis factor: precursor structure, expression and  
homology to lymphotoxin.";  
RT Nature 312:724-729(1984).  
RN [3]  
RP SEQUENCE FROM N.A.  
RA MEDLINE-85137898; PubMed-3883195;  
RA Shirai T., Yamaguchi H., Ito H., Todd C.W., Wallace R.B.;  
RT "Cloning and expression in Escherichia coli of the gene for human  
tumor necrosis factor.";  
RT Nature 313:803-806(1985).  
RN [4]  
RP SEQUENCE FROM N.A.  
RA MEDLINE-86016093; PubMed-2995927;  
RA Nedwin G.E., Naylor S.L., Sakaguchi A.Y., Smith D.H.,  
RA Jarrett-Nedwin J., Pennica D., Goeddel D.V., Gray P.W.;  
RT "Human lymphotoxin and tumor necrosis factor genes: structure,  
homology and chromosomal localization.";  
RT Nucleic Acids Res. 13:6361-6373(1985).  
RN [5]  
RP SEQUENCE FROM N.A.  
RA MEDLINE-85142190; PubMed-3856324;  
RA Wang A.M., Cressey A.A., Lachner M.B., Lin L.S., Strickler J.,  
RA van Arsdale J.N., Yamamoto R., Mark D.F.;  
RT "Molecular cloning of the complementary DNA for human tumor necrosis  
factor.";  
RT Science 228:149-154(1985).  
RN [6]  
RP SEQUENCE FROM N.A.  
RA MEDLINE-86030296; PubMed-3932069;  
RA Marrenhout A., Eransen L., Tavernier J., van der Heyden J., Tizard R.,  
RA Kawashima E., Shaw A., Johnson M.J., Semon D., Mueller R.,  
RA Ruysschaert M.R., van Vliet A., Fiers W.;  
RT "Molecular cloning and expression of human tumor necrosis factor and

RT comparison with mouse tumor necrosis factor.";  
RN Eur. J. Biochem. 152:515-522(1985).  
RN [7]  
RP SEQUENCE FROM N.A.  
RA MEDLINE-93272029; PubMed-8499947;  
RA Iris F.J.M., Bougueleret L., Prieur S., Caterina D., Primas G.,  
RA Perrot V., Jurka J., Rodriguez-Rome P., Claverie J.-M., Dausset J.,  
RA Cohen D.;  
RT "Dense Alu clustering and a potential new member of the NF kappa B  
family within a 90 kilobase HLA class III segment.";  
RN Nat. Genet. 3:137-145(1993).  
RN [8]  
RP SEQUENCE FROM N.A.  
RA Bowen L., Madan A., Qin S., Shafer T., James R., Ratcliffe A.,  
RA Abbasi N., Dickhoff R., Loretz C., Madan A., Dors M., Young J.,  
RA Lasky S., Hood L.;  
RT "Sequence of the human major histocompatibility complex class III  
region.";  
RN Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.  
RN [9]  
RP SEQUENCE FROM N.A.  
RA Shina S., Tamiya G., Oka A., Inoko H.;  
RT "Homo sapiens 2,229,817bp genomic DNA of 6p21.3 HLA class I region.";  
RN Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.  
RN [10]  
RP SEQUENCE FROM N.A.  
RA Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poel C.L., Yi Q.,  
RA Nickerson D.A.;  
RN Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.  
RN [11]  
RP SEQUENCE FROM N.A.  
RA Straussberg R.;  
RT Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.  
RN [12]  
RP PHOSPHORYLATION (MEMBRANE FORM).  
RA PubMed-8597870;  
RT "Phosphorylation of the 26 kDa TNF precursor in monocytic cells and in  
transfected HeLa cells.";  
RN J. Inflamm. 45:152-160(1995).  
RN [13]  
RP PHOSPHORYLATION BY CK1 AND DEPHOSPHORYLATION.  
RA PubMed-10205166;  
RA Watts A.D., Hunt N.H., Wanigasakara Y., Bloomfield G., Wallach D.,  
RA Roufogalis B.D., Chaudhuri G.;  
RT "A casein kinase I motif present in the cytoplasmic domain of members  
of the tumor necrosis factor ligand family is implicated in 'reverse  
signaling'.";  
RN EMBO J. 18:2119-2126(1999).  
RN [14]  
RP MUTAGENESIS.  
RA MEDLINE-91184128; PubMed-2009860;  
RA Ostrade X.V., Tavernier J., Prange T., Fiers W.;  
RT "Localization of the active site of human tumor necrosis factor  
(hTNF) by mutational analysis.";  
RN EMBO J. 10:827-836(1991).  
RN [15]  
RP MYRISTOYLATION.  
RA MEDLINE-93018820; PubMed-1402651;  
RA Stevenson F.T., Bursten S.L., Locksley R.M., Lovett D.H.;  
RT "Myristyl acylation of the tumor necrosis factor alpha precursor on  
specific lysine residues.";  
RN J. Exp. Med. 176:1053-1062(1992).  
RN [16]  
RP CLEAVAGE BY ADAM17.  
RA MEDLINE-97186575; PubMed-9034191;  
RA Moss M.L., Jin S.-L.C., Milla M.E., Burkhardt W., Carter H.L.,  
RA Chen W.-J., Clay W.C., Didsbury J.R., Hassler D., Hoffman C.R.,  
RA Kost T.A., Lambert M.H., Leesnitzer M.A., McCauley P., McGehee G.,  
RA Mitchell J., Moyer M., Patel G., Rocque W., Overton L.K., Schoenen F.,  
RA Seton T., Su J.-L., Warner J., Willard D., Becherer J.D.;  
RT "Cloning of a disintegrin metalloproteinase that processes precursor

RT tumor-necrosis factor-alpha. ",  
RL Nature 385:733-736(1997).  
RN [17]  
RX X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).  
RA MEDLINE=89159409; PubMed=2922050;  
RT Jones E.Y., Stuart D.I., Walker N.P.;  
RL "Structure of tumour necrosis factor. ",  
RN Nature 338:225-228(1989).  
RX X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).  
RA MEDLINE=91193276; PubMed=1964681;  
RT Jones E.Y., Stuart D.I., Walker N.P.;  
RL "The structure of tumour necrosis factor -- implications for  
RT biological function. ";  
RN J. Cell Sci. Suppl. 13:11-18(1990).  
RX [19]  
RN X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).  
RX MEDLINE=90008932; PubMed=2551905;  
RA Eck M.J., Sprang S.R.;  
RT "The structure of tumor necrosis factor-alpha at 2.6-A resolution.  
RL Implications for receptor binding. ";  
RN J. Biol. Chem. 264:17595-17605(1989).  
RX [20]  
RN X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF MUTANT ARG-107.  
RX MEDLINE=981147459; PubMed=94488135;  
RA Reed C., Fu Z.Q., Wu J., Xue Y.N., Harrison R.W., Chen M.J.,  
RT Weber I.T.;  
RL "Crystal structure of TNF-alpha mutant R1D with greater affinity for  
RT receptor R1 compared with R2. ";  
RN Protein Eng. 10:1101-1107(1997).  
RX [21]  
RN X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF MUTANT M35.  
RX MEDLINE=98113178; PubMed=9442056;  
RA Cha S.S., Kim J.S., Cho H.S., Shin N.K., Jeong W., Shin H.C.,  
RT Kim Y.C., Hahn J.H., Oh B.H.;  
RL "High resolution crystal structure of a human tumor necrosis factor-  
RT alpha mutant with low systemic toxicity. ";  
RN J. Biol. Chem. 273:2153-2160(1998).  
RX -1- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and  
TNFRSF1B/TNFR. It is mainly secreted by macrophages and can  
CC induce cell death of certain tumor cell lines. It is potent  
CC pyrogen causing fever by direct action or by stimulation of  
CC interleukin 1 secretion and is implicated in the induction of  
CC cachexia, under certain conditions it can stimulate cell  
CC proliferation and induce cell differentiation.  
CC -1- SUBUNIT: Homotrimer.  
CC -1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN  
CC EXTRACELLULAR SOLUBLE FORM.  
CC -1- PM: THE SOLUBLE FORM DERIVES FROM THE MEMBRANE FORM BY  
CC PROTEOLYTIC PROCESSING.  
CC -1- PM: The membrane form, but not the soluble form, is  
CC phosphorylated on serine residues. Dephosphorylation of the  
CC membrane form occurs by binding to soluble TNFRSF1A/TNFR1.  
CC -1- DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF DISEASES, INCLUDING  
CC CANCER AND INFECTION, AND IS CHARACTERIZED BY GENERAL ILL HEALTH  
CC AND MALNUTRITION.  
CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.  
CC -----  
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CC EMBL/ X02910.CAA26669.1; -

Query Match	77.48;	Score 65;	DB 1;	Length 233;
Best Local Similarity	76.98;	Pred. No. 0.0024;		
Matches 10; Conservative	2;	Mismatches 1;	Indels 0;	Gaps 0;
OY	2	KDPEGAEIKPMY	14	

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Db      179  RETPEGAARKPMY 191

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ID      TNFA_MACFA  STANDARD:  PRT:  233 AA.
AC      TNFA_MACFA  79337;
DT      15-JUL-1998 (Rel. 36, Created)
DT      15-JUL-1998 (Rel. 36, Last sequence update)
DT      15-JUN-2002 (Rel. 41, Last annotation update)
DE      Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor
DE      ligand superfamily member 2) (Cachectin).
DE      TNF OR TNFSF2 OR TNFA.
OS      Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Cerepithedeidae;
OC      Cercopitheciae; Macaca.
OX      NCBI_TaxID=9541;
RX      (1)
RN      SEQUENCE FROM N.A.
RP      TISSUE=Lymphocytes;
RA      Tatsumi M.;
RL      Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
CC      -I- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and
CC      TNFRSF1B/TNFR. It is mainly secreted by macrophages and can
CC      induce cell death of certain tumor cell lines. It is potent
CC      pyrogen causing fever by direct action or by stimulation of
CC      interleukin 1 secretion and is implicated in the induction of
CC      cachexia. Under certain conditions, it can stimulate cell
CC      proliferation and induce cell differentiation.
CC      -I- SUBUNIT: Homotrimer (By similarity).
CC      -I- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an
CC      extracellular soluble form (By similarity).
CC      -I- PIM: The soluble form derives from the membrane form by
CC      proteolytic processing (By similarity).
CC      -I- PIM: The membrane form, but not the soluble form, is
CC      phosphorylated on serine residues. Dephosphorylation of the
CC      membrane form occurs by binding to soluble TNFRSF1A/TNFR1 (By
CC      similarity).
CC      -I- DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF DISEASES, INCLUDING
CC      CANCER AND INFECTION, AND IS CHARACTERIZED BY GENERAL ILL HEALTH
CC      AND MALNUTRITION.
CC      -I- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
CC      -----
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CC      entities requires a license agreement. (See http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch.)
CC      -----
CC      EMBL; AB000513; BAA19131.1; -.
CC      HSSP; P01375; 4TSV.
CC      InterPro; IPR003636; TNF_abc.
CC      InterPro; IPR000478; TNF_family.
CC      Pfam; PF00229; TNF_1.
CC      PRINTS; PR01234; TNECROSISFCT.
CC      ProDom; PD002012; TNF_abc; 1.
CC      SMART; SM00207; TNF_1.
CC      PROSITE; PS00251; TNF_1; 1.
CC      PROSITE; PSS0049; TNF_2; 1.
CC      Cytokine; Cytotoxin; Transmembrane; Phosphorylation; Signal-anchor.
CC      KW      CHAIN 1 233
CC      FT      CHAIN 1 233
CC      FT      CHAIN 77 233
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CC      FT      DOMAIN 57 233
CC      FT      SITE 76 77
CC      FT      MOD_RES 2 2
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CC      CLEAVAGE (BY ADAM17) (BY SIMILARITY).
CC      PHOSPHORYLATION (BY CK1) (BY SIMILARITY).
CC      BY SIMILARITY.

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5Q SEQUENCE 233 AA; 25558 MW; 6ABF2C3AB132C217 CRC64;  
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 Best Local Similarity 76.9%; Pred. No. 0.0024;  
 Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 0Y 2 KDPEGAELEKPMY 14  
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 Db 179 RETPEGAELKPMY 191

RESULT 10  
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 ID TNFA\_MACMU STANDARD; PRT; 233 AA.  
 AC P48094:  
 DT 01-FEB-1996 (Rel. 33, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor  
 ligand superfamily member 2) (Cachectin).  
 GN TNF OR TNFSF2 OR TNFA.  
 OS Macaca mulatta (Rhesus macaque).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
 OC Cercopithecinae; Macaca.  
 OX NCBI\_TaxID=9544;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE-96003435; PubMed-7561102;  
 RA Villinger F.J., Brar S.S., Mayne A.E., Chikkala N., Ansari A.A.;  
 RT "Comparative sequence analysis of cytokine genes from human and  
 RT nonhuman primates."  
 RL J. Immunol. 155:3946-3954(1995).  
 CC -I- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and  
 CC TNFRSF1B/TNFR. It is mainly secreted by macrophages and can  
 CC induce cell death of certain tumor cell lines. It is potent  
 CC pyrogen causing fever by direct action or by stimulation of  
 CC interleukin 1 secretion and is implicated in the induction of  
 CC cachexia, under certain conditions it can stimulate cell  
 CC proliferation and induce cell differentiation.  
 CC -I- SUBUNIT: Homotrimer (By similarity).  
 CC -I- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an  
 CC extracellular soluble form (By similarity).  
 CC -I- PTM: The soluble form derives from the membrane form by  
 CC proteolytic processing (By similarity).  
 CC -I- PTM: The membrane form, but not the soluble form, is  
 CC phosphorylated on serine residues. Dephosphorylation of the  
 CC membrane form occurs by binding to soluble TNFRSF1A/TNFR1 (By  
 CC similarity).  
 CC -I- DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF DISEASES, INCLUDING  
 CC CANCER AND INFECTION, AND IS CHARACTERIZED BY GENERAL ILL HEALTH  
 CC AND MALNUTRITION.  
 CC -I- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.  
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 CC -----  
 CC EMBL: P01375; AAA86712.1; -  
 CC HSSP: P01375; 4TSV.  
 CC InterPro: IPR003636; TNF\_abc.  
 CC InterPro: IPR000478; TNF\_family.  
 CC Pfam: PF00229; TNF.1.  
 CC PRINTS: P01234; TNCRSISFCT.  
 CC ProDom: PD002012; TNF\_abc; 1.  
 CC SMART: SMO0207; TNF.1.  
 CC PROSITE: PS00251; TNF\_1; 1.  
 CC PROSITE: PS0049; TNF\_2; 1.  
 KW Cytokine; Cytotoxin; Transmembrane; Phosphorylation; Signal-anchor.

FT CHAIN 1 233 TUMOR NECROSIS FACTOR, MEMBRANE FORM.  
 FT CHAIN 77 233 TUMOR NECROSIS FACTOR, SOLUBLE FORM.  
 FT DOMAIN 1 35 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 36 56 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)  
 FT DOMAIN 57 233 (POTENTIAL).  
 FT SITE 76 77 EXTRACELLULAR (POTENTIAL).  
 FT MOD\_RES 2 2 CLEAVAGE (BY ADAM17) (BY SIMILARITY).  
 FT DISULFID 145 177 PHOSPHORYLATION (BY CK1) (BY SIMILARITY).  
 FT DISULFID 145 177 BY SIMILARITY.  
 SQ SEQUENCE 233 AA; 25630 MW; 96F85050595FD59 CRC64;  
 Query Match 77.4%; Score 65; DB 1; Length 233;  
 Best Local Similarity 76.9%; Pred. No. 0.0024;  
 Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 0Y 2 KDPEGAELEKPMY 14  
 :|||||  
 Db 179 RETPEGAELKPMY 191

RESULT 11  
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 ID TNFA\_PAPHU STANDARD; PRT; 233 AA.  
 AC 077510;  
 DT 15-DEC-1998 (Rel. 37, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor  
 ligand superfamily member 2) (Cachectin).  
 GN TNF OR TNFSF2 OR TNFA.  
 OS Papio hamadryas ursinus (chacma baboon).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
 OC Cercopithecinae; Papio.  
 OX NCBI\_TaxID=36229;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE-98147379; PubMed-9488055;  
 RA Haudek S.B., Redl H., Schlag G., Giroir B.P.;  
 RT "Complementary DNA (cDNA) sequence of baboon tumor necrosis factor  
 RT alpha."  
 RL Mol. Immunol. 34:1041-1042(1997).  
 CC -I- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and  
 CC TNFRSF1B/TNFR. It is mainly secreted by macrophages and can  
 CC induce cell death of certain tumor cell lines. It is potent  
 CC pyrogen causing fever by direct action or by stimulation of  
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 CC cachexia, under certain conditions it can stimulate cell  
 CC proliferation and induce cell differentiation.  
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 CC -I- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an  
 CC extracellular soluble form (By similarity).  
 CC -I- PTM: The soluble form derives from the membrane form by  
 CC proteolytic processing (By similarity).  
 CC -I- PTM: The membrane form, but not the soluble form, is  
 CC phosphorylated on serine residues. Dephosphorylation of the  
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 CC AND MALNUTRITION.  
 CC -I- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.  
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 CC -----  
 CC EMBL: AF019963; AAC31675.1; -  
 CC HSSP: P01375; 4TSV.



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DR InterPro: IPR003636; TNF_abc.
DR InterPro: IPR000478; TNF_family.
DR Pfam: PF00229; TNF_1.
DR PRINTS: PR01234; TNFCROSISFCT.
DR ProDom: PD002012; TNF_abc; 1.
DR SMART: SM00207; TNF_1.
DR PROSITE: PS00251; TNF_1; 1.
DR PROSITE: PS50049; TNF_2; 1.
DR CYTOKINE: Cytotoxin; Transmembrane; Phosphorylation; Signal-anchor.
KW CHAIN 1 233 TUMOR NECROSIS FACTOR, MEMBRANE FORM.
FT CHAIN 77 233 TUMOR NECROSIS FACTOR, SOLUBLE FORM.
FT DOMAIN 1 35 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 36 36 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
(POTENTIAL).
FT DOMAIN 57 233 EXTRACELLULAR (POTENTIAL).
FT SITE 76 77 CLEAVAGE (BY ADAM17) (BY SIMILARITY).
FT MOD_RES 2 2 PHOSPHORYLATION (BY CK1) (BY SIMILARITY).
FT DISULFID 145 177 BY SIMILARITY.
SQ SEQUENCE 233 AA; 25658 MW; B940325058D4A03 CRC64;

Query Match 77.4%; Score 65; DB 1; Length 233;
Best Local Similarity 76.9%; Pred. No. 0.0024;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 KDTPEGAELKRPWY 14
Db 179 RETPEGAELKRPWY 191

RESULT 12
TNFA_PAPSP STANDARD; PRT; 233 AA.
AC P33620;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor
ligand superfamily member 2) (Cachectin).
GN TNF OR TNFSF2 OR TNFA.
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
Papio.
NCBI_TaxID=61183;
[1]
SEQUENCE FROM N.A.
RA Santanvala M., Edwards A.;
RL Submitted (SEP-1991) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and
induce cell death of certain tumor cell lines. It is potent
pyrogen causing fever by direct action or by stimulation of
interleukin 1 secretion and is implicated in the induction of
cachexia, under certain conditions it can stimulate cell
proliferation and induce cell differentiation.
CC -1- SUBUNIT: Homotrimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an
extracellular soluble form (By similarity).
CC -1- PTM: The soluble form derives from the membrane form by
proteolytic processing (By similarity).
CC -1- PTM: The membrane form, but not the soluble form, is
phosphorylated on serine residues. Dephosphorylation of the
membrane form occurs by binding to soluble TNFRSF1A/TNFR1 (By
similarity).
CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
-----
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CC EMBL: X62141; CAA44068.1; -.
DR PIR: S22052; S22052.
DR HSSP: P01375; 1A8M.
DR InterPro: IPR003636; TNF_abc.
DR InterPro: IPR000478; TNF_family.
DR Pfam: PF00229; TNF_1.
DR PRINTS: PR01234; TNFCROSISFCT.
DR ProDom: PD002012; TNF_abc; 1.
DR SMART: SM00207; TNF_1.
DR PROSITE: PS00251; TNF_1; 1.
DR PROSITE: PS50049; TNF_2; 1.
KW CYTOKINE: Cytotoxin; Transmembrane; Phosphorylation; Signal-anchor;
Myristate.
FT CHAIN 1 233 TUMOR NECROSIS FACTOR, MEMBRANE FORM.
FT CHAIN 77 233 TUMOR NECROSIS FACTOR, SOLUBLE FORM.
FT DOMAIN 1 35 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 36 56 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
(POTENTIAL).
FT DOMAIN 57 233 EXTRACELLULAR (POTENTIAL).
FT SITE 76 77 CLEAVAGE (BY ADAM17) (BY SIMILARITY).
FT MOD_RES 2 2 PHOSPHORYLATION (BY CK1) (BY SIMILARITY).
FT LIPID 19 19 MYRISTATE (BY SIMILARITY).
FT LIPID 20 20 MYRISTATE (BY SIMILARITY).
FT DISULFID 145 177 BY SIMILARITY.
SQ SEQUENCE 233 AA; 25557 MW; 455360B48DC74173 CRC64;

Query Match 77.4%; Score 65; DB 1; Length 233;
Best Local Similarity 76.9%; Pred. No. 0.0024;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 KDTPEGAELKRPWY 14
Db 179 RETPEGAELKRPWY 191

RESULT 13
TNFA_TURTR STANDARD; PRT; 233 AA.
AC Q9BEA1;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor
ligand superfamily member 2) (Cachectin).
GN TNF OR TNFSF2 OR TNFA.
OS Turislops truncatus (Atlantic bottle-nosed dolphin).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Cetacea; Odontoceti; Delphinidae;
Ox Turislops.
NCBI_TaxID=9739;
[1]
SEQUENCE FROM N.A.
RX PubMed=11587733;
RA Shoji Y., Inoue Y., Sugisawa H., Ito T., Sakai T.;
RT "Molecular cloning and functional characterization of bottlenose
dolphin (Turislops truncatus) tumor necrosis factor alpha.";
RL Vet. Immunol. Immunopathol. 82:183-192(2001).
CC -1- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and
induce cell death of certain tumor cell lines. It is potent
pyrogen causing fever by direct action or by stimulation of
interleukin 1 secretion and is implicated in the induction of
cachexia, under certain conditions it can stimulate cell
proliferation and induce cell differentiation (By similarity).
CC -1- SUBUNIT: Homotrimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an
extracellular soluble form (By similarity).
CC -1- PTM: The soluble form derives from the membrane form by
proteolytic processing (By similarity).
CC -1- PTM: The membrane form, but not the soluble form, is
phosphorylated on serine residues. Dephosphorylation of the
membrane form occurs by binding to soluble TNFRSF1A/TNFR1 (By
similarity).

```

CC similarity).

CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.

CC -----

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CC -----

DR EMBL; AB049358; BAB39855.1; -

DR HSSP; P01375; 4TSV.

DR InterPro; IPR003636; TNF\_abc.

DR InterPro; IPR000478; TNF\_family.

DR Pfam; PF00229; TNF\_1.

DR PRINTS; PR01234; TNECROSISFCT.

DR PRODOM; PD002012; TNF\_abc; 1.

DR SMART; SM00207; TNF\_1.

DR PROSITE; PS00251; TNF\_1; 1.

DR PROSITE; PS50049; TNF\_2; 1.

DR Cytochrome; Cytochrome; Transmembrane; Glycoprotein; Phosphorylation;

KW Signal-anchor.

KW CHAIN 1 233 TUMOR NECROSIS FACTOR, MEMBRANE FORM.

FT CHAIN 78 233 TUMOR NECROSIS FACTOR, SOLUBLE FORM.

FT DOMAIN 1 35 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 36 56 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)

FT (POTENTIAL).

FT DOMAIN 57 233 EXTRACELLULAR (POTENTIAL).

FT SITE 77 78 CLEAVAGE (BY ADAM17) (BY SIMILARITY).

FT MOD\_RES 2 2 PHOSPHORYLATION (BY CK1) (BY SIMILARITY).

FT DISULFID 145 177 BY SIMILARITY.

FT CARBOHYD 95 95 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT SEQUENCE 233 AA; 25404 MW; 71CC39C699CC49D9 CRC64;

SQ

Query Match 77.4%; Score 65; DB 1; Length 233;

Best Local Similarity 76.9%; Pred. No. 0.0024;

Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 2 KDPGGAELKRPWY 14

Db 179 RETPEGAELKRPWY 191

RESULT 14

TNFA\_CAPHI STANDARD; PRT; 234 AA.

ID TNFA\_CAPHI STANDARD; PRT; 234 AA.

AC P13296; Q28320; Q9MYZ2;

DT 01-JAN-1990 (Rel. 13, Created)

DT 15-JUN-2002 (Rel. 41, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor

DE ligand superfamily member 2) (Cachectin).

GN TNF OR TNFSF2 OR TNFA.

OS Capra hircus (Goat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

OC Bovidae; Caprinae; Capra.

OC NCBI\_taxid=9925;

OX [1]

RN SEQUENCE FROM N.A.

RC TISSUE-Splenocyte;

RA Takakura H., Mori Y., Tatsumi M.;

RT "Molecular cloning of caprine TNF-alpha cDNA and its expression in

RT E.coli and insect cells."

RL Submitted (JUL-1996) to the EMBL/Genbank/DBJ databases.

RN [2]

RP SEQUENCE OF 41-234 FROM N.A.

RA Goldstein I.M., Henner D., Talhouk A.;

RL Submitted (MAR-1989) to the EMBL/Genbank/DBJ databases.

RN [3]

RP SEQUENCE OF 44-234 FROM N.A.

RC TISSUE-Ovarian follicle;

RA Wang B., Zhang Y.;

RT "Goat ovarian TNF alpha cDNA sequence."

RL Submitted (JUN-2000) to the EMBL/Genbank/DBJ databases.

RN [4]

RP SEQUENCE OF 75-234 FROM N.A.

RC TISSUE-Blood;

RA Rument E.;

RL Submitted (JAN-1994) to the EMBL/Genbank/DBJ databases.

CC -1- FUNCTION: Cytokine that binds to TNFSF1A/TNFR1 and

CC TNFSF1B/TNFR. It is mainly secreted by macrophages and can

CC induce cell death of certain tumor cell lines. It is potent

CC pyrogen causing fever by direct action or by stimulation of

CC interleukin 1 secretion and is implicated in the induction of

CC cachexia, under certain conditions it can stimulate cell

CC proliferation and induce cell differentiation.

CC -1- SUBUNIT: Homotrimer (By similarity).

CC -1- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an

CC extracellular soluble form (By similarity).

CC -1- PTM: The soluble form derives from the membrane form by

CC proteolytic processing (By similarity).

CC -1- PTM: The membrane form, but not the soluble form, is

CC phosphorylated on serine residues. Dephosphorylation of the

CC membrane form occurs by binding to soluble TNFSF1A/TNFR1 (By

CC similarity).

CC -1- DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF DISEASES, INCLUDING

CC CANCER AND INFECTION, AND IS CHARACTERIZED BY GENERAL ILL HEALTH

CC AND MAINTENANCE.

CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.

CC -1- CAUTION: Ref.2 sequence differs from that shown due to a

CC frameshift in position 60.

CC -----

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CC between the Swiss Institute of Bioinformatics and the EMBL outstation-

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CC -----

DR EMBL; D86587; BAA13130.1; -

DR EMBL; X14828; CAA32937.1; ALT\_FRAME.

DR EMBL; AF276985; AAF87741.1; -

DR EMBL; X77317; CAA54523.1; -

DR PIR; S06192; S06192.

DR HSSP; P01375; 4TSV.

DR InterPro; IPR003636; TNF\_abc.

DR InterPro; IPR000478; TNF\_family.

DR Pfam; PF00229; TNF\_1.

DR PRODOM; PD002012; TNF\_abc; 1.

DR SMART; SM00207; TNF\_1.

DR PROSITE; PS00251; TNF\_1; 1.

DR PROSITE; PS50049; TNF\_2; 1.

DR Cytochrome; Cytochrome; Transmembrane; Phosphorylation; Signal-anchor.

KW CHAIN 1 234

FT CHAIN 79 234

FT DOMAIN 1 35

FT TRANSMEM 36 56

FT (POTENTIAL).

FT DOMAIN 57 233

FT MOD\_RES 2 2

FT SITE 78 79

FT DISULFID 146 178

FT CARBOHYD 96 96

FT CONFLICT 79 79

FT CONFLICT 119 119

FT CONFLICT 129 129

FT CONFLICT 155 155

FT CONFLICT 164 164

FT CONFLICT 184 184

FT CONFLICT 185 185

FT CONFLICT 215 215

SQ SEQUENCE 234 AA; 25519 MW; 9768E33BBBAB041 CRC64;

EXTRACELLULAR (POTENTIAL).

PHOSPHORYLATION (BY CK1) (BY SIMILARITY).

CLEAVAGE (BY ADAM17) (BY SIMILARITY).

BY SIMILARITY.

N-LINKED (GLCNAC. . .) (POTENTIAL).

R -> S (IN REF. 4).

E -> A (IN REF. 4).

T -> N (IN REF. 4).

H -> Q (IN REF. 4).

Y -> D (IN REF. 4).

E -> EG (IN REF. 4).

MISSING (IN REF. 2).

Q -> L (IN REF. 3 AND 4).



Query Match 77.4%; Score 65; DB 1; Length 234;  
 Best Local Similarity 76.9%; Pred. No. 0.0024;  
 Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 2 KDPTEGAELKPMY 14  
 DB 180 KETPEGAELKPMY 192

## RESULT 15

TNFA\_MARMO STANDARD; PRT; 233 AA.  
 AC 035734;  
 DT 15-JUL-1999 (Rel. 38, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor  
 ligand superfamily member 2) (Cachectin).  
 GN TNF OR TNFSF2 OR TNFA.  
 OS Marmota monax (Woodchuck).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;  
 OC Marmota.  
 OX NCBI\_TaxID=9995;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Peripheral blood;  
 RX MEDLINE=9819553; PubMed=9472070;  
 RA Lohrangel B., Lu M., Rogendorf M.;  
 RT "Molecular cloning of the woodchuck cytokines: TNF-alpha, IFN-gamma,  
 and IL-6."  
 RL Immunogenetics 47:332-335(1998).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Peripheral blood;  
 RA Zhou H., Hu J., Seeger C.;  
 RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Peripheral blood;  
 RX MEDLINE=20184748; PubMed=10721723;  
 RA Li D.H., Havelle E.A., Brown C.L., Cullen J.M.;  
 RT "Woodchuck lymphotoxin-alpha, -beta and tumor necrosis factor genes:  
 structure, characterization and biological activity."  
 RL Gene 242:295-305(2000).  
 CC -1- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and  
 TNFRSF1B/TNFR. It is mainly secreted by macrophages and can  
 induce cell death of certain tumor cell lines. It is potent  
 pyrogen causing fever by direct action or by stimulation of  
 interleukin 1 secretion and is implicated in the induction of  
 cachexia, under certain conditions it can stimulate cell  
 proliferation and induce cell differentiation.  
 CC -1- SUBUNIT: Homotrimer (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an  
 extracellular soluble form (By similarity).  
 CC -1- PTM: The soluble form derives from the membrane form by  
 proteolytic processing (By similarity).  
 CC -1- PTM: The membrane form, but not the soluble form, is  
 phosphorylated on serine residues. Dephosphorylation of the  
 membrane form occurs by binding to soluble TNFRSF1A/TNFR1 (By  
 similarity).  
 CC -1- DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF DISEASES, INCLUDING  
 CANCER AND INFECTION, AND IS CHARACTERIZED BY GENERAL ILL HEALTH  
 AND MALNUTRITION.  
 CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.  
 CC -----  
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CC EMBL: Y14137; CA74569.1; -  
 DR EMBL: AF062491; AAC32615.1; -  
 DR EMBL: AF012910; AAF34863.1; -  
 DR HSSP: P06804; 2TNF.  
 DR InterPro: IPR003636; TNF\_abc.  
 DR InterPro: IPR000478; TNF\_family.  
 DR Pfam: PF00229; TNF; 1.  
 DR PRINTS: PR01234; TNECROSISFCT.  
 DR PRODOM: PD002012; TNF\_abc; 1.  
 DR SMART: SM00207; TNF; 1.  
 DR PROSITE: PS00251; TNF\_1; 1.  
 DR PROSITE: PS50049; TNF\_2; 1.  
 KW Cytokine; Cytotoxin; Transmembrane; Phosphorylation; Signal-anchor.  
 FT CHAIN 1 233  
 FT CHAIN 78 233  
 FT DOMAIN 1 35  
 FT TRANSMEM 36 56  
 FT DOMAIN 57 233  
 FT SITE 77 78  
 FT MOD\_RES 2 2  
 FT DISULFID 146 177  
 SQ SEQUENCE 233 AA; 25764 MW; 34D3D1965DAE0E7 CRC64;  
 (POTENTIAL).  
 (POTENTIAL).  
 EXTRACELLULAR (POTENTIAL).  
 CLEAVAGE (BY ADAM17) (BY SIMILARITY).  
 PHOSPHORYLATION (BY CK1) (BY SIMILARITY).  
 BY SIMILARITY.

OY 1 KDPTEGAELKPMY 14  
 DB 178 KESLEGAELKPMY 191

Search completed: April 4, 2003, 08:40:26  
 Job time : 5.64516 secs

GenCore version 5.1.4.p5.4578  
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OM protein - protein search, using sw model

Run on: April 4, 2003, 08:37:16 ; Search time 20.3226 Seconds  
(without alignments)  
141.944 Million cell updates/sec

Title: US-09-779-703-2

Perfect score: 84

Sequence: 1 PKDTREGALRPMY 14

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

SPTREMBL\_21:\*

- 1: sp.archaea:\*
- 2: sp.bacteria:\*
- 3: sp.fungi:\*
- 4: sp.human:\*
- 5: sp.invertebrate:\*
- 6: sp.mammal:\*
- 7: sp.mhc:\*
- 8: sp.organelle:\*
- 9: sp.phage:\*
- 10: sp.plant:\*
- 11: sp rodent:\*
- 12: sp.virus:\*
- 13: sp.vertibrate:\*
- 14: sp.unclassified:\*
- 15: sp.virus:\*
- 16: sp.bacteriap:\*
- 17: sp.archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	84	100.0	235	11	Q9J126	Q9J126 rattus norv
2	80	95.2	235	11	Q9J127	Q9J127 rattus norv
3	77	91.7	156	11	Q9J124	Q9J124 sigmodon hi
4	77	91.7	217	11	Q9JRG6	Q9JRG6 peromyscus
5	75	89.3	216	11	Q70332	Q70332 mesocricetu
6	65	77.4	66	4	Q9P102	Q9P102 homo sapien
7	65	77.4	149	6	Q97543	Q97543 actus nancy
8	65	77.4	217	6	Q9BEF4	Q9BEF4 cabassous u
9	65	77.4	232	4	Q9UIV3	Q9UIV3 homo sapien
10	62	73.8	215	11	Q9JND1	Q9JND1 tamiasciuru
11	62	73.8	216	6	Q9BEC4	Q9BEC4 talpa europ
12	62	73.8	217	6	Q9BEC5	Q9BEC5 tenrec ecan
13	60	71.4	157	4	Q43647	Q43647 homo sapien
14	60	71.4	215	6	Q9BEF8	Q9BEF8 erinaceus e
15	60	71.4	217	6	Q9BEC0	Q9BEC0 cyclopes di
16	58	69.0	217	6	Q9BEC1	Q9BEC1 bradypus tr

17	57	67.9	104	6	Q27978	Q27978 bos taurus
18	51	60.7	138	6	Q9TIG7	Q9TIG7 actus lemur
19	51	60.7	149	6	Q97538	Q97538 actus vocif
20	51	60.7	149	6	Q9TNG8	Q9TNG8 actus nigri
21	51	60.7	234	6	Q9TJ3	Q9TJ3 equus caball
22	48	57.1	216	6	Q9BEC9	Q9BEC9 ochnona pr
23	48	57.1	674	11	Q60979	Q60979 mus musculu
24	48	57.1	1649	16	Q9CFA2	Q9CFA2 lactococcus
25	47	56.0	259	12	Q86972	Q86972 western equ
26	47	56.0	1235	12	Q9IBP3	Q9IBP3 western equ
27	47	56.0	1241	12	Q66579	Q66579 eastern equ
28	47	56.0	1242	12	Q86678	Q86678 eastern equ
29	47	56.0	1242	12	Q9PZX7	Q9PZX7 eastern equ
30	47	56.0	1242	12	Q9PZX6	Q9PZX6 eastern equ
31	47	56.0	1242	12	Q9PZX5	Q9PZX5 eastern equ
32	47	56.0	1242	12	Q9PZX4	Q9PZX4 eastern equ
33	47	56.0	1242	12	Q9PZX3	Q9PZX3 eastern equ
34	47	56.0	1242	12	Q9PZX2	Q9PZX2 eastern equ
35	47	56.0	1242	12	Q9PZX1	Q9PZX1 eastern equ
36	47	56.0	1242	12	Q9PZX0	Q9PZX0 eastern equ
37	47	56.0	1242	12	Q9PZW9	Q9PZW9 eastern equ
38	47	56.0	1242	12	Q9PZW8	Q9PZW8 eastern equ
39	47	56.0	1242	12	Q9PZW7	Q9PZW7 eastern equ
40	47	56.0	1242	12	Q9PZW6	Q9PZW6 eastern equ
41	47	56.0	1242	12	Q88790	Q88790 eastern equ
42	47	56.0	1242	12	Q88792	Q88792 eastern equ
43	47	56.0	1242	12	Q88793	Q88793 eastern equ
44	47	56.0	1242	12	Q88794	Q88794 eastern equ
45	47	56.0	1242	12	Q88795	Q88795 eastern equ

#### ALIGNMENTS

##### RESULT 1

Q9J126 PRELIMINARY; PRT; 235 AA.

AC Q9J126;  
 DT 01-OCT-2000 (TREMBLrel. 15, Created)  
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE TNF-alpha propeptide 3 (Fragment).  
 OS Rattus norvegicus (Rat).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID-10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-DARK AGOUTI;  
 RA Seidel M.F., Junter M.-P., Vetter H.;  
 RT "TNF-alpha polymorphism in rats with collagen-induced arthritis.";  
 RL Submitted (MAY-2000) to the EMBL/Genbank/DBJ databases.  
 DR EMBL; AF269160; AAF82568.1; -;  
 DR HSSP; P06804; 2TNF.  
 DR InterPro: IPR003636; TNF\_abc.  
 DR InterPro: IPR00478; TNF\_family.  
 DR Pfam; PF00229; TNF\_1.  
 DR PRINTS; PRO1234; TNFROSISFCT.  
 DR PRODOM; PD002012; TNF\_abc; 1.  
 DR SMART; SM00207; TNF\_1.  
 DR PROSITE; PS00251; TNF\_1; 1.  
 DR PROSITE; PS50049; TNF\_2; 1.  
 FT NON-TER  
 SQ SEQUENCE 235 AA; 25789 MW; C801B92D049C2F2E CRC64;

##### Query Match

Best Local Similarity 100.0%; Score 84; DB 11; Length 235;  
 Pred. No. 9.8e-06;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 PKDTREGALRPMY 14  
 DB 180 PKDTREGALRPMY 193

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RESULT 2
09J127 PRELIMINARY: PRT: 235 AA.
AC 09J127:
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE TNF-alpha propeptide 5 (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
XX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DARK AGOUTI;
RA Seidel M.F., Junter M.-P., Vetter H.;
RT "TNF-alpha polymorphism in rats with collagen-induced arthritis.";
RL Submitted (MAY-2000) to the EMBL/Genbank/DBJ databases.
DR EMBL: AF269159; AAF82567.1; -
DR HSSP: P06804; 2TNF.
DR InterPro: IPR003636; TNF_abc.
DR InterPro: IPR00478; TNF_family.
DR Pfam: PF00229; TNF_1.
DR PRINTS: PRO1234; TNECROSISFCT.
DR ProDom: PD002012; TNF_abc; 1.
DR SMART: SM00207; TNF_1.
DR PROSITE: PS00251; TNF_1; 1.
DR PROSITE: PS50049; TNF_2; 1.
FT NON_TER 235
SQ SEQUENCE 235 AA; 25806 MW; 12A8EC6D0491428D CRC64;

Query Match 95.2%; Score 80; DB 11; Length 235;
Best Local Similarity 92.9%; Pred. No. 4.4e-05;
Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKDPEGAELKPMY 14
Db 180 PKDPEGAELKPMY 193

RESULT 3
09J124 PRELIMINARY: PRT: 156 AA.
AC 09J124:
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Tumor necrosis factor alpha (Fragment).
OS Sigmodon hispidus (Hispid cotton rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
OC Sigmodon.
XX NCBI_TaxID=42415;
RN [1]
RP SEQUENCE FROM N.A.
RA Blanco J.C., Pletneva L.M., Prince G.A.;
RT "Sigmodon hispidus cytokines, chemokines and interferons.";
RL Submitted (SEP-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL: AF421388; AAL18818.1; -
DR InterPro: IPR003636; TNF_abc.
DR InterPro: IPR00478; TNF_family.
DR Pfam: PF00229; TNF_1.
DR ProDom: PD002012; TNF_abc; 1.
DR PROSITE: PS00251; TNF_1; UNKNOWN.1.
DR PROSITE: PS50049; TNF_2; 1.
FT NON_TER 1
SQ SEQUENCE 156 AA; 17303 MW; DC565F3BC3C826E4 CRC64;

Query Match 91.7%; Score 77; DB 11; Length 156;
Best Local Similarity 85.7%; Pred. No. 8.6e-05;
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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QY 1 PKDPEGAELKPMY 14
Db 101 PKDPEGAELKPMY 114

RESULT 4
09ERG6 PRELIMINARY: PRT: 217 AA.
AC 09ERG6:
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Tumor necrosis factor alpha (Fragment).
OS Peromyscus maniculatus (Deer mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
OC Peromyscus.
XX NCBI_TaxID=10042;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=SPLEEN;
RA Herbst M.M., Schountz T.;
RT "Cloning of the deer mouse interferon gamma, interleukin-10 and tumor
necrosis factor genes.";
RL Submitted (SEP-2000) to the EMBL/Genbank/DBJ databases.
DR EMBL: AF307013; AAG30264.1; -
DR HSSP: P06804; 2TNF.
DR InterPro: IPR003636; TNF_abc.
DR InterPro: IPR00478; TNF_family.
DR Pfam: PF00229; TNF_1.
DR PRINTS: PRO1234; TNECROSISFCT.
DR ProDom: PD002012; TNF_abc; 1.
DR SMART: SM00207; TNF_1.
DR PROSITE: PS00251; TNF_1; 1.
DR PROSITE: PS50049; TNF_2; 1.
FT NON_TER 217
SQ SEQUENCE 217 AA; 23964 MW; D6F90C74C0B3021F CRC64;

Query Match 91.7%; Score 77; DB 11; Length 217;
Best Local Similarity 85.7%; Pred. No. 0.00012;
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKDPEGAELKPMY 14
Db 172 PKDPEGAELKPMY 185

RESULT 5
07O332 PRELIMINARY: PRT: 216 AA.
AC 07O332:
DT 01-AUG-1998 (TREMBLrel. 07, Created)
DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
DT 01-OCT-2001 (TREMBLrel. 18, Last annotation update)
DE Tumor necrosis factor-alpha (Fragment).
OS Mesocricetus auratus (Golden hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Mesocricetus.
XX NCBI_TaxID=10036;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=SPLEEN;
RA MEDLINE=98234044; PubMed=9573100;
RA Melby P.C., Tryon V.V., Chandrasekar B., Freeman G.L.;
RT "Cloning of Syrian hamster (Mesocricetus auratus) cytokine cDNAs and
analysis of cytokine mRNA expression in experimental visceral
leishmaniasis.";
RT Infect. Immun. 66:2135-2142(1998).
DR EMBL: AF046215; AAC40100.1; -
DR HSSP: P06804; 2TNF.
DR InterPro: IPR003636; TNF_abc.

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DR InterPro: IPR000478; TNF_family.
DR Pfam: PF00229; TNF_1.
DR PRINTS: PR01234; TNECROSISFCT.
DR PRODOM: PD002012; TNF_abc; 1.
DR SMART: SM00207; TNF_1.
DR PROSITE: PS00251; TNF_1; 1.
DR PROSITE: PS50049; TNF_2; 1.
DR NON_TER 1
FT NON_TER 1
SQ SEQUENCE 216 AA; 23793 MW; BADAE3F8345B533 CRC64;

Query Match
Best Local Similarity 89.3%; Score 75; DB 11; Length 216;
Pred. No. 0.0026;
Matches 12; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 KDTPEGAELKPMY 14
Db 170 KETPEGELKPMY 183

RESULT 6
O9P1Q2 PRELIMINARY; PRT; 66 AA.
AC O9P1Q2:
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE APC1 protein (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-PROSTATE TUMOR;
RA Shao C., Yan W., Zhu F., Yue W., Chai Y., Zhao Z., Wang C.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF098751; AAF7192.1; -.
DR HSSP: P01375; 5TSW.
DR InterPro: IPR003636; TNF_abc.
DR InterPro: IPR000478; TNF_family.
DR Pfam: PF00229; TNF_1.
DR PRINTS: PR01234; TNECROSISFCT.
DR PRODOM: PD002012; TNF_abc; 1.
DR PROSITE: PS50049; TNF_2; 1.
FT NON_TER 66
SQ SEQUENCE 66 AA; 7300 MW; C58DC3537E6D368 CRC64;

Query Match
Best Local Similarity 77.4%; Score 65; DB 4; Length 66;
Pred. No. 0.003;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 2 KDTPEGAELKPMY 14
Db 31 RETPEGAELKPMY 43

RESULT 7
O9T543 PRELIMINARY; PRT; 149 AA.
AC O9T543:
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-OCT-2001 (TREMBlrel. 18, Last annotation update)
DE Tumor necrosis factor alpha (Fragment).
OS TNF-ALPHA.
GN Aotus nancyanae (Owl monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotidae; Aotus.
OX NCBI_TaxID=37293;
RN [1]
RP SEQUENCE FROM N.A.
RA Echeverry S.J., Hernandez E., Moreno A., Patarroyo M.E., Murillo L.A.;

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RT "Identification, cloning and sequencing of different interleukin genes
in 4 Aotus species."
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF014513; AAD01539.1; -.
DR HSSP: P01375; 4TSV.
DR InterPro: IPR003636; TNF_abc.
DR InterPro: IPR000478; TNF_family.
DR Pfam: PF00229; TNF_1.
DR PRINTS: PR01234; TNECROSISFCT.
DR PRODOM: PD002012; TNF_abc; 1.
DR SMART: SM00207; TNF_1.
DR PROSITE: PS00251; TNF_1; 1.
DR PROSITE: PS50049; TNF_2; 1.
DR NON_TER 1
FT NON_TER 1
SQ SEQUENCE 149 AA; 16466 MW; 3C2A6140778FFA8A CRC64;

Query Match
Best Local Similarity 77.4%; Score 65; DB 6; Length 149;
Pred. No. 0.0072;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 2 KDTPEGAELKPMY 14
Db 96 RETPEGAELKPMY 108

RESULT 8
O9BEF4 PRELIMINARY; PRT; 217 AA.
AC O9BEF4:
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Tumor necrosis factor (Fragment).
OS TNFA.
OC Capassous uelinctus (Southern naked-tailed armadillo).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Edentata; Dasypodidae; Capassous.
OX NCBI_TaxID=48852;
RN [1]
RP SEQUENCE FROM N.A.
RA van Dijk M.A.M., de Jong W.W.;
RT "Indels indicate that rodents are monophyletic and lagomorphs are
their sister group."
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ268829; CAC28518.1; -.
DR HSSP: P01375; 4TSV.
DR InterPro: IPR003636; TNF_abc.
DR InterPro: IPR000478; TNF_family.
DR Pfam: PF00229; TNF_1.
DR PRINTS: PR01234; TNECROSISFCT.
DR PRODOM: PD002012; TNF_abc; 1.
DR SMART: SM00207; TNF_1.
DR PROSITE: PS00251; TNF_1; 1.
DR PROSITE: PS50049; TNF_2; 1.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 217 AA; 23742 MW; 83C591DD6883FD86 CRC64;

Query Match
Best Local Similarity 77.4%; Score 65; DB 6; Length 217;
Pred. No. 0.011;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 2 KDTPEGAELKPMY 14
Db 171 RETPEGAELKPMY 183

RESULT 9
O9UIV3 PRELIMINARY; PRT; 232 AA.
AC O9UIV3:
DT 01-MAY-2000 (TREMBlrel. 13, Created)

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01-MAY-2000 (TREMblrel. 13, last sequence update)  
 01-DEC-2001 (TREMblrel. 19, last annotation update)  
 Tumor necrosis factor.  
 TNF.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 NCBI\_TaxID=9606;  
 [1]  
 RN SEQUENCE FROM N.A.  
 RP MEDLINE=93272029; PubMed=849947;  
 RX Iris F., Bougueleret L., Prieur S., Caterina D., Primas G., Perrot V.,  
 RA Jurta J., Rodriguez-Rome P., Clavierie J., Cohen D., Dausset J.,  
 RT "Dense Alu clustering and a potential new member of the NFkappa  
 family within a 90 Kilobase HLA class III segment.",  
 RL Nat. Genet. 3:137-145(1993).  
 [2]  
 RN SEQUENCE FROM N.A.  
 RP MEDLINE=96215741; PubMed=8629302;  
 RX Utans U., Quist W.C., Mehnans B.M., Wilson J.E., Arceci R.J.,  
 RA Wallace A.F., Russell M.E.,  
 RT "Allograft inflammatory factor-1. A cytokine-responsive macrophage  
 molecule expressed in transplanted human hearts.",  
 RL Transplantation 61:1387-1392(1996).  
 [3]  
 RN SEQUENCE FROM N.A.  
 RP MEDLINE=96006565; PubMed=7590964;  
 RX Holinger I., de Baey A., Messer G., Kick G., Zwierzina H.,  
 RA Weiss E.H.,  
 RT "Cloning and genomic characterization of LST1: a new gene in the human  
 TNF region.",  
 RL Immunogenetics 42:315-322(1995).  
 [4]  
 RN SEQUENCE FROM N.A.  
 RP MEDLINE=93208881; PubMed=7916655;  
 RX Browning J.L., Ngam-ek A., Lawton P., Demarinis J., Tizard R.,  
 RA Chow E.P., Hession C., O'Brine-Greco B., Foley S.F., Ware C.F.,  
 RT "Lymphotoxin-beta: A new member of the TNF family that forms a  
 heteromeric complex with lymphotoxin on the cell surface.",  
 RL Cell 72:847-856(1993).  
 [5]  
 RN SEQUENCE FROM N.A.  
 RP MEDLINE=86016093; PubMed=2995927;  
 RX Nedwin G.E., Naylor S.L., Sakaguchi A.Y., Smith D., Jarrett-Nedwin J.,  
 RA Pennica D., Goeddel D.V., Gray P.W.,  
 RT "Human lymphotoxin and tumor necrosis factor genes: structure,  
 homology and chromosomal localization.",  
 RL Nucleic Acids Res. 13:6361-6373(1985).  
 [6]  
 RN SEQUENCE FROM N.A.  
 RP MEDLINE=91086846; PubMed=1670638;  
 RX Messer G., Spengler U., Jung M.C., Honold G., Bloemer K., Pape G.R.,  
 RA Rietmuller G., Weiss E.H.,  
 RT "Polymorphic Structure of the Tumor Necrosis Factor (TNF) Locus: An  
 NcoI Polymorphism in the First Intron of the Human TNF-beta Gene  
 Correlates with a Variant Amino Acid in Position 26 and a Reduced  
 Level of TNF-beta Production.",  
 RL J. Exp. Med. 173:209-219(1991).  
 [7]  
 RN SEQUENCE FROM N.A.  
 RP MEDLINE=91139175; PubMed=1671667;  
 RX Abraham L.J., Du D.C., Zahedi K., Dawkins R.L., Whitehead A.S.,  
 RT "Haploypic polymorphisms of the TNF gene.",  
 RL Immunogenetics 33:50-53(1991).  
 [8]  
 RN SEQUENCE FROM N.A.  
 RP MEDLINE=94362679; PubMed=8081366;  
 RX Albertella M.R., Campbell D.R.,  
 RT "Characterization of a novel gene in the human major  
 histocompatibility complex that encodes a potential new member of the  
 I kappa B family of proteins.",  
 RL Hum. Mol. Genet. 3:793-799(1994).  
 [9]

RP SEQUENCE FROM N.A.  
 RX MEDLINE=95324911; PubMed=7601445;  
 RA Peelman L., Chardon P., Nunes M., Renard C., Geffroyet C., Vaiman M.,  
 RA Van Zeveren A., Coppieters W., Van de Weghe A., Bouquet Y., Choy W.,  
 RA Strominger J., Spies T.,  
 RT "The BART Gene in the MHC Encodes an Evolutionarily Conserved Putative  
 Nuclear RNA Helicase of the D-E-A-D Family.",  
 RL Genomics 26:210-218(1995).  
 [10]  
 RN SEQUENCE FROM N.A.  
 RP MEDLINE=20132445; PubMed=10668961;  
 RX Neville M.J., Campbell R.D.,  
 RT "Alternative splicing of the LST-1 gene located in the major  
 histocompatibility complex on human chromosome 6.",  
 RL DNA Seq. 8:155-160(1997).  
 [11]  
 RN SEQUENCE FROM N.A.  
 RP MEDLINE=98035883; PubMed=9367684;  
 RX de Baey A., Fellerhoff B., Meier S., Martinozzi S., Weidle U.,  
 RA Weiss E.H.,  
 RT "Complex expression pattern of the TNF region gene LST1 through  
 differential regulation, initiation, and alternative splicing.",  
 RL Genomics 45:591-600(1997).  
 [12]  
 RN SEQUENCE FROM N.A.  
 RP MEDLINE=98149985; PubMed=9480751;  
 RX Shilina T., Tamiya G., Oka A., Yamagata T., Yamagata N., Kikkawa E.,  
 RA Goto K., Mizuki N., Watanabe K., Fukuzumi Y., Taguchi S., Sugawara C.,  
 RA Ono A., Chen L., Yamazaki M., Tashiro H., Ando A., Ikemura T.,  
 RA Kimura M., Inoko H.,  
 RT "Nucleotide sequencing analysis of the 146-kilobase segment around the  
 IKBL and MICA genes at the centromeric end of the HLA class I  
 region.",  
 RL Genomics 47:372-382(1998).  
 DR EMBL: Y14768; CAA75070.1; -.  
 DR HSSP: P01375; ATSV.  
 DR InterPro: IPR003636; TNF\_abc.  
 DR InterPro: IPR000478; TNF\_family.  
 DR Pfam: PF00229; TNF\_1.  
 DR PRINTS: PR01234; TNECROSISFCT.  
 DR ProDom: PD002012; TNF\_abc; 1.  
 DR SMART: SM00207; TNF\_1.  
 DR PROSITE: PS00251; TNF\_1; 1.  
 DR PROSITE: PS0049; TNF\_2; 1.  
 SQ SEQUENCE 232 AA; 25446 MW; E4D71B19C6AE0D03 CRC64;  
 Query Match 77.4%; Score 65; DB 4; Length 232;  
 Best Local Similarity 76.9%; Pred. No. 0.012;  
 Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 QY 2 KDPFGAEIKRPY 14  
 DB 178 RPEFGAEKRPY 190  
 ID O99ND1 PRELIMINARY; PRT; 215 AA.  
 AC O99ND1;  
 DT 01-JUN-2001 (TREMblrel. 17, Created)  
 DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)  
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)  
 DE Tumor necrosis factor (Fragment).  
 GN TNFA.  
 OS Tamiasciurus hudsonicus (American red squirrel).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;  
 OC Tamiasciurus.  
 NCBI\_TaxID=10009;  
 OX [1]  
 RP SEQUENCE FROM N.A.  
 RA van Dijk M.A.M., de Jong W.W.,  
 RT "Indels indicate that rodents are monophyletic and lagomorphs are

RT their sister group.";  
 RL Submitted (FEB-2000) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: AJ286824; CAC28540.1; -.  
 DR HSSP: P06804; TNF.  
 DR InterPro: IPR003636; TNF\_abc.  
 DR InterPro: IPR00478; TNF\_family.  
 DR Pfam: PF00229; TNF\_1.  
 DR PRINTS: PR01234; TNECROSISFCT.  
 DR ProDom: PD002012; TNF\_abc; 1.  
 DR SMART: SM00207; TNF\_1.  
 DR PROSITE: PS00251; TNF\_1; 1.  
 DR PROSITE: PS0049; TNF\_2; 1.  
 DR NON\_TER 1  
 FT NON\_TER 1  
 SQ SEQUENCE 215 AA; 23739 MW; 36441309CA5E9898 CRC64;  
 Query Match 73.8%; Score 62; DB 11; Length 215;  
 Best Local Similarity 71.4%; Pred. No. 0.032;  
 Matches 10; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
 OY 1 PRDPGAEALKPWY 14  
 DB 168 PRLEGAEKFPWY 181  
 RESULT 11  
 O9BEC4 PRELIMINARY; PRT; 216 AA.  
 AC O9BEC4;  
 DT 01-JUN-2001 (TREMblrel. 17, Created)  
 DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)  
 DE 01-DEC-2001 (TREMblrel. 19, Last annotation update)  
 DE Tumor necrosis factor (Fragment).  
 GN TNFA.  
 OS Talpa europaea (European mole).  
 OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Insectivora; Talpidae; Talpa.  
 OX NCBI\_TaxID=9375;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA van Dijk M.A.M., de Jong W.W.;  
 RT "Indels indicate that rodents are monophyletic and lagomorphs are  
 RT their sister group.";  
 RL Submitted (FEB-2000) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: AJ286831; CAC28539.1; -.  
 DR HSSP: P01375; IABM.  
 DR InterPro: IPR003636; TNF\_abc.  
 DR InterPro: IPR00478; TNF\_family.  
 DR Pfam: PF00229; TNF\_1.  
 DR PRINTS: PR01234; TNECROSISFCT.  
 DR ProDom: PD002012; TNF\_abc; 1.  
 DR SMART: SM00207; TNF\_1.  
 DR PROSITE: PS00251; TNF\_1; 1.  
 DR PROSITE: PS0049; TNF\_2; 1.  
 DR NON\_TER 1  
 FT NON\_TER 1  
 SQ SEQUENCE 216 AA; 23542 MW; FFFEE8DBD27836 CRC64;  
 Query Match 73.8%; Score 62; DB 6; Length 216;  
 Best Local Similarity 69.2%; Pred. No. 0.033;  
 Matches 9; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
 OY 2 KDTPGAEALKPWY 14  
 DB 170 REPPEGAELRPWY 182  
 RESULT 12  
 O9BEC5 PRELIMINARY; PRT; 217 AA.  
 AC O9BEC5;  
 DT 01-JUN-2001 (TREMblrel. 17, Created)  
 DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)

DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)  
 DE Tumor necrosis factor (Fragment).  
 GN TNFA.  
 OS Tenrec ecaudatus (tailless tenrec).  
 OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Insectivora; Tenrecidae; Tenrecinae; Tenrec.  
 OX NCBI\_TaxID=94439;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA van Dijk M.A.M., de Jong W.W.;  
 RT "Indels indicate that rodents are monophyletic and lagomorphs are  
 RT their sister group.";  
 RL Submitted (FEB-2000) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: AJ286826; CAC28538.1; -.  
 DR HSSP: P01375; ATSV.  
 DR InterPro: IPR003636; TNF\_abc.  
 DR InterPro: IPR00478; TNF\_family.  
 DR Pfam: PF00229; TNF\_1.  
 DR PRINTS: PR01234; TNECROSISFCT.  
 DR ProDom: PD002012; TNF\_abc; 1.  
 DR SMART: SM00207; TNF\_1.  
 DR PROSITE: PS00251; TNF\_1; 1.  
 DR PROSITE: PS0049; TNF\_2; 1.  
 DR NON\_TER 1  
 FT NON\_TER 1  
 SQ SEQUENCE 217 AA; 23845 MW; 1C5013E9B777B54A CRC64;  
 Query Match 73.8%; Score 62; DB 6; Length 217;  
 Best Local Similarity 69.2%; Pred. No. 0.033;  
 Matches 9; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
 OY 2 KDTPGAEALKPWY 14  
 DB 171 REPPEGSETRKPWY 183  
 RESULT 13  
 O43647 PRELIMINARY; PRT; 157 AA.  
 AC O43647;  
 DT 01-JUN-1998 (TREMblrel. 06, Created)  
 DT 01-JUN-1998 (TREMblrel. 06, Last sequence update)  
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)  
 DE Tumor necrosis factor alpha (Fragment).  
 GN TNFA.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Jang J.S., Kim B.E.;  
 RL Submitted (JAN-1998) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: AF043342; AAC03542.1; -.  
 DR HSSP: P01375; IABM.  
 DR InterPro: IPR003636; TNF\_abc.  
 DR InterPro: IPR00478; TNF\_family.  
 DR Pfam: PF00229; TNF\_1.  
 DR PRINTS: PR01234; TNECROSISFCT.  
 DR ProDom: PD002012; TNF\_abc; 1.  
 DR SMART: SM00207; TNF\_1.  
 DR PROSITE: PS00251; TNF\_1; 1.  
 DR PROSITE: PS0049; TNF\_2; 1.  
 DR NON\_TER 1  
 FT NON\_TER 1  
 SQ SEQUENCE 157 AA; 17380 MW; D134482267B9F20 CRC64;  
 Query Match 71.4%; Score 60; DB 4; Length 157;  
 Best Local Similarity 69.2%; Pred. No. 0.049;  
 Matches 9; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
 OY 2 KDTPGAEALKPWY 14  
 DB 103 REPPEGAELKPWY 115

```

RESULT 14
Q9BEE8 PRELIMINARY; PRT; 215 AA.
AC Q9BEE8;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Tumor necrosis factor (Fragment).
GN TNFA.
OS Eriaceus europaeus (Western European hedgehog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Insectivora; Erinaceidae; Erinaceinae; Erinaceus.
OX NCBI_TaxID=9365;
RN [1]
RP SEQUENCE FROM N.A.
RA van Dijk M.A.M., de Jong W.W.;
RT "Indels indicate that rodents are monophyletic and lagomorphs are
RT their sister group."
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ266830; CAC28522.1; -.
DR HSSP; P01375; 4TSV.
DR InterPro; IPR003636; TNF_abc.
DR InterPro; IPR00478; TNF_family.
DR Pfam; PF00229; TNF; 1.
DR PRINTS; PR01234; TNECROSISFCT.
DR ProDom; PD002012; TNF_abc; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS50049; TNF_2; 1.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 215 AA; 23696 MW; 3E337E7E65F074EA CRC64;

Query Match 71.4%; Score 60; DB 6; Length 215;
Best Local Similarity 75.0%; Pred. No. 0.068;
Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 DPEGAEKPMY 14
Db 170 ETPEGAERPMY 181

RESULT 15
Q9BEG0 PRELIMINARY; PRT; 217 AA.
AC Q9BEG0;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Tumor necrosis factor (Fragment).
GN TNFA.
OS Cyclopes didactylus (silky anteater).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Edentata; Myrmecophagidae; Cyclopes.
OX NCBI_TaxID=84074;
RN [1]
RP SEQUENCE FROM N.A.
RA van Dijk M.A.M., de Jong W.W.;
RT "Indels indicate that rodents are monophyletic and lagomorphs are
RT their sister group."
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ266828; CAC28514.1; -.
DR HSSP; P01375; 1ABM.
DR InterPro; IPR003636; TNF_abc.
DR InterPro; IPR00478; TNF_family.
DR Pfam; PF00229; TNF; 1.
DR PRINTS; PR01234; TNECROSISFCT.
DR ProDom; PD002012; TNF_abc; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS50049; TNF_2; 1.

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FT NON_TER 1 1
FT NON_TER 217 217
SQ SEQUENCE 217 AA; 23753 MW; F760E887FC29EBB CRC64;

Query Match 71.4%; Score 60; DB 6; Length 217;
Best Local Similarity 69.2%; Pred. No. 0.069;
Matches 9; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 KDPGEAEKPMY 14
Db 171 RETPEGAERPMY 183

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Search completed: April 4, 2003, 08:42:05  
Job time : 21.3226 secs

GenCore version 5.1.4\_p5.4578  
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## OM protein - protein search, using sw model

Run on: April 4, 2003, 08:37:56 ; Search time 9.03226 Seconds  
(without alignments)  
45.606 Million cell updates/sec

Title: US-09-779-703-2

Perfect score: 84

Sequence: 1 PKDFEGAEKPMW 14

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:\*

1: /cgcn2\_6/prodata/1/1aa/5A\_COMB.pep:\*

2: /cgcn2\_6/prodata/1/1aa/5A\_COMB.pep:\*

3: /cgcn2\_6/prodata/1/1aa/5A\_COMB.pep:\*

4: /cgcn2\_6/prodata/1/1aa/5A\_COMB.pep:\*

5: /cgcn2\_6/prodata/1/1aa/5A\_COMB.pep:\*

6: /cgcn2\_6/prodata/1/1aa/5A\_COMB.pep:\*

## SUMMARIES

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

Result No.	Score	Query Match Length	ID	Description
1	84	100.0	17 2 US-08-500-860A-24	Sequence 24, Appl
2	84	100.0	156 2 US-08-500-860A-36	Sequence 36, Appl
3	84	100.0	157 5 PCT-US93-02475-8	Sequence 8, Appl
4	84	100.0	157 5 PCT-US93-02475-9	Sequence 9, Appl
5	84	100.0	235 4 US-08-883-086-7	Sequence 7, Appl
6	84	100.0	17 2 US-08-500-860A-25	Sequence 25, Appl
7	65	77.4	147 1 US-07-668-517-1	Sequence 2, Appl
8	65	77.4	148 1 US-07-668-517-2	Sequence 1, Appl
9	65	77.4	148 1 US-07-668-517-15	Sequence 15, Appl
10	65	77.4	149 1 US-07-668-517-3	Sequence 3, Appl
11	65	77.4	149 1 US-07-668-517-16	Sequence 16, Appl
12	65	77.4	150 1 US-07-668-517-4	Sequence 4, Appl
13	65	77.4	150 1 US-07-668-517-5	Sequence 5, Appl
14	65	77.4	150 1 US-07-668-517-6	Sequence 6, Appl
15	65	77.4	150 1 US-07-668-517-9	Sequence 9, Appl
16	65	77.4	150 1 US-07-668-517-10	Sequence 10, Appl
17	65	77.4	150 1 US-07-668-517-11	Sequence 11, Appl
18	65	77.4	150 1 US-07-668-517-12	Sequence 12, Appl
19	65	77.4	150 1 US-07-668-517-13	Sequence 13, Appl
20	65	77.4	150 1 US-07-668-517-14	Sequence 14, Appl
21	65	77.4	150 1 US-07-668-517-17	Sequence 17, Appl
22	65	77.4	150 1 US-07-668-517-19	Sequence 19, Appl
23	65	77.4	150 1 US-07-668-517-29	Sequence 29, Appl
24	65	77.4	150 1 US-07-668-517-31	Sequence 31, Appl
25	65	77.4	150 1 US-07-668-517-35	Sequence 35, Appl
26	65	77.4	150 1 US-07-668-517-37	Sequence 37, Appl
27	65	77.4	150 1 US-07-994-469A-6	Sequence 6, Appl

28	65	77.4	150 1 US-07-994-469A-7	Sequence 7, Appl
29	65	77.4	150 1 US-07-994-469A-8	Sequence 8, Appl
30	65	77.4	150 1 US-07-994-469A-57	Sequence 57, Appl
31	65	77.4	150 4 US-09-286-529-25	Sequence 25, Appl
32	65	77.4	151 1 US-07-668-517-7	Sequence 7, Appl
33	65	77.4	151 1 US-07-668-517-18	Sequence 18, Appl
34	65	77.4	151 1 US-07-668-517-19	Sequence 19, Appl
35	65	77.4	151 1 US-07-668-517-20	Sequence 20, Appl
36	65	77.4	151 1 US-07-668-517-22	Sequence 22, Appl
37	65	77.4	151 1 US-07-668-517-23	Sequence 23, Appl
38	65	77.4	151 1 US-07-668-517-24	Sequence 24, Appl
39	65	77.4	151 1 US-07-668-517-25	Sequence 25, Appl
40	65	77.4	151 1 US-07-668-517-26	Sequence 26, Appl
41	65	77.4	151 1 US-07-668-517-27	Sequence 27, Appl
42	65	77.4	151 1 US-07-668-517-28	Sequence 28, Appl
43	65	77.4	151 1 US-07-668-517-30	Sequence 30, Appl
44	65	77.4	151 1 US-07-668-517-32	Sequence 32, Appl
45	65	77.4	151 1 US-07-668-517-36	Sequence 36, Appl

## ALIGNMENTS

RESULT 1  
US-08-500-860A-24

; Sequence 24, Application US/08500860A

; Patent No. 5891679

GENERAL INFORMATION:

APPLICANT: LUCAS, RUDOLPH

APPLICANT: DE BAETSELER, PATRICK

APPLICANT: FRANSSEN, LUCIE

APPLICANT: SABON, ERWIN

TITLE OF INVENTION: TNP-MUTAINS, A PROCESS FOR PREPARING THEM AND

NUMBER OF SEQUENCES: 36

CORRESPONDENCE ADDRESS:

ADDRESSEE: NIXON & VANDERHAYE P.C.

STREET: 1100 NORTH GLEBE ROAD

CITY: ARLINGTON

STATE: VIRGINIA

COUNTRY: U.S.A.

ZIP: 22201-4714

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/500,860A

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: BYRNE, THOMAS E.

REGISTRATION NUMBER: 32,205

REFERENCE/DOCKET NUMBER: 1487-8

TELEPHONE: (703)816-4000

TELEFAX: (703)816-4100

INFORMATION FOR SEQ ID NO: 24:

SEQUENCE CHARACTERISTICS:

LENGTH: 17 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

FEATURE:

NAME/KEY: Modified-site

LOCATION: 1

OTHER INFORMATION: /note= "Biotin-Gly-Gly is coupled

OTHER INFORMATION: to the N-terminus of the peptide"

US-08-500-860A-24



Query Match 100.0%; Score 84; DB 2; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 9e-08;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PKDTPGAEKLPWY 14  
 |||||  
 DB 3 PKDTPGAEKLPWY 16

## RESULT 2

US-08-500-860A-36  
 ; Sequence 36, Application US/08500860A  
 ; Patent No. 5891679

GENERAL INFORMATION:  
 APPLICANT: LUCAS, RUDOLPH  
 APPLICANT: DE BAETSELIER, PATRICK  
 APPLICANT: FRANKEN, LUCIE  
 APPLICANT: SABON, EMIL  
 TITLE OF INVENTION: TNF-MUTAINS, A PROCESS FOR PREPARING THEM AND  
 TITLE OF INVENTION: THEIR USE AS ACTIVE SUBSTANCES IN PHARMACEUTICAL COMPOSITIONS  
 NUMBER OF SEQUENCES: 36  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: NIXON & VANDERHAYE P.C.  
 STREET: 1100 NORTH GLEBE ROAD  
 CITY: ARLINGTON  
 STATE: VIRGINIA  
 COUNTRY: U.S.A.  
 ZIP: 22201-4714

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/500,860A

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:  
 NAME: BYRNE, THOMAS E.

REGISTRATION NUMBER: 32,205

REFERENCE/DOCKET NUMBER: 1487-8

TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (703)816-4100

TELEFAX: (703)816-4100

TELEX: 200797 NIXN UR

INFORMATION FOR SEQ ID NO: 36:

SEQUENCE CHARACTERISTICS:  
 LENGTH: 156 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 US-08-500-860A-36

Query Match 100.0%; Score 84; DB 2; Length 156;  
 Best Local Similarity 100.0%; Pred. No. 1e-06;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PKDTPGAEKLPWY 14  
 |||||  
 DB 101 PKDTPGAEKLPWY 114

## RESULT 3

PCT-US93-02475-8  
 ; Sequence 8, Application PC/TUS9302475  
 ; GENERAL INFORMATION:

APPLICANT: Wisniewski, Bernadine J.  
 TITLE OF INVENTION: Tumor Necrosis Factor with Modified  
 TITLE OF INVENTION: Ion Channel  
 NUMBER OF SEQUENCES: 13  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Donald G. Lewis

STREET: 8328 Regents Road #1E  
 CITY: San Diego  
 STATE: California  
 COUNTRY: USA

ZIP: 92122

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.5 inch, 1.44 M storage  
 COMPUTER: VE System 386  
 OPERATING SYSTEM: MS-DOS 5

SOFTWARE: Word Perfect

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: PCT/US93/02475

FILING DATE: 19930412

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/852,625

FILING DATE: 12 March 1992

ATTORNEY/AGENT INFORMATION:

NAME: Donald G. Lewis

REGISTRATION NUMBER: 28636

REFERENCE/DOCKET NUMBER: BJW-2

TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (619) 554-2421

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 157 amino acids

TYPE: AMINO ACIDS

TOPOLOGY: linear

MOLECULE TYPE: protein

FEATURE:

NAME/KEY: Tumor Necrosis Factor (rat)

OTHER INFORMATION: "Xaa" is inserted after residue No. 70 of rat TNF

OTHER INFORMATION: and the sequence numbering is augmented by 1

OTHER INFORMATION: starting with residue No. 71 in order to maximize

PUBLICATION INFORMATION:  
 AUTHORS: Shirai, T., Shimizu, N., Horiguchi,

AUTHORS: S., and Ito, H.

TITLE: Cloning and Expression in

TITLE: Escherichia coli of the gene for

TITLE: Rat

JOURNAL: Agric. Biol. Chem.

VOLUME: 53

PAGES: 1733-1736

DATE: 1989

RELEVANT RESIDUES IN SEQ ID NO: 8: 1-157 (includes

RELEVANT RESIDUES IN SEQ ID NO: one blank)

PCT-US93-02475-8

Query Match 100.0%; Score 84; DB 5; Length 157;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-06;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PKDTPGAEKLPWY 14  
 |||||  
 DB 102 PKDTPGAEKLPWY 115

## RESULT 4

PCT-US93-02475-9  
 ; Sequence 9, Application PC/TUS9302475  
 ; GENERAL INFORMATION:

APPLICANT: Wisniewski, Bernadine J.  
 TITLE OF INVENTION: Tumor Necrosis Factor with Modified  
 TITLE OF INVENTION: Ion Channel  
 NUMBER OF SEQUENCES: 13  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Donald G. Lewis  
 STREET: 8328 Regents Road #1E  
 CITY: San Diego  
 STATE: California

COUNTRY: USA  
ZIP: 92122  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 M storage  
COMPUTER: VE System 386  
OPERATING SYSTEM: MS-DOS 5  
SOFTWARE: Word Perfect  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/02475  
FILING DATE: 19930412  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/852,625  
FILING DATE: 12 March 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Donald G. Lewis  
REGISTRATION NUMBER: 28636  
REFERENCE/DOCKET NUMBER: BJW-2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 554-2421  
TELEFAX: (619) 554-6312  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 157 amino acids  
TYPE: AMINO ACIDS  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FEATURE:  
NAME/KEY: Tumor Necrosis Factor (murine)  
OTHER INFORMATION: A blank residue designated by  
OTHER INFORMATION: "Xaa" is inserted after residue No. 70 of murine  
OTHER INFORMATION: TNF and the sequence numbering is augmented by 1  
OTHER INFORMATION: starting with residue No. 71 in order to maximize  
OTHER INFORMATION: the sequence homology with human TNF.  
PUBLICATION INFORMATION:  
AUTHORS: Caput, D., Beutler, B. Harzog, K.  
AUTHORS: Thayer, R., Brown-Shlmer, S. and  
AUTHORS: Cerami, A.  
TITLE: Identification of a Common Nucleotide  
TITLE: Sequence in the 3'-Untranslated Region of mRNA  
TITLE: Molecules Specifying Inflammatory Mediators.  
JOURNAL: Proc. National Academy of Science,  
VOLUME: 83  
PAGES: 1670-1674  
DATE: 1986  
RELEVANT RESIDUES IN SEQ ID NO: 9: 1-157 (includes  
RELEVANT RESIDUES IN SEQ ID NO: one blank)  
PCT-US93-02475-9  
Query Match 100.0%; Score 84; DB 5; Length 157;  
Best Local Similarity 100.0%; Pred. No. 1.1e-06;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 PKDPEGAELKPMY 14  
|||||  
Db 102 PKDPEGAELKPMY 115

RESULT 5  
US-08-883-086-7  
Sequence 7, Application US/08883086  
Patent No. 6171787  
GENERAL INFORMATION:  
APPLICANT: WILEY, STEVEN  
TITLE OF INVENTION: MEMBER OF THE TNF FAMILY USEFUL  
TITLE OF INVENTION: FOR TREATMENT AND DIAGNOSIS OF DISEASE  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Abbott Laboratories  
STREET: 100 Abbott Park Road  
CITY: Abbott Park  
STATE: IL

COUNTRY: USA  
ZIP: 60064-3500  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/883,086  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Potembski, Priscilla E.  
REGISTRATION NUMBER: 33,207  
REFERENCE/DOCKET NUMBER: 6134 US.01  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 847-937-0378  
TELEFAX: 847-938-2623  
TELEX:  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 235 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: No. 6171787e  
US-08-883-086-7  
Query Match 100.0%; Score 84; DB 4; Length 235;  
Best Local Similarity 100.0%; Pred. No. 1.6e-06;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 PKDPEGAELKPMY 14  
|||||  
Db 180 PKDPEGAELKPMY 193

RESULT 6  
US-08-500-860A-25  
Sequence 25, Application US/08500860A  
Patent No. 5891679  
GENERAL INFORMATION:  
APPLICANT: LUCAS, RUDOLPH  
APPLICANT: DE BAETSELIER, PATRICK  
APPLICANT: FRANSSEN, LUCIE  
APPLICANT: SABON, ERWIN  
TITLE OF INVENTION: TNF-MUTAINS, A PROCESS FOR PREPARING THEM AND  
TITLE OF INVENTION: THEIR USE AS ACTIVE SUBSTANCES IN PHARMACEUTICAL COMPOSITIO  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: NIXON & VANDERHAYE P.C.  
STREET: 1100 NORTH GLEBE ROAD  
CITY: ARLINGTON  
STATE: VIRGINIA  
COUNTRY: U.S.A.  
ZIP: 22201-4714  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/500,860A  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: BYRNE, THOMAS E.  
REGISTRATION NUMBER: 32,205  
REFERENCE/DOCKET NUMBER: 1487-8  
TELECOMMUNICATION INFORMATION:

TELEPHONE: (703)816-4000  
TELEFAX: (703)816-4100  
TELEX: 200797 NIXN UR  
INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Binding-site  
LOCATION: 1  
OTHER INFORMATION: /note= "Biotin-Gly-Gly is coupled  
OTHER INFORMATION: to the N-terminus of the peptide"  
US-08-500-860A-25

Query Match 77.4%; Score 65; DB 2; Length 17;  
Best Local Similarity 76.9%; Pred. No. 0.00013;  
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 KDPGAEAKPMY 14  
Db 4 RETPGAEAKPMY 16

RESULT 7  
US-07-668-517-1  
Sequence 1, Application US/07668517  
Patent No. 5262309  
GENERAL INFORMATION:  
APPLICANT: Satoshi NAKAMURA et al.  
TITLE OF INVENTION: No. 5262309el Physiologically Active  
TITLE OF INVENTION: Polypeptide, Recombinant Plasmid, Recombinant Microorganism  
TITLE OF INVENTION: Cell, Pharmaceutical Composition and Method of Recovering  
NUMBER OF SEQUENCES: 50  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wenderoth, Lind & Ponack  
STREET: 805 Fifteenth Street, N.W., #700  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch, 500 Kb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Displaywrite  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/668, 517  
FILING DATE: 19910322  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Matthew Jacob  
REGISTRATION NUMBER: 25,154  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-8850  
TELEFAX: 202-371-8856  
TELEX:  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 147 amino acids  
TYPE: AMINO ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY:  
LOCATION:  
IDENTIFICATION METHOD:  
OTHER INFORMATION:

OTHER INFORMATION:  
US-07-668-517-1

Query Match 77.4%; Score 65; DB 1; Length 147;  
Best Local Similarity 76.9%; Pred. No. 0.0014;  
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 KDPGAEAKPMY 14  
Db 93 RETPGAEAKPMY 105

RESULT 8  
US-07-668-517-2  
Sequence 2, Application US/07668517  
Patent No. 5262309  
GENERAL INFORMATION:  
APPLICANT: Satoshi NAKAMURA et al.  
TITLE OF INVENTION: No. 5262309el Physiologically Active  
TITLE OF INVENTION: Polypeptide, Recombinant Plasmid, Recombinant Microorganism  
TITLE OF INVENTION: Cell, Pharmaceutical Composition and Method of Recovering  
NUMBER OF SEQUENCES: 50  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wenderoth, Lind & Ponack  
STREET: 805 Fifteenth Street, N.W., #700  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch, 500 Kb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Displaywrite  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/668, 517  
FILING DATE: 19910322  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Matthew Jacob  
REGISTRATION NUMBER: 25,154  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-8850  
TELEFAX: 202-371-8856  
TELEX:  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 148 amino acids  
TYPE: AMINO ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY:  
LOCATION:  
IDENTIFICATION METHOD:  
OTHER INFORMATION:  
US-07-668-517-2

Query Match 77.4%; Score 65; DB 1; Length 148;  
Best Local Similarity 76.9%; Pred. No. 0.0014;  
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 KDPGAEAKPMY 14  
Db 94 RETPGAEAKPMY 106

RESULT 9  
US-07-668-517-15

Sequence 15, Application US/07668517  
Patent No. 5262309  
GENERAL INFORMATION:  
APPLICANT: SATOSHI NAKAMURA et al.  
TITLE OF INVENTION: No. 5262309el Physiologically Active  
TITLE OF INVENTION: Polypeptide, Recombinant Plasmid, Recombinant Microorganism  
TITLE OF INVENTION: Cell, Pharmaceutical Composition and Method of Recovering  
NUMBER OF SEQUENCES: 50  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wenderoth, Lind & Ponack  
STREET: 805 Fifteenth Street, N.W., #700  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch, 500 Kb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: DisplayWrite  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/668,517  
FILING DATE: 19910322  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Matthew Jacob  
REGISTRATION NUMBER: 25,154  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-8850  
TELEFAX: 202-371-8856  
TELEX:  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 148 amino acids  
TYPE: AMINO ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY:  
LOCATION:  
IDENTIFICATION METHOD:  
OTHER INFORMATION:  
US-07-668-517-15

Query Match 77.4%; Score 65; DB 1; Length 148;  
Best Local Similarity 76.9%; Pred. No. 0.0014;  
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 KDPGGAELKPMY 14  
DB 94 RETPEGAELKPMY 106

RESULT 10  
US-07-668-517-3  
Sequence 3, Application US/07668517  
Patent No. 5262309  
GENERAL INFORMATION:  
APPLICANT: SATOSHI NAKAMURA et al.  
TITLE OF INVENTION: No. 5262309el Physiologically Active  
TITLE OF INVENTION: Polypeptide, Recombinant Plasmid, Recombinant Microorganism  
TITLE OF INVENTION: Cell, Pharmaceutical Composition and Method of Recovering  
NUMBER OF SEQUENCES: 50  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wenderoth, Lind & Ponack  
STREET: 805 Fifteenth Street, N.W., #700  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.

ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch, 500 Kb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: DisplayWrite  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/668,517  
FILING DATE: 19910322  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Matthew Jacob  
REGISTRATION NUMBER: 25,154  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-8850  
TELEFAX: 202-371-8856  
TELEX:  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 149 amino acids  
TYPE: AMINO ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY:  
LOCATION:  
IDENTIFICATION METHOD:  
OTHER INFORMATION:  
US-07-668-517-3

Query Match 77.4%; Score 65; DB 1; Length 149;  
Best Local Similarity 76.9%; Pred. No. 0.0014;  
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 KDPGGAELKPMY 14  
DB 95 RETPEGAELKPMY 107

RESULT 11  
US-07-668-517-16  
Sequence 16, Application US/07668517  
Patent No. 5262309  
GENERAL INFORMATION:  
APPLICANT: SATOSHI NAKAMURA et al.  
TITLE OF INVENTION: No. 5262309el Physiologically Active  
TITLE OF INVENTION: Polypeptide, Recombinant Plasmid, Recombinant Microorganism  
TITLE OF INVENTION: Cell, Pharmaceutical Composition and Method of Recovering  
NUMBER OF SEQUENCES: 50  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wenderoth, Lind & Ponack  
STREET: 805 Fifteenth Street, N.W., #700  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch, 500 Kb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: DisplayWrite  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/668,517  
FILING DATE: 19910322  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:

NAME: Matthew Jacob  
REGISTRATION NUMBER: 25,154  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-8850  
TELEFAX: 202-371-8856  
TELEX:  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 149 amino acids  
TYPE: AMINO ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY:  
LOCATION:  
IDENTIFICATION METHOD:  
OTHER INFORMATION:  
US-07-668-517-16

Query Match 77.4%; Score 65; DB 1; Length 149;  
Best Local Similarity 76.9%; Pred. No. 0.0014;  
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 2 KDPTEGAEKPMY 14  
Db 95 RETPEGAEKPMY 107

RESULT 12  
US-07-668-517-4  
Sequence 4, Application US/07668517  
Patent No. 5262309  
GENERAL INFORMATION:  
APPLICANT: Satoshi NAKAMURA et al.  
TITLE OF INVENTION: No. 5262309el Physiologically Active  
TITLE OF INVENTION: Polypeptide, Recombinant Plasmid, Recombinant Microorganism  
NUMBER OF SEQUENCES: 50  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wenderoth, Lind & Ponack  
STREET: 805 Fifteenth Street, N.W., #700  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch, 500 Kb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: DisplayWrite  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/668,517  
FILING DATE: 19910322  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Matthew Jacob  
REGISTRATION NUMBER: 25,154  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-8850  
TELEFAX: 202-371-8856  
TELEX:  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 150 amino acids  
TYPE: AMINO ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:

NAME/KEY:  
LOCATION:  
IDENTIFICATION METHOD:  
OTHER INFORMATION:  
US-07-668-517-4

Query Match 77.4%; Score 65; DB 1; Length 150;  
Best Local Similarity 76.9%; Pred. No. 0.0014;  
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 2 KDPTEGAEKPMY 14  
Db 96 RETPEGAEKPMY 108

RESULT 13  
US-07-668-517-5  
Sequence 5, Application US/07668517  
Patent No. 5262309  
GENERAL INFORMATION:

APPLICANT: Satoshi NAKAMURA et al.  
TITLE OF INVENTION: No. 5262309el Physiologically Active  
TITLE OF INVENTION: Polypeptide, Recombinant Plasmid, Recombinant Microorganism  
NUMBER OF SEQUENCES: 50  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wenderoth, Lind & Ponack  
STREET: 805 Fifteenth Street, N.W., #700  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch, 500 Kb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: DisplayWrite  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/668,517  
FILING DATE: 19910322  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Matthew Jacob  
REGISTRATION NUMBER: 25,154  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-8850  
TELEFAX: 202-371-8856  
TELEX:

INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 150 amino acids  
TYPE: AMINO ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY:  
LOCATION:  
IDENTIFICATION METHOD:  
OTHER INFORMATION:  
US-07-668-517-5

Query Match 77.4%; Score 65; DB 1; Length 150;  
Best Local Similarity 76.9%; Pred. No. 0.0014;  
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 2 KDPTEGAEKPMY 14  
Db 96 RETPEGAEKPMY 108

RESULT 14  
US-07-668-517-6  
Sequence 6, Application US/07668517  
Patent No. 5262309  
GENERAL INFORMATION:  
APPLICANT: Satoshi NAKAMURA et al.  
TITLE OF INVENTION: No. 5262309el Physiologically Active  
TITLE OF INVENTION: Polypeptide, Recombinant Plasmid, Recombinant Microorganism  
NUMBER OF SEQUENCES: 50  
CELL, Pharmaceutical Composition and Method of Recovering  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wenderoth, Lind & Ponack  
STREET: 805 Fifteenth Street, N.W., #700  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch, 500 KB  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: DisplayWrite  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/668,517  
FILING DATE: 19910322  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Matthew Jacob  
REGISTRATION NUMBER: 25,154  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-8850  
TELEFAX: 202-371-8856  
TELEX:  
INFORMATION FOR SEQ. ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 150 amino acids  
TYPE: AMINO ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY:  
LOCATION:  
IDENTIFICATION METHOD:  
OTHER INFORMATION:  
US-07-668-517-6

Query Match 77.4%; Score 65; DB 1; Length 150;  
Best Local Similarity 76.9%; Pred. No. 0.0014;  
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 2 KDTPEGAELKPMY 14  
Db 96 RETPEGAELKPMY 108

RESULT 15  
US-07-668-517-8  
Sequence 8, Application US/07668517  
Patent No. 5262309  
GENERAL INFORMATION:  
APPLICANT: Satoshi NAKAMURA et al.  
TITLE OF INVENTION: No. 5262309el Physiologically Active  
TITLE OF INVENTION: Polypeptide, Recombinant Plasmid, Recombinant Microorganism  
NUMBER OF SEQUENCES: 50  
CELL, Pharmaceutical Composition and Method of Recovering  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wenderoth, Lind & Ponack  
STREET: 805 Fifteenth Street, N.W., #700  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch, 500 KB  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: DisplayWrite  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/668,517  
FILING DATE: 19910322  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Matthew Jacob  
REGISTRATION NUMBER: 25,154  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-8850  
TELEFAX: 202-371-8856  
TELEX:  
INFORMATION FOR SEQ. ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 150 amino acids  
TYPE: AMINO ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY:  
LOCATION:  
IDENTIFICATION METHOD:  
OTHER INFORMATION:  
US-07-668-517-8

CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch, 500 KB  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: DisplayWrite  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/668,517  
FILING DATE: 19910322  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Matthew Jacob  
REGISTRATION NUMBER: 25,154  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-8850  
TELEFAX: 202-371-8856  
TELEX:  
INFORMATION FOR SEQ. ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 150 amino acids  
TYPE: AMINO ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY:  
LOCATION:  
IDENTIFICATION METHOD:  
OTHER INFORMATION:  
US-07-668-517-8

Query Match 77.4%; Score 65; DB 1; Length 150;  
Best Local Similarity 76.9%; Pred. No. 0.0014;  
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 2 KDTPEGAELKPMY 14  
Db 96 RETPEGAELKPMY 108

Search completed: April 4, 2003, 08:43:41  
Job time: 9.03226 secs

GenCore version 5.1.4-p5.4578  
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OM protein - protein search, using sw model

Run on: April 4, 2003, 08:42:11 ; Search time 8.80645 Seconds  
(without alignments)  
97.191 Million cell updates/sec

Title: US-09-779-703-2  
Perfect score: 84  
Sequence: 1 PKDTPGAEKLPWY 14

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 248812 seqs, 61136040 residues  
Total number of hits satisfying chosen parameters: 248812

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published\_Applications\_AA:\*

- 1: /cgn2\_6/ptodata/2/pubppa/US08\_NEW\_PUB pep:\*
- 2: /cgn2\_6/ptodata/2/pubppa/PCF\_NEW\_PUB pep:\*
- 3: /cgn2\_6/ptodata/2/pubppa/US06\_NEW\_PUB pep:\*
- 4: /cgn2\_6/ptodata/2/pubppa/US07\_NEW\_PUB pep:\*
- 5: /cgn2\_6/ptodata/2/pubppa/US07\_PUBCOMB pep:\*
- 6: /cgn2\_6/ptodata/2/pubppa/PCFUS\_PUBCOMB pep:\*
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- 9: /cgn2\_6/ptodata/2/pubppa/US10\_NEW\_PUB pep:\*
- 10: /cgn2\_6/ptodata/2/pubppa/US10\_PUBCOMB pep:\*
- 11: /cgn2\_6/ptodata/2/pubppa/US10\_PUBCOMB pep:\*
- 12: /cgn2\_6/ptodata/2/pubppa/US60\_NEW\_PUB pep:\*
- 13: /cgn2\_6/ptodata/2/pubppa/US60\_PUBCOMB pep:\*
- 14: /cgn2\_6/ptodata/2/pubppa/US60\_PUBCOMB pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	84	100.0	151	9	US-09-779-050A-40
2	84	100.0	235	9	US-10-017-910-8
3	84	100.0	268	9	US-10-185-425-6
4	65	77.4	150	10	US-09-877-156-25
5	65	77.4	150	12	US-10-116-378-28
6	65	77.4	152	9	US-09-779-050A-24
7	65	77.4	157	9	US-09-903-327A-7
8	65	77.4	157	9	US-10-043-432-1
9	65	77.4	157	10	US-09-756-301A-1
10	65	77.4	157	10	US-09-927-703-1
11	65	77.4	157	10	US-09-854-280-19
12	65	77.4	157	10	US-09-934-465-13
13	65	77.4	157	10	US-09-766-535A-1
14	65	77.4	157	10	US-09-854-208-19
15	65	77.4	157	10	US-09-756-161A-1
16	65	77.4	157	12	US-10-010-229-1
17	65	77.4	157	12	US-10-043-450-1
18	65	77.4	157	12	US-10-044-534-1
19	65	77.4	164	10	US-09-798-789-2

20	65	77.4	164	10	US-09-981-289-2	Sequence 2, Appl1
21	65	77.4	193	9	US-10-145-014-3	Sequence 3, Appl1
22	65	77.4	193	10	US-09-982-308-3	Sequence 3, Appl1
23	65	77.4	233	8	US-08-971-317A-5	Sequence 5, Appl1
24	65	77.4	233	9	US-10-136-511-3	Sequence 3, Appl1
25	65	77.4	233	9	US-10-145-014-22	Sequence 22, Appl1
26	65	77.4	233	9	US-09-131-237-3	Sequence 9, Appl1
27	65	77.4	233	9	US-10-174-654-9	Sequence 42, Appl1
28	65	77.4	233	9	US-10-151-882-42	Sequence 5, Appl1
29	65	77.4	233	10	US-09-193-663-5	Sequence 5, Appl1
30	65	77.4	233	10	US-09-879-919-5	Sequence 43, Appl1
31	65	77.4	233	10	US-09-782-980-43	Sequence 14, Appl1
32	65	77.4	233	10	US-09-840-707A-14	Sequence 3, Appl1
33	65	77.4	233	10	US-09-246-129B-3	Sequence 3, Appl1
34	65	77.4	233	10	US-09-345-790-3	Sequence 3, Appl1
35	65	77.4	233	10	US-09-929-493-3	Sequence 3, Appl1
36	65	77.4	233	10	US-09-899-059-3	Sequence 3, Appl1
37	65	77.4	233	12	US-10-082-260-5	Sequence 5, Appl1
38	65	77.4	233	12	US-10-012-452-10	Sequence 11, Appl1
39	65	77.4	597	9	US-09-903-327A-11	Sequence 5707, Ap
40	49	58.3	104	10	US-09-911-777-5	Sequence 16, Appl
41	46	54.8	404	9	US-09-738-626-5707	Sequence 627, App
42	43	51.2	3298	9	US-10-160-758-16	Sequence 7, Appl1
43	42	50.0	226	9	US-09-866-050A-627	
44	41	48.8	235	9	US-09-131-237-7	
45	41	48.8	235	10	US-09-246-129B-7	

## ALIGNMENTS

RESULT 1  
US-09-779-050A-40  
Sequence 40, Application US/09779050A  
Patent No. US20020160416A1  
GENERAL INFORMATION:  
APPLICANT: BOYE, WILLIAM  
APPLICANT: HSU, HAILING  
TITLE OF INVENTION: RECEPTOR FROM TNF FAMILY  
FILE REFERENCE: A-570B  
CURRENT APPLICATION NUMBER: US/09/779, 050A  
PRIOR FILING DATE: 2001-02-12  
PRIOR APPLICATION NUMBER: 60/181,800  
PRIOR FILING DATE: 2000-02-11  
NUMBER OF SEQ ID NOS: 52  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 40  
LENGTH: 151  
TYPE: PRT  
ORGANISM: Mus musculus  
US-09-779-050A-40

Query Match 100.0% Score 84 DB 9 Length 151  
Best Local Similarity 100.0% Pred. No. 2.9e-06  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKDTPGAEKLPWY 14  
Db 96 PKDTPGAEKLPWY 109

RESULT 2  
US-10-017-910-8  
Sequence 8, Application US/10017910  
Patent No. US20020159970A1  
GENERAL INFORMATION:  
APPLICANT: Choi, Yongwon  
Wong, Brian  
Josien, Regis  
Steinman, Ralph  
TITLE OF INVENTION: A PROTEIN BELONGING TO THE TNF SUPERFAMILY  
INVOLVED IN SIGNAL TRANSDUCTION, NUCLEIC ACIDS ENCODING  
METHODS OF USE THEREOF

```

NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue, 4th Floor
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/017,910
FILING DATE: 14-Dec-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/447,035
FILING DATE: 1999-11-22
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-200
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-343-1684
TELEFAX: 201-343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 235 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Mus musculus
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-10-017-910-8

Query Match      100.0%; Score 84; DB 9; Length 235;
Best Local Similarity 100.0%; Pred. No. 4.6e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 PKDPGAEELKPMY 14
DB      180 PKDPGAEELKPMY 193

RESULT 3
US-10-185-425-6
; Sequence 6, Application US/10185425
; Publication No. US20030053984A1
; GENERAL INFORMATION:
; APPLICANT: Apotech Research and Development Ltd.
; APPLICANT: Tschopp, Jurg
; APPLICANT: Schneider, Pascal
; APPLICANT: Holler, Nils
; TITLE OF INVENTION: A Bimer or an Oligomer of a Dimer, Trimer, Quadromer, or Pentamer
; FILE REFERENCE: 1708.0010S1
; CURRENT APPLICATION NUMBER: US/10/185,425
; PRIOR FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: PCT/EP00/13032
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: DE 199 63 859.4
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 268
; TYPE: PRT

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ORGANISM: Artificial Sequence
FEATURE:
; OTHER INFORMATION: TNFa-ACRP30
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (1) ... (8)
; OTHER INFORMATION: Flag
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (9) ... (16)
; OTHER INFORMATION: Linker
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (17) ... (108)
; OTHER INFORMATION: mouseACRP30 aa 18-111
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (109) ... (110)
; OTHER INFORMATION: Linker
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (111) ... (268)
; OTHER INFORMATION: mouseTNFa aa 77-235
US-10-185-425-6

Query Match      100.0%; Score 84; DB 9; Length 268;
Best Local Similarity 100.0%; Pred. No. 5.3e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 PKDPGAEELKPMY 14
DB      213 PKDPGAEELKPMY 226

RESULT 4
US-09-877-156-25
; Sequence 25, Application US/09877156
; Patent No. US20020055625A1
; GENERAL INFORMATION:
; APPLICANT: Catherine Tribouley
; TITLE OF INVENTION: NEW MEMBERS OF TNF AND TNFR FAMILIES
; FILE REFERENCE: 1408.003/200130.439C1
; CURRENT APPLICATION NUMBER: US/09/877,156
; CURRENT FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 09/286,529
; PRIOR FILING DATE: 1998-04-05
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 25
; LENGTH: 150
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-877-156-25

Query Match      77.4%; Score 65; DB 10; Length 150;
Best Local Similarity 76.9%; Pred. No. 0.0032;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      2 KDPGAEELKPMY 14
DB      96 KDPGAEELKPMY 108

RESULT 5
US-10-116-378-28
; Sequence 28, Application US/10116378
; Patent No. US20020150935A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Goddard, Audrey
; APPLICANT: Gurney, Austin
; APPLICANT: Marsters, Scott A.
; APPLICANT: Pitti, Robert M.

```



```
APPLICANT: WOOD, William
TITLE OF INVENTION: NOVEL TUMOR NECROSIS FACTOR RECEPTOR HOMOLOG AND
TITLE OF INVENTION: NOVEL TUMOR NECROSIS FACTOR RECEPTOR HOMOLOG AND
TITLE OF INVENTION: NOVEL TUMOR NECROSIS FACTOR RECEPTOR HOMOLOG AND
TITLE OF INVENTION: NOVEL TUMOR NECROSIS FACTOR RECEPTOR HOMOLOG AND
FILE REFERENCE: P1206R1
CURRENT APPLICATION NUMBER: US/10/116,378
CURRENT FILING DATE: 2002-04-04
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/247,225
PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-09
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/074,087
PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-09
NUMBER OF SEQ ID NOS: 31
SEQ ID NO 28
LENGTH: 150
TYPE: PRT
ORGANISM: Homo sapiens
US-10-116-378-28

Query Match          77.4%: Score 65; DB 9; Length 150;
Best Local Similarity 76.9%: Pred. No. 0.0032;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      2 KDPPEGAELKPMY 14
DB      96 RETPEGAELKPMY 108

RESULT 6
US-09-779-050A-24
Sequence 24, Application US/09779050A
Patent No. US20020160416A1
GENERAL INFORMATION:
APPLICANT: BOYLE, WILLIAM
APPLICANT: HSU, HAILING
TITLE OF INVENTION: RECEPTOR FROM TNF FAMILY
FILE REFERENCE: A-570B
CURRENT APPLICATION NUMBER: US/09/779,050A
CURRENT FILING DATE: 2001-02-12
PRIOR APPLICATION NUMBER: 60/181,800
PRIOR FILING DATE: 2000-02-11
NUMBER OF SEQ ID NOS: 52
SOFTWARE: PatentIn version 3.0
SEQ ID NO 24
LENGTH: 152
TYPE: PRT
ORGANISM: Homo sapiens
US-09-779-050A-24

Query Match          77.4%: Score 65; DB 9; Length 152;
Best Local Similarity 76.9%: Pred. No. 0.0032;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      2 KDPPEGAELKPMY 14
DB      98 RETPEGAELKPMY 110

RESULT 7
US-09-903-327A-7
Sequence 7, Application US/09903327A
Patent No. US20020164333A1
GENERAL INFORMATION:
APPLICANT: Nemerow, Glen R.
APPLICANT: Li, Erlang
TITLE OF INVENTION: BIFUNCTIONAL MOLECULES AND VECTORS COMPLEXED THEREWITH FOR TARGET
TITLE OF INVENTION: GENE
TITLE OF INVENTION: DELIVERY
FILE REFERENCE: 22908-1228
CURRENT APPLICATION NUMBER: US/09/903,327A
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 09/613,017
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 33
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SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 7
LENGTH: 157
TYPE: PRT
ORGANISM: Human
FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (0)...(0)
OTHER INFORMATION: Tumor necrosis factor-alpha (TNF alpha, mature
US-09-903-327A-7

Query Match          77.4%: Score 65; DB 9; Length 157;
Best Local Similarity 76.9%: Pred. No. 0.0033;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      2 KDPPEGAELKPMY 14
DB      103 RETPEGAELKPMY 115

RESULT 8
US-10-043-432-1
Sequence 1, Application US/10043432
Publication No. US20030054004A1
GENERAL INFORMATION:
APPLICANT: Le, Junming
APPLICANT: Vilcek, Jan
APPLICANT: Daddona, Peter
APPLICANT: Ghayab, John
APPLICANT: Knight, David M.
APPLICANT: Siegel, Scott
TITLE OF INVENTION: Anti-TNF Antibodies and Peptides of
FILE REFERENCE: 0975,1005-013
CURRENT APPLICATION NUMBER: US/10/043,432
CURRENT FILING DATE: 2002-01-10
PRIOR APPLICATION NUMBER: 09/927,703
PRIOR FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: U.S. 09/756,398
PRIOR FILING DATE: 2001-01-08
PRIOR APPLICATION NUMBER: U.S. 09/133,119
PRIOR FILING DATE: 1998-08-12
PRIOR APPLICATION NUMBER: U.S. 08/570,674
PRIOR FILING DATE: 1995-12-11
PRIOR APPLICATION NUMBER: U.S. 08/324,799
PRIOR FILING DATE: 1994-10-18
PRIOR APPLICATION NUMBER: U.S. 08/192,102
PRIOR FILING DATE: 1994-02-04
PRIOR APPLICATION NUMBER: U.S. 08/192,861
PRIOR FILING DATE: 1994-02-04
PRIOR APPLICATION NUMBER: U.S. 08/192,093
PRIOR FILING DATE: 1994-02-04
PRIOR APPLICATION NUMBER: U.S. 08/010,406
PRIOR FILING DATE: 1993-01-29
PRIOR APPLICATION NUMBER: U.S. 08/013,413
PRIOR FILING DATE: 1993-02-02
PRIOR APPLICATION NUMBER: U.S. 07/943,852
PRIOR FILING DATE: 1992-09-11
PRIOR APPLICATION NUMBER: U.S. 07/853,606
PRIOR FILING DATE: 1992-03-18
PRIOR APPLICATION NUMBER: U.S. 07/670,827
PRIOR FILING DATE: 1991-03-18
NUMBER OF SEQ ID NOS: 19
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 157
TYPE: PRT
ORGANISM: Homo sapiens
US-10-043-432-1

Query Match          77.4%: Score 65; DB 9; Length 157;
Best Local Similarity 76.9%: Pred. No. 0.0033;
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Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 2 KDTPEGAELKPMY 14
Db 103 RETPEGAELKPMY 115
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RESULT 9
US-09-756-301A-1
; Sequence 1, Application US/09756301A
; Patent No. US20010027249A1
; GENERAL INFORMATION:
; APPLICANT: Le, Junming
; APPLICANT: Vilcek, Jan
; APPLICANT: Daddona, Peter
; APPLICANT: Ghayeb, John
; APPLICANT: Knight, David M.
; APPLICANT: Siegel, Scott
; TITLE OF INVENTION: Anti-TNF Antibodies and Peptides of
; FILE REFERENCE: 0975.1005-008
; CURRENT APPLICATION NUMBER: US/09/756,301A
; CURRENT FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: U.S. 09/133,119
; PRIOR FILING DATE: 1998-08-12
; PRIOR APPLICATION NUMBER: U.S. 08/570,674
; PRIOR FILING DATE: 1995-12-11
; PRIOR APPLICATION NUMBER: U.S. 08/324,799
; PRIOR FILING DATE: 1994-10-18
; PRIOR APPLICATION NUMBER: U.S. 08/192,102
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/192,861
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/192,093
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/010,406
; PRIOR FILING DATE: 1993-01-29
; PRIOR APPLICATION NUMBER: U.S. 08/013,413
; PRIOR FILING DATE: 1993-02-02
; PRIOR APPLICATION NUMBER: U.S. 07/943,852
; PRIOR FILING DATE: 1992-09-11
; PRIOR APPLICATION NUMBER: U.S. 07/853,606
; PRIOR FILING DATE: 1992-03-18
; PRIOR APPLICATION NUMBER: U.S. 07/670,827
; PRIOR FILING DATE: 1991-03-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 157
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-756-301A-1
Query Match 77.4%; Score 65; DB 10; Length 157;
Best Local Similarity 76.9%; Pred. No. 0.0033;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 2 KDTPEGAELKPMY 14
Db 103 RETPEGAELKPMY 115
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RESULT 10
US-09-927-703-1
; Sequence 1, Application US/09927703
; Patent No. US20020022720A1
; GENERAL INFORMATION:
; APPLICANT: Le, Junming
; APPLICANT: Vilcek, Jan
; APPLICANT: Daddona, Peter
; APPLICANT: Ghayeb, John
; APPLICANT: Knight, David M.
; APPLICANT: Siegel, Scott
```

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; TITLE OF INVENTION: Anti-TNF Antibodies and Peptides of
; FILE REFERENCE: 0975.1005-013
; CURRENT APPLICATION NUMBER: US/09/927,703
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: U.S. 09/756,398
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: U.S. 09/133,119
; PRIOR FILING DATE: 1998-08-12
; PRIOR APPLICATION NUMBER: U.S. 08/570,674
; PRIOR FILING DATE: 1995-12-11
; PRIOR APPLICATION NUMBER: U.S. 08/324,799
; PRIOR FILING DATE: 1994-10-18
; PRIOR APPLICATION NUMBER: U.S. 08/192,102
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/192,861
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/192,093
; PRIOR FILING DATE: 1993-01-29
; PRIOR APPLICATION NUMBER: U.S. 08/013,413
; PRIOR FILING DATE: 1993-02-02
; PRIOR APPLICATION NUMBER: U.S. 07/943,852
; PRIOR FILING DATE: 1992-09-11
; PRIOR APPLICATION NUMBER: U.S. 07/853,606
; PRIOR FILING DATE: 1992-03-18
; PRIOR APPLICATION NUMBER: U.S. 07/670,827
; PRIOR FILING DATE: 1991-03-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 157
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-927-703-1
Query Match 77.4%; Score 65; DB 10; Length 157;
Best Local Similarity 76.9%; Pred. No. 0.0033;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 2 KDTPEGAELKPMY 14
Db 103 RETPEGAELKPMY 115
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RESULT 11
US-09-854-280-19
; Sequence 19, Application US/09854280
; Patent No. US20020052027A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Jian
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Gurney, Austin
; APPLICANT: Li, Hanzhong
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF
; FILE REFERENCE: P1381R1C2
; CURRENT APPLICATION NUMBER: US/09/854,280
; CURRENT FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: US 09/311,832
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: US 60/085,579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: US 60/113,621
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 26
; SEQ ID NO 19
; LENGTH: 157
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-280-19
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Query Match          77.4%; Score 65; DB 10; Length 157;
Best Local Similarity 76.9%; Pred. No. 0.0033;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 KDTPEGAELKPMY 14
Db 103 RETPEGAELKPMY 115

RESULT 12
US-09-934-465-13
; Sequence 13, Application US/09934465
; Patent No. US20020102233A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J
; TITLE OF INVENTION: APO-2 LIGAND
; FILE REFERENCE: 11669.22US03
; CURRENT APPLICATION NUMBER: US/09/934,465
; PRIOR FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: 08/584,031
; PRIOR FILING DATE: 1996-01-09
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 157
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-934-465-13

Query Match          77.4%; Score 65; DB 10; Length 157;
Best Local Similarity 76.9%; Pred. No. 0.0033;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 KDTPEGAELKPMY 14
Db 103 RETPEGAELKPMY 115

RESULT 13
US-09-766-535A-1
; Sequence 1, Application US/09766535A
; Patent No. US20020106372A1
; GENERAL INFORMATION:
; APPLICANT: Le, Junming
; APPLICANT: Villcek, Jan
; APPLICANT: Daddona, Peter
; APPLICANT: Chrayeb, John
; APPLICANT: Knight, David M.
; APPLICANT: Siegel, Scott
; TITLE OF INVENTION: Anti-TNF Antibodies and Peptides of
; TITLE OF INVENTION: Human Tumor Necrosis Factor
; FILE REFERENCE: 0975.1005-010
; CURRENT APPLICATION NUMBER: US/09/766,535A
; PRIOR FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: U.S. 09/133,119
; PRIOR FILING DATE: 1998-08-12
; PRIOR APPLICATION NUMBER: U.S. 08/570,674
; PRIOR FILING DATE: 1995-12-11
; PRIOR APPLICATION NUMBER: U.S. 08/324,799
; PRIOR FILING DATE: 1994-10-18
; PRIOR APPLICATION NUMBER: U.S. 08/192,102
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/192,861
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/192,093
; PRIOR FILING DATE: 1993-01-29
; PRIOR APPLICATION NUMBER: U.S. 08/010,406
; PRIOR FILING DATE: 1993-01-29
; PRIOR APPLICATION NUMBER: U.S. 08/013,413
; PRIOR FILING DATE: 1992-09-11
; PRIOR APPLICATION NUMBER: U.S. 07/943,852
; FILE REFERENCE: 1992-09-11
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; PRIOR APPLICATION NUMBER: U.S. 07/853,606
; PRIOR FILING DATE: 1992-03-18
; PRIOR APPLICATION NUMBER: U.S. 07/670,827
; PRIOR FILING DATE: 1991-03-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 157
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-766-535A-1

Query Match          77.4%; Score 65; DB 10; Length 157;
Best Local Similarity 76.9%; Pred. No. 0.0033;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 KDTPEGAELKPMY 14
Db 103 RETPEGAELKPMY 115

RESULT 14
US-09-854-208-19
; Sequence 19, Application US/09854208
; Patent No. US20020106743A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Jian
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Gurney, Austin
; APPLICANT: Li, Hanzhong
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES
; TITLE OF INVENTION: THERPEOF
; FILE REFERENCE: P1381-R1
; CURRENT APPLICATION NUMBER: US/09/854,208
; CURRENT FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: US/09/311,832
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: US 60/085,579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: US 60/113,621
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 26
; SEQ ID NO 19
; LENGTH: 157
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-208-19

Query Match          77.4%; Score 65; DB 10; Length 157;
Best Local Similarity 76.9%; Pred. No. 0.0033;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 KDTPEGAELKPMY 14
Db 103 RETPEGAELKPMY 115

RESULT 15
US-09-756-161A-1
; Sequence 1, Application US/09756161A
; Patent No. US2002013307A1
; GENERAL INFORMATION:
; APPLICANT: Le, Junming
; APPLICANT: Villcek, Jan
; APPLICANT: Daddona, Peter
; APPLICANT: Chrayeb, John
; APPLICANT: Knight, David M.
; APPLICANT: Siegel, Scott
; TITLE OF INVENTION: Anti-TNF Antibodies and Peptides of
; TITLE OF INVENTION: Human Tumor Necrosis Factor
; FILE REFERENCE: 0975.1005-007
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; CURRENT APPLICATION NUMBER: US/09/756,161A
; CURRENT FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: U.S. 09/133,119
; PRIOR FILING DATE: 1998-08-12
; PRIOR APPLICATION NUMBER: U.S. 08/570,674
; PRIOR FILING DATE: 1995-12-11
; PRIOR APPLICATION NUMBER: U.S. 08/324,799
; PRIOR FILING DATE: 1994-10-18
; PRIOR APPLICATION NUMBER: U.S. 08/192,102
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/192,861
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/192,093
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/010,406
; PRIOR FILING DATE: 1993-01-29
; PRIOR APPLICATION NUMBER: U.S. 08/013,413
; PRIOR FILING DATE: 1993-02-02
; PRIOR APPLICATION NUMBER: U.S. 07/943,852
; PRIOR FILING DATE: 1992-09-11
; PRIOR APPLICATION NUMBER: U.S. 07/853,606
; PRIOR FILING DATE: 1992-03-18
; PRIOR APPLICATION NUMBER: U.S. 07/670,827
; PRIOR FILING DATE: 1991-03-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 157
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-756-161A-1

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Query Match      77.4%; Score 65; DB 10; Length 157;
Best Local Similarity 76.9%; Pred. No. 0.0033;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
OY      2 KDTPEGAEIKPMY 14
      ::||| |||
Db      103 RETPEGAEAKPMY 115

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 Job time : 8.80645 secs

GenCore version 5.1.4\_p5\_4578  
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OM protein - protein search, using sw model

Run on: April 4, 2003, 08:36:10 ; Search time 31.5323 Seconds  
(without alignments)  
71.839 Million cell updates/sec

Title: US-09-779-703-4  
Perfect score: 105  
Sequence: 1 CGOREPGEAKPMYC 17

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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5	88	83.8	19	21	AA182198
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7	81	77.1	17	11	AA805469
8	81	77.1	25	11	AA805513
9	81	77.1	140	16	AA172456
10	81	77.1	145	9	AA182043

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12	81	77.1	147	22	AA67245	Human tumour necro
13	81	77.1	147	22	AA171982	C-terminal region
14	81	77.1	149	10	AA191635	Polypeptide derive
15	81	77.1	149	11	AA191635	Antitumour peptide
16	81	77.1	150	8	AA170528	Synthetic tumour n
17	81	77.1	150	8	AA171245	TNF-derived polype
18	81	77.1	150	9	AA181236	Modified tumour ne
19	81	77.1	150	9	AA182190	TNF analogue. AA
20	81	77.1	150	9	AA182303	TNF analogue. AA
21	81	77.1	150	9	AA181066	Sequence of new ph
22	81	77.1	150	9	AA181068	Anti-tumour active
23	81	77.1	150	10	AA195660	New polypeptide wi
24	81	77.1	150	11	AA195286	Polypeptide with a
25	81	77.1	150	11	AA195286	TNF-like polypepti
26	81	77.1	150	12	AA110111	Tumour Necrosis fa
27	81	77.1	150	12	AA117723	TNF analogue #1.
28	81	77.1	150	13	AA12808	TNF analogue #2.
29	81	77.1	150	13	AA12809	Human TNF mutein.
30	81	77.1	150	13	AA12811	Human TNF mutein.
31	81	77.1	150	13	AA12811	Human TNF mutein.
32	81	77.1	150	15	AA16579	Human TNF mutein.
33	81	77.1	150	15	AA16579	Human TNF mutein.
34	81	77.1	150	15	AA16580	Human TNF mutein.
35	81	77.1	150	15	AA16581	Human TNF mutein.
36	81	77.1	150	15	AA16582	Human TNF mutein.
37	81	77.1	151	9	AA181251	Human TNF mutein.
38	81	77.1	151	9	AA181251	Tumouride polypep
39	81	77.1	151	9	AA181231	Anti-tumour peptid
40	81	77.1	151	10	AA19187	Sequence of modifi
41	81	77.1	151	10	AA19187	Polypeptide with a
42	81	77.1	151	11	AA195865	Anti-tumour peptid
43	81	77.1	151	11	AA195865	Antitumour polypep
44	81	77.1	151	12	AA11615	Tumour Necrosis fa
45	81	77.1	151	12	AA11613	Tumour Necrosis fa

#### ALIGNMENTS

RESULT 1	
AA60233	
ID	AA60233 standard; peptide: 17 AA.
AC	
AA60233:	
16-MAR-1995 (first entry)	
XX	
hTNF-alpha tip.	
DE	
XX	
TNF-alpha; tumor necrosis factor-alpha; tip peptide; muten; cancer;	
KW	sepsis; inflammation; cytokine; metastasis; lectin; adhesion;
KM	mutagenesis; trypanoside.
KX	
OS	Synthetic.
XX	
Key	Location/Qualifiers
FT	Misc-difference 1 /note="N-terminal biotin Gly-Gly"
XX	
PN	W09418325-A.
PD	18-AUG-1994.
XX	
PE	02-FEB-1994; 94NO-EP00286.
XX	
PR	03-FEB-1993; 93EP-0400262.
XX	
PA	(INNO-) INNOGENETICS NV SA.
XX	
PI	De Betseleer P, Franssen L, Lucas R, Sablon E;
XX	
DR	WPI, 1994-279746/34.

XX New tumour necrosis factor -alpha muteins, antibodies and  
 PT antisense peptide(s) - used in the treatment of diseases and  
 PT conditions associated with the in vivo activities of TNF- $\alpha$  eg  
 PT cancer, sepsis, inflammation, etc  
 PS Disclosure; Page 61; 132pp; English.  
 XX  
 CC The TNF- $\alpha$  tip peptides given in AAR60232-42 were modified with  
 CC N-terminal biotin-gly-moieties and were used to demonstrate  
 CC that the tip region of mouse and human TNF- $\alpha$  contains the  
 CC trypanosomal and lectin-like activities of the molecule and is  
 CC involved in TNF-induced lethal shock.  
 XX  
 SQ Sequence 17 AA;  
 Query Match 100.0%; Score 105; DB 15; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 3.8e-09;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 CGORETPEGAEAKPMYC 17  
 Db 1 CGORETPEGAEAKPMYC 17  
 RESULT 2  
 AAY82196  
 ID AAY82196 standard; peptide; 17 AA.  
 XX  
 AC AAY82196;  
 XX  
 DT 08-JUN-2000 (first entry)  
 XX  
 DE Tumour necrosis factor alpha derived circularised peptide #1.  
 XX  
 KW Tumour necrosis factor alpha; TNF- $\alpha$ ; human; mouse; oedema;  
 KW proinflammatory; pulmonary oedema; cyclic.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Disulfide-bond 1..17  
 XX  
 PN WO200009149-A1.  
 XX  
 PD 24-FEB-2000.  
 XX  
 PE 10-AUG-1999; 99WO-EP05806.  
 XX  
 PR 14-AUG-1998; 98EP-0870180.  
 PR 18-SEP-1998; 98EP-0870198.  
 PR 21-OCT-1998; 98EP-0870222.  
 XX  
 PA (INNO-) INNOGENETICS NV.  
 XX  
 PI Lucas R, De Baetselier P, Pugin J, Bloc A, Fransen L;  
 XX  
 DR WPI; 2000-282855/24.  
 XX  
 PT Use of peptides derived from human or mouse tissue necrosis  
 PT factor-alpha (TNF- $\alpha$ ), and comprising 7-17 contiguous amino acids,  
 PT for preventing or treating oedema -  
 XX  
 PS Claim 8; Page 16; 26pp; English.  
 XX  
 CC The present invention describes the use of peptides comprising a chain  
 CC of 7-17 contiguous amino acids derived from the Ser100-Glu116 region  
 CC of human tumour necrosis factor-alpha (TNF- $\alpha$ ), or Ser99-Glu115  
 CC region of mouse TNF- $\alpha$ , for treating oedema. The peptides form  
 CC pharmaceutical compositions for treating oedema, especially pulmonary  
 CC oedema. The peptides are non-toxic, whilst retaining the oedema  
 CC resorption-inducing capacity as TNF. The present sequence represents  
 CC a specifically claimed TNF- $\alpha$  circularised peptide from the present

CC invention.  
 XX  
 SQ Sequence 17 AA;  
 Query Match 100.0%; Score 105; DB 21; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 3.8e-09;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 CGORETPEGAEAKPMYC 17  
 Db 1 CGORETPEGAEAKPMYC 17  
 RESULT 3  
 AAR60232  
 ID AAR60232 standard; peptide; 17 AA.  
 XX  
 AC AAR60232;  
 XX  
 DT 16-MAR-1995 (first entry)  
 XX  
 DE mTNF- $\alpha$  tip.  
 XX  
 KW TNF- $\alpha$ ; tumor necrosis factor-alpha; tip peptide; mutein; cancer;  
 KW sepsis; inflammation; cytokine; metastasis; lectin; adhesion;  
 KW mutagenesis; trypanoside.  
 XX  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 1  
 FT note="N-terminal biotin Gly-Gly"  
 XX  
 PN WO9418325-A.  
 XX  
 PD 18-AUG-1994.  
 XX  
 PE 02-FEB-1994; 94WO-EP00266.  
 XX  
 PR 03-FEB-1993; 93EP-0400262.  
 XX  
 PA (INNO-) INNOGENETICS NV SA.  
 XX  
 PI De Baetselier P, Fransen L, Lucas R, Sablon E;  
 XX  
 DR WPI; 1994-279746/34.  
 XX  
 PE New tumour necrosis factor -alpha muteins, antibodies and  
 PT antisense peptide(s) - used in the treatment of diseases and  
 PT conditions associated with the in vivo activities of TNF- $\alpha$  eg  
 PT cancer, sepsis, inflammation, etc  
 XX  
 PS Disclosure; Page 61; 132pp; English.  
 XX  
 CC The TNF- $\alpha$  tip peptides given in AAR60232-42 were modified with  
 CC N-terminal biotin-gly-moieties and were used to demonstrate  
 CC that the tip region of mouse and human TNF- $\alpha$  contains the  
 CC trypanosomal and lectin-like activities of the molecule and is  
 CC involved in TNF-induced lethal shock.  
 XX  
 SQ Sequence 17 AA;  
 Query Match 83.8%; Score 88; DB 15; Length 17;  
 Best Local Similarity 76.5%; Pred. No. 1.4e-06;  
 Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
 OY 1 CGORETPEGAEAKPMYC 17  
 Db 1 CGPVDTEPGAEAKPMYC 17  
 RESULT 4  
 AAY82197

ID AAY82197 standard; peptide: 17 AA.  
 AC AAY82197;  
 XX  
 DT 08-JUN-2000 (first entry)  
 DE Tumour necrosis factor alpha derived circularised peptide #2.  
 XX  
 KM Tumour necrosis factor alpha; TNF-alpha; human; mouse; oedema;  
 XX  
 KM proinflammatory; pulmonary oedema; cyclic.  
 OS Mus sp.  
 XX  
 FH Key Location/Qualifiers  
 FT Disulfide-bond 1..17  
 XX  
 PN WO200009149-A1.  
 XX  
 PD 24-FEB-2000.  
 XX  
 PF 10-AUG-1999; 99WO-EP05806.  
 XX  
 PR 14-AUG-1998; 98EP-0870180.  
 PR 18-SEP-1998; 98EP-0870198.  
 PR 21-OCT-1998; 98EP-0870222.  
 XX  
 PA (INNO-) INNOGENETICS NV.  
 XX  
 PI Lucas R, De Baetselier P, Pugin J, Bloc A, Franssen L;  
 XX  
 DR WPI: 2000-282855/24.  
 XX  
 PT Use of peptides derived from human or mouse tissue necrosis  
 PT factor-alpha (TNF-alpha), and comprising 7-17 contiguous amino acids,  
 PT for preventing or treating oedema  
 XX  
 PS Claim 8; Page 16; 26pp; English.  
 XX  
 CC The present invention describes the use of peptides comprising a chain  
 CC of 7-17 contiguous amino acids derived from the Ser100-Glu116 region  
 CC of human tumour necrosis factor-alpha (TNF-alpha), or Ser99-Glu115  
 CC region of mouse TNF-alpha, for treating oedema. The peptides form  
 CC pharmaceutical compositions for treating oedema, especially pulmonary  
 CC oedema. The peptides are non-toxic, whilst retaining the oedema  
 CC resorption-inducing capacity as TNF. The present sequence represents  
 CC a specifically claimed TNF-alpha circularised peptide from the present  
 CC invention.  
 CC  
 SQ Sequence 17 AA;  
 XX  
 Query Match 83.8%; Score 88; DB 21; Length 17;  
 Best Local Similarity 76.5%; Pred. No. 1.4e-06;  
 Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
 OY 1 CGQRETPGAGAKPYC 17  
 II::IIIIIIIIII  
 DB 1 CGPKDTPGAGELKPYC 17  
 XX  
 RESULT 5  
 AAY82198  
 ID AAY82198 standard; peptide: 19 AA.  
 AC AAY82198;  
 XX  
 DT 08-JUN-2000 (first entry)  
 DE Murine TNF derived peptide long tip peptide 99-115 (LTIP).  
 XX  
 KM Tumour necrosis factor alpha; TNF-alpha; human; mouse; oedema;  
 XX  
 KM proinflammatory; pulmonary oedema.  
 OS Mus sp.

XX  
 PN WO200009149-A1.  
 XX  
 PD 24-FEB-2000.  
 XX  
 PF 10-AUG-1999; 99WO-EP05806.  
 XX  
 PR 14-AUG-1998; 98EP-0870180.  
 PR 18-SEP-1998; 98EP-0870198.  
 PR 21-OCT-1998; 98EP-0870222.  
 XX  
 PA (INNO-) INNOGENETICS NV.  
 XX  
 PI Lucas R, De Baetselier P, Pugin J, Bloc A, Franssen L;  
 XX  
 DR WPI: 2000-282855/24.  
 XX  
 PT Use of peptides derived from human or mouse tissue necrosis  
 PT factor-alpha (TNF-alpha), and comprising 7-17 contiguous amino acids,  
 PT for preventing or treating oedema  
 XX  
 PS Example 1; Page 7; 26pp; English.  
 XX  
 CC The present invention describes the use of peptides comprising a chain  
 CC of 7-17 contiguous amino acids derived from the Ser100-Glu116 region  
 CC of human tumour necrosis factor-alpha (TNF-alpha), or Ser99-Glu115  
 CC region of mouse TNF-alpha, for treating oedema. The peptides form  
 CC pharmaceutical compositions for treating oedema, especially pulmonary  
 CC oedema. The peptides are non-toxic, whilst retaining the oedema  
 CC resorption-inducing capacity as TNF. The present sequence represents  
 CC a murine TNF derived peptide used in an example from the present  
 CC invention.  
 CC  
 SQ Sequence 19 AA;  
 XX  
 Query Match 83.8%; Score 88; DB 21; Length 19;  
 Best Local Similarity 76.5%; Pred. No. 1.6e-06;  
 Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
 OY 1 CGQRETPGAGAKPYC 17  
 II::IIIIIIIIII  
 DB 3 CGPKDTPGAGELKPYC 19  
 XX  
 RESULT 6  
 AAY82194  
 ID AAY82194 standard; peptide: 14 AA.  
 AC AAY82194;  
 XX  
 DT 08-JUN-2000 (first entry)  
 DE Tumour necrosis factor alpha derived peptide #1.  
 XX  
 KM Tumour necrosis factor alpha; TNF-alpha; human; mouse; oedema;  
 XX  
 KM proinflammatory; pulmonary oedema.  
 OS Homo sapiens.  
 XX  
 PN WO200009149-A1.  
 XX  
 PD 24-FEB-2000.  
 XX  
 PF 10-AUG-1999; 99WO-EP05806.  
 XX  
 PR 14-AUG-1998; 98EP-0870180.  
 PR 18-SEP-1998; 98EP-0870198.  
 PR 21-OCT-1998; 98EP-0870222.  
 XX  
 PA (INNO-) INNOGENETICS NV.  
 XX  
 PI Lucas R, De Baetselier P, Pugin J, Bloc A, Franssen L;

DR WPI; 2000-282855/24.  
 XX  
 PT Use of peptides derived from human or mouse tissue necrosis  
 PT factor-alpha (TNF-alpha), and comprising 7-17 contiguous amino acids,  
 PT for preventing or treating oedema  
 XX  
 PS Claim 5; Page 16; 26pp; English.  
 CC The present invention describes the use of peptides comprising a chain  
 CC of 7-17 contiguous amino acids derived from the Ser100-Glu116 region  
 CC of human tumour necrosis factor-alpha (TNF-alpha), or Ser99-Glu115  
 CC region of mouse TNF-alpha, for treating oedema. The peptides form  
 CC pharmaceutical compositions for treating oedema, especially pulmonary  
 CC oedema. The peptides are non-toxic, whilst retaining the oedema  
 CC resorption-inducing capacity as TNF. The present sequence represents  
 CC a specifically claimed TNF-alpha peptide from the present invention.  
 XX  
 SQ Sequence 14 AA;  
 Query Match 77.1%; Score 81; DB 21; Length 14;  
 Best Local Similarity 100.0%; Pred. NO. 1.4e-05;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 QRETPEGAEAKPMY 16  
 DB 1 QRETPEGAEAKPMY 14  
 RESULT 7  
 AAR05469  
 XX AAR05469 standard; protein; 17 AA.  
 AC AAR05469;  
 XX  
 DT 23-OCT-1990 (first entry)  
 DE Tumour necrosis factor derived peptide.  
 XX  
 KM Tumour necrosis factor; TNF; neoplastic disease; autoimmune  
 KM disease; infection; inflammation; transplant rejection.  
 XX  
 OS Synthetic.  
 XX  
 PN DE3841759-A.  
 XX  
 PD 13-JUN-1990.  
 XX  
 PF 12-DEC-1988; 88DE-3841759.  
 XX  
 PR 12-DEC-1988; 88DE-3841759.  
 XX  
 PA (BADT ) BASF AG.  
 PI Bohm HJ, Daum L, Haupt A, Schmied B, Walker N, Zechel JC;  
 DR WPI; 1990-186576/25.  
 XX  
 PT New tumour necrosis factor derived peptides- for treating or preventing  
 PT neoplastic and autoimmune diseases, infection, inflammation and  
 PT transplant rejection.  
 XX  
 PS Example 1; Page 7; 16pp; German.  
 CC To residue S1 is attached Ac and to residue T17 NH2.  
 CC This peptide is an example of a highly generic sequence of the  
 CC formula X-A-Y.  
 CC A= QRETPEGAEAKP, HRETPENAEAKP, HRETPENAEAPMA, PROTPEGAEELKP, PGLOEP,  
 CC PGPOGP or PGLOGP;  
 CC X= G-NH-CHM-CO, G-NH-CHM-CO-W, G-R-NH-CHM-CO or G-R-NH-CHM-CO-W;  
 CC Y= Z, NH-CHQ-COZ, V-NH-CHQ-COZ, NH-CHQ-CO-U-Z or V-NH-CHQ-CO-U-Z;  
 CC G= H or an amino protecting group;  
 CC Z= OH, NH2 or carboxy protecting group; or G and Z together are a  
 CC covalent bond or the gp. CO(CH2)2NH; a=1-12;

CC R, U, V and W= peptide chains of 1-4 naturally occurring alpha aminoacids;  
 CC M and O= H, isopropyl, CHMe-Et, phenyl, CH(OH), 3-indolyl- or  
 CC 4-midazolyl-methyl or (CH2)BT; b=1-6;  
 CC T= OH, MeO, MeS, isopropyl, phenyl (opt. 4-OH, substd.), HS, NH2, COOH,  
 CC CONH2, or NH2 C (NH) NH; or  
 CC M and O together are (CH2)c-S-S-(CH2)d, (CH2)eCO NH-(CH2)f or  
 CC (CH2)2eNH CO(CH2)2gNH CO(CH2)h; c and d=1-4; e and f=1-6; g=1-12.  
 CC The peptide is a low mol. wt. deriv. of TNF.  
 CC See also DE3841753-55, DE3841759, DE3841761-64, DE3841767-68.  
 XX  
 SQ Sequence 17 AA;  
 Query Match 77.1%; Score 81; DB 11; Length 17;  
 Best Local Similarity 100.0%; Pred. NO. 1.7e-05;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 QRETPEGAEAKPMY 16  
 DB 4 QRETPEGAEAKPMY 17  
 RESULT 8  
 AAR05513  
 XX AAR05513 standard; protein; 25 AA.  
 AC AAR05513;  
 XX  
 DT 23-OCT-1990 (first entry)  
 DE Tumour necrosis factor derived peptide.  
 XX  
 KM Tumour necrosis factor; TNF; neoplastic disease; autoimmune  
 KM disease; infection; inflammation; transplant rejection.  
 XX  
 OS Synthetic.  
 XX  
 PN DE3841759-A.  
 XX  
 PD 13-JUN-1990.  
 XX  
 PF 12-DEC-1988; 88DE-3841759.  
 XX  
 PR 12-DEC-1988; 88DE-3841759.  
 XX  
 PA (BADT ) BASF AG.  
 PI Bohm HJ, Daum L, Haupt A, Schmied B, Walker N, Zechel JC;  
 DR WPI; 1990-186576/25.  
 XX  
 PT New tumour necrosis factor derived peptides- for treating or preventing  
 PT neoplastic and autoimmune diseases, infection, inflammation and  
 PT transplant rejection.  
 XX  
 PS Example 37; Page 12; 16pp; German.  
 CC To residue S1 is attached Ac and to residue Y22 NH2.  
 CC Residues Orn4 and Asp22 together form a covalent bond.  
 CC This peptide is an example of a highly generic sequence of the  
 CC formula X-A-Y.  
 CC A= QRETPEGAEAKP, HRETPENAEAKP, HRETPENAEAPMA, PROTPEGAEELKP, PGLOEP,  
 CC PGPOGP or PGLOGP;  
 CC X= G-NH-CHM-CO, G-NH-CHM-CO-W, G-R-NH-CHM-CO or G-R-NH-CHM-CO-W;  
 CC Y= Z, NH-CHQ-COZ, V-NH-CHQ-COZ, NH-CHQ-CO-U-Z or V-NH-CHQ-CO-U-Z;  
 CC G= H or an amino protecting group;  
 CC Z= OH, NH2 or carboxy protecting group; or G and Z together are a  
 CC covalent bond or the gp. CO(CH2)2NH; a=1-12;  
 CC R, U, V and W= peptide chains of 1-4 naturally occurring alpha aminoacids;



CC M and Q-H, isopropyl, CHMe.Et, phenyl, CH(OH), 3-indolyl - or  
 CC 4-Imidazolyl-methyl or (CH<sub>2</sub>)<sub>2</sub>Br; b-1-6;  
 CC T-OH, MeO, MeS, isopropyl, phenyl (opt. 4-OH, substd.), HS, NH<sub>2</sub>, COOH,  
 CC CONH<sub>2</sub>, or NH<sub>2</sub> C (NH) NH; or  
 CC M and Q together are (CH<sub>2</sub>)<sub>2</sub>C-S-S-(CH<sub>2</sub>)<sub>2</sub>d, (CH<sub>2</sub>)<sub>2</sub>CO NH-(CH<sub>2</sub>)<sub>2</sub>f or  
 CC (CH<sub>2</sub>)<sub>2</sub>CO(CH<sub>2</sub>)<sub>2</sub>CO(CH<sub>2</sub>)<sub>2</sub>f; c and d-1-4; e and f-1-6; g-1-12.  
 CC The peptide is a low mol. wt. deriv. of TNF.  
 CC See also DB3841753-55, DB3841759, DB3841761-64, DB3841767-68.  
 CC  
 XX  
 SQ Sequence 25 AA;

Query Match 77.1%; Score 81; DB 11; Length 25;  
 Best Local Similarity 100.0%; Pred. No. 2.5e-05;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 QRETPGAEAKPMY 16  
 |||||  
 DB 8 QRETPGAEAKPMY 21

## RESULT 9

AAR72456  
 ID AAR72456 standard; protein; 140 AA.

AC AAR72456;

DT 19-DEC-1995 (first entry)

DE Tumour necrosis factor-alpha 4th exon fragment.

KW Tumour necrosis factor; fusion protein; metastasis; inhibition.

XX Synthetic.

OS  
 FH Key Location/Qualifiers

FT Misc-difference 1 /note= "This residue has the peptide AAR72454  
 FT attached at the N-terminus"  
 XX

PN TW239078-A.

PD 21-JAN-1995.

PF 12-OCT-1993; 93TW-0108498.

PR 29-SEP-1993; 93JP-0020556.

PA (MIZU/) MIZUNO D.  
 PA (SONA/) SONAMOTO I.

PI Sonamoto I;

DR WPI; 1995-168947/22.

XX Pharmaceutical and veterinary composition for inhibiting metastasis  
 PT - can be made into tablet form

PS Disclosure; Page 5; 14pp; Chinese.

XX The amino acid sequence of a part of the 4th exon from the tumour  
 CC necrosis factor (TNF)-alpha. The protein has the peptide AAR72454  
 CC attached to the N-terminal amino acid. The fusion protein can be  
 CC used in pharmaceutical compositions for inhibiting metastasis.  
 CC  
 XX

SQ Sequence 140 AA;

Query Match 77.1%; Score 81; DB 16; Length 140;  
 Best Local Similarity 100.0%; Pred. No. 0.00014;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 QRETPGAEAKPMY 16  
 |||||  
 DB 85 QRETPGAEAKPMY 98

## RESULT 10

AAP82043  
 ID AAP82043 standard; protein; 145 AA.

AC AAP82043;

DT 12-DEC-1990 (first entry)

DE Sequence of new tumour necrosis factor (TNF).

KW Anticancer drug; lymphokine; antitumour.

XX Homo sapiens.

PN JP63032486-A.

PD 12-FEB-1988.

PF 25-JUL-1986; 86JP-0173822.

PR 25-JUL-1986; 86JP-0173822.

PA (TEIJ ) TEIJIN KK.

DR WPI; 1988-080331/12.

XX New biologically active polypeptide - useful as anticancer agent  
 PS Claim 2(1); Page 547; 17pp; Japanese.

CC New biologically active polypeptide has cytotoxic activity specifically  
 CC for tumour cells and, therefore, is expected to be used as an anticancer  
 CC drug. It is derived from human TNF by deleting 11 N-terminal AAs. (See  
 CC also J63188396, AAN81624 and AAP81236).  
 CC  
 XX

SQ Sequence 145 AA;

Query Match 77.1%; Score 81; DB 9; Length 145;  
 Best Local Similarity 100.0%; Pred. No. 0.00014;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 QRETPGAEAKPMY 16  
 |||||  
 DB 91 QRETPGAEAKPMY 104

## RESULT 11

AAP81853  
 ID AAP81853 standard; protein; 147 AA.

AC AAP81853;

DT 17-DEC-1990 (first entry)

DE Sequence of modified human tumour necrosis factor (hTNF).

KW Antitumour; anticancer; cytostatic.

XX Homo sapiens.

PN JP62272991-A.

PD 27-NOV-1987.

PF 21-MAY-1986; 86JP-0114754.

PR 21-MAY-1986; 86JP-0114754.

PA (TEIJ ) TEIJIN KK.

DR WPI; 1988-010365/02.

DR N-PSDB: AAN82306.

XX New bioactive polypeptide -  
 PT has antitumour activity, and is obtd. by culturing bacteria  
 PT transformed with plasmid contg. DNA sequence of the polypeptide  
 XX  
 PS Claim 2(1): Page 761, 20pp; Japanese.

CC DNA sequence encoding hTNF was synthesised chemically and inserted into  
 CC vector plasmid. Recombinant plasmid was cut with restriction enzyme and  
 CC DNA fragment coding for new bioactive polypeptide was obtd. The new  
 CC bioactive polypeptide has ten N-terminal AAs deleted. It has antitumour  
 CC activity greater than hTNF and can be produced by culturing bacteria  
 CC transformed with a plasmid contg. DNA encoding the polypeptide.  
 XX

SO Sequence 147 AA;

Query Match 77.1%; Score 81; DB 9; Length 147;  
 Best Local Similarity 100.0%; Pred. No. 0.00014;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 QRETPGAEAKPMY 16  
 |||||

DB 92 QRETPGAEAKPMY 105

# RESULT 12

AAB67245  
 ID AAB67245 standard; protein; 147 AA.

XX AAB67245;

DT 18-APR-2001 (first entry)

DE Human tumour necrosis factor alpha.

KW Human; Apo2 ligand; divalent metal ions; viral infection; cancer.

OS Homo sapiens.

PN WO200100832-A1.

PD 04-JAN-2001.

PF 26-JUN-2000; 2000WO-US17579.

PR 28-JUN-1999; 99US-0141342.

PA (GETH ) GENENTECH INC.

PI Ashkenazi AJ, Hymowitz S, Kelley RF, Koumenis I, Leung S;  
 PI O'Connell M, Pai R, Shahrokhi Z, Simmons L;

DR WPI; 2001-123012/13.

PT Use of divalent metal ions for making Apo-2 ligand and in formulations  
 PT containing Apo-2 ligand for increasing yield and stability of ligand  
 PT trimers, useful for therapeutic applications -

PS Disclosure; Fig 3; 60pp; English.

CC The present invention relates to a formulation comprising Apo-2  
 CC ligand and divalent metal ions. Apo-2 ligand and the formulation  
 CC are useful for treating cancers and viral infections. Addition  
 CC of divalent metal ions for making Apo-2 ligand and formulations  
 CC containing Apo-2 ligand results in increased yield and stability  
 CC of Apo-2 ligand trimers.

SO Sequence 147 AA;

Query Match 77.1%; Score 81; DB 22; Length 147;

Best Local Similarity 100.0%; Pred. No. 0.00014;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 QRETPGAEAKPMY 16  
 |||||

DB 92 QRETPGAEAKPMY 105

# RESULT 13

AAY71982  
 ID AAY71982 standard; Protein; 147 AA.

XX AAY71982;

DT 28-MAR-2001 (first entry)

DE C-terminal region of human Tumour Necrosis Factor (TNF).

KW Human; Tumour Necrosis Factor; TNF; Immunosuppressant; TALL-1;

KW Tumour necrosis factor and Apol-related leucocyte expressed ligand 1;

KW therapy; autoimmune disorder; rheumatoid arthritis; multiple sclerosis;

KW systemic lupus erythematosus; SLE; insulin dependent diabetes mellitus;

KW thrombocytopenia purpura; acute rheumatic fever; myasthenia gravis;

KW haemolytic anaemia; Grave's disease; Goodpasture's syndrome;

KW post-streptococcal glomerulonephritis; polyarteritis nodosa; BCMA;

KW B cell maturation factor; pemphigus vulgaris; B-lymphocyte proliferation.

OS Homo sapiens.

PN WO200068378-A1.

PD 16-NOV-2000.

PF 05-MAY-2000; 2000WO-US12266.

PR 06-MAY-1999; 99US-0132892.

PA (NAJE-) NAT JEWISH MEDICAL & RES CENT.

PI Shu HS;

DR WPI; 2001-016094/02.

PT Isolated TALL-1 protein is used to identify compounds that regulate B  
 PT lymphocyte proliferation, used to treat B lymphocyte associated  
 PT autoimmune disorders -

PS Example 1; Fig 1b; 112pp; English.

SO The present invention relates to Tumour necrosis factor (TNF) and

CC Apol-related leucocyte expressed ligand 1 (TALL-1) nucleic acid  
 CC molecules, proteins (including homologues), and their antibodies. The  
 CC invention in particular relates to methods for regulating the  
 CC interaction between TALL-1 and TALL-1 receptors (RGM referred as B cell  
 CC maturation factor) to regulate monocyte, macrophage and B lymphocyte  
 CC mediated immune responses. TALL-1 protein is useful for identifying  
 CC compounds that regulate B lymphocyte proliferation. It is also useful for  
 CC treating B lymphocyte associated autoimmune disorders like rheumatoid  
 CC arthritis, systemic lupus erythematosus (SLE), insulin dependent diabetes  
 CC mellitus, multiple sclerosis, myasthenia gravis, Grave's disease,  
 CC autoimmune haemolytic anaemia, autoimmune thrombocytopenia purpura,  
 CC Goodpasture's syndrome, pemphigus vulgaris, acute rheumatic fever,  
 CC post-streptococcal glomerulonephritis, or polyarteritis nodosa.  
 CC The TALL-1 protein and its corresponding nucleic acid sequence are also  
 CC useful in diagnostic assays.  
 CC The present sequence is a C-terminal region of human Tumour necrosis  
 CC factor (TNF) which has 20-25% sequence identity with C-terminal region of  
 CC human TALL-1 protein extracellular domain.  
 CC  
 XX Sequence 147 AA;

Query Match 77.1%; Score 81; DB 22; Length 147;  
 Best Local Similarity 100.0%; Pred. No. 0.00014;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 QRETPGAEAKPMY 16  
 |||||  
 DB 92 QRETPGAEAKPMY 105

RESULT 14  
 AAP91635  
 ID AAP91635 standard; protein; 149 AA.  
 XX  
 AC AAP91635;

DT 25-JUN-1990 (first entry)

XX Polypeptide derived from human tumour necrosis factor.

DE Tumour necrosis factor; antitumour activity; pTNF482.

XX Homo sapiens.

XX JP01023898-A.

XX 26-JAN-1989.

PD 17-JUL-1987; 87JP-0177284.

PF 17-JUL-1987; 87JP-0177284.

XX 17-JUL-1987; 87JP-0177284.

PR (TEIJ ) TEIJIN KK.

XX WPI; 1989-072158/10.

XX N-PSDB; AAN94432.

DR New physiologically active polypeptide - with antitumour activity.

XX Claim 1, page 1; 18pp; Japanese.

PS The recombinant polypeptide expressed by E.coli transformed with pTNF482,

XX has antitumour activity with greater specific activity and stability than

CC natural h-TNF, and which causes less side effects.

XX Sequence 149 AA;

OY 3 QRETPGAEAKPMY 16  
 |||||

DB 94 QRETPGAEAKPMY 107

RESULT 15

ID AAR05612 standard; protein; 149 AA.

XX AAR05612;

XX 29-OCR-1990 (first entry)

DE Antitumour peptide.

XX Antitumour; cancer; tumour necrosis factor; ds.

XX Synthetic.

PN JP02128696-A.

XX 17-MAY-1990.

XX 09-NOV-1988; 88JP-0281364.

XX 09-NOV-1988; 88JP-0281364.

XX (TEIJ ) TEIJIN KK.

XX WPI; 1990-196692/26.

DR N-PSDB; AAQ05038.

XX New physiologically active polypeptide -

PT contains specific amino acid sequence, shows antitumour effect

PT and has low side effect.

XX Disclosure; 18pp; Japanese.

XX DNA is synthesised from 17 oligonucleotides TNF-1 to TNF-17.

CC The gene product may be truncated by 12 N-terminal AAs, and

CC residue Leu-157 may be replaced by Phe

XX Sequence 149 AA;

OY 3 QRETPGAEAKPMY 16  
 |||||  
 DB 95 QRETPGAEAKPMY 108

Query Match 77.1%; Score 81; DB 11; Length 149;  
 Best Local Similarity 100.0%; Pred. No. 0.00015;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Search completed: April 4, 2003, 08:39:55  
 Job time : 31.5323 secs

GenCore version 5.1.4.p5.4578  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 4, 2003, 08:37:36 ; Search time 12.3387 Seconds  
(without alignments)  
132.452 Million cell updates/sec

Title: US-09-779-703-4

Perfect score: 105

Sequence: 1 CGOREPGEAKPWC 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

1: PIR\_73:\*  
2: PIR1:\*  
3: PIR3:\*  
4: PIR4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	81	77.1	232	1	SI2606
2	81	77.1	233	1	QWHUN
3	81	77.1	233	1	S22052
4	81	77.1	233	2	SI1688
5	68	64.8	185	2	S52715
6	68	64.8	233	1	S24642
7	66	62.9	234	1	JH0529
8	65	61.9	235	1	QWMSN
9	65	61.9	235	2	JU0029
10	65	61.9	235	2	S06192
11	59.5	56.7	193	1	J01344
12	59	56.2	234	1	D69373
13	49.5	47.1	347	2	D69373
14	49	46.7	234	1	A25451
15	48	45.7	328	2	AH2218
16	47	44.8	711	2	F75440
17	46.5	44.3	733	2	F82965
18	46	43.8	647	2	G75060
19	45	42.9	469	2	T48783
20	45	42.9	553	2	T45596
21	45	41.9	1386	2	T00257
22	44	41.9	142	2	A47169
23	44	41.9	195	2	T43227
24	44	41.9	669	2	T47484
25	44	41.9	713	2	G96286
26	44	41.9	713	2	AB2997
27	43.5	41.4	1677	2	T14267
28	43	41.0	157	2	AF3344
29	43	41.0	289	2	AH0060

30	43	41.0	733	2	B40595	methylnalonyl-CoA
31	43	41.0	879	1	QRRTD	IDL receptor precu
32	43	41.0	1021	2	F82230	conserved hypothet
33	43	41.0	1216	2	T09224	spindle assembly c
34	42.5	40.5	1297	2	T30274	proteolisin - se
35	42	40.0	187	2	C75136	hypothetical prote
36	42	40.0	220	2	E72204	hypothetical prote
37	42	40.0	350	2	A10924	probable bacteriop
38	42	40.0	402	2	D70602	probable arginine
39	42	40.0	800	1	S31575	interleukin-4 rece
40	42	40.0	836	2	JE0248	ATP-binding cassat
41	42	40.0	1539	2	G70630	probable ctpH prot
42	42	40.0	4544	1	S02392	alpha-2-macroglobu
43	42	40.0	4545	1	S25111	alpha-2-macroglobu
44	41.5	39.5	1002	2	T43236	carboxypeptidase C
45	41	39.0	331	2	A83678	hypothetical prote

#### ALIGNMENTS

##### RESULT 1

SI2606

tumor necrosis factor alpha precursor - pig

C:Species: Sus scrofa domestica (domestic pig)

C>Date: 10-Sep-1999 #sequence, revision 10-Sep-1999 #text\_change 04-Feb-2000

C:Accession: SI2606; SI7290; SI8965; I46659

R:Draws: R.T.; Coffee, B.W.; Prestwood, A.K.; McGraw, R.A.

Nucleic Acids Res. 18, 5564, 1990

A>Title: Gene sequence of porcine tumor necrosis factor alpha.

A:Reference number: SI2606; MUID:91016861; PMID:2216741

A:Accession: SI2606

A:Molecule type: DNA

A:Residues: 1-232 <DRE>

A:Cross-references: EMBL:X54001; NID:g2135; PIDN:CAA37949.1; PID:g2136

R:Kuhnert, P.; Wuehlich, C.; Peterhans, E.; Pauli, U.

Gene 102, 171-178, 1991

A>Title: The porcine tumor necrosis factor-encoding genes: sequence and comparative a

A:Reference number: SI7289; MUID:91340150; PMID:1874444

A:Accession: SI7290

A:Molecule type: DNA

A:Residues: 1-232 <KUH>

A:Cross-references: EMBL:X54859; NID:g2132; PIDN:CAA38639.1; PID:g2134

A>Note: The authors translated the codon GAG for residue 202 as Gly

R:Choi, C.S.; Mollitor, T.W.; Lin, G.F.; Murtaugh, M.P.

submitted to the EMBL data library, January 1991

A>Description: Complete nucleotide sequence of a cDNA encoding porcine tumor necrosis

A:Accession: SI8965

A:Molecule type: mRNA

A:Residues: 1-232 <CHO>

A:Cross-references: EMBL:X57321; NID:g2137; PIDN:CAA40591.1; PID:g2138

R:Pauli, U.; Beutler, B.; Peterhans, E.

Gene 81, 185-191, 1989

A>Title: Porcine tumor necrosis factor alpha: Cloning with the polymerase chain react

A:Reference number: I46659; MUID:90034181; PMID:2478420

A:Accession: I46659

A:Molecule type: mRNA

A:Residues: 44-232 <PAU>

A:Cross-references: GB:M29079; NID:g164694; PIDN:AAA31128.1; PID:g164695

C:Genetics: 62/3; 78/1; 93/1

C:Superfamily: tumor necrosis factor

C:Keywords: cytokine; cytotoxic; glycoprotein; lipoprotein; lymphokine; macrophage; m

F:1-77/Domain: propeptide #status predicted <PRO>

F:78-222/Product: tumor necrosis factor alpha #status predicted <MAT>

F:19/20/Binding site: myristate (lys) (covalent) #status predicted

F:91/Binding site: carbohydrate (Ser) (covalent) #status predicted

F:144-176/Disulfide bonds: #status predicted

Query Match 77.1%; Score 81; DB 1; Length 232;

Best Local Similarity 100.0%; Pred. No. 3.6e-05;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 3 QRETPGAEKAPMW 16  
 |||||||  
 Db 177 QRETPGAEKAPMW 190

## RESULT 2

OMHUN

tumor necrosis factor alpha precursor [validated] - human

M:Alternate names: cachectin; TNFA

C:Species: Homo sapiens (man)

C:Date: 28-Aug-1985 #sequence, revision 28-Aug-1985 #text, change 08-Dec-2000

C:Accession: A93585; S36153; A93351; A44189; B61478; I53311; S62610; I54522; A01646; B23

R:Nedwin, G.E.; Naylor, S.L.; Sakaguchi, A.Y.; Smith, D.; Jarrett-Nedwin, J.; Pennica, D

Nucleic Acids Res. 13, 6361-6373, 1985

A:Title: Human lymphotoxin and tumor necrosis factor genes: structure, homology and chrc

A:Reference number: A93585; MUID:86016093; PMID:2995927

A:Accession: A93585

A:Molecule type: DNA

A:Residues: 1-233 &lt;MED&gt;

A:Cross-references: GB:X02910; GB:X02159; NID:937209; PIDN:CAA26669.1; PID:937210

R:Rits, F.J.M.; Bouguetere, L.; Pileur, S.; Caterina, D.; Primas, G.; Perrot, V.; Jurka

Nature Genet. 3, 137-145, 1993

A:Title: Dense Alu clustering and a potential new member of the NFkappaB family within a

A:Reference number: S36152; MUID:93272029; PMID:8499947

A:Accession: S36153

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-233 &lt;IRI&gt;

A:Cross-references: EMBL:215026; NID:937211; PIDN:CAA8745.1; PID:937212

A:Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1992

R:Pennica, D.; Nedwin, G.E.; Hayflick, J.S.; Seeburg, P.H.; Derynck, R.; Palladino, M.A.

Nature 312, 724-729, 1984

A:Title: Human tumor necrosis factor: precursor structure, expression and homology to

A:Reference number: A93351; MUID:85086244; PMID:6392892

A:Accession: A93351

A:Molecule type: mRNA

A:Residues: 1-233 &lt;PEN&gt;

A:Cross-references: GB:X02910; GB:X02159; NID:937209; PIDN:CAA26669.1; PID:937210

A:Note: this protein was isolated from the monocytic-like cell line HL-60 from a promyelid

R:Wang, A.M.; Creasey, A.A.; Ladner, M.B.; Lin, L.S.; Strickler, J.; Van Arsdel, J.N.;

Science 228, 149-154, 1985

A:Title: Molecular cloning of the complementary DNA for human tumor necrosis factor.

A:Reference number: A44189; MUID:85142190; PMID:3856324

A:Accession: A44189

A:Molecule type: mRNA

A:Residues: 1-62, S', 64-233 &lt;MAN&gt;

A:Cross-references: GB:M10988; NID:9339737; PIDN:AAA61198.1; PID:9339738

R:Fukuda, S.; Ando, S.; Sanou, O.; Tanai, M.; Fujii, M.; Masaki, N.; Nakamura, K.I.; An

Lymphokine Res. 7, 175-185, 1988

A:Title: Simultaneous production of natural human tumor necrosis factor-alpha, -beta and

A:Reference number: A61478; MUID:88301617; PMID:2841543

A:Accession: B61478

A:Molecule type: Protein

A:Residues: 83-102,109-119,121-128, 'X', 130-131,142-144, 'X', 146, 'XXX', 150-152,159-174,180

R:Marmenout, A.; Fransen, L.; Tavenier, J.; Van Der Heyden, J.; Tizard, R.; Kawashima,

Eur. J. Biochem. 152, 515-522, 1985

A:Title: Molecular cloning and expression of human tumor necrosis factor and comparison

A:Reference number: I53311; MUID:86030296; PMID:3932069

A:Accession: I53311

A:Molecule type: DNA

A:Residues: 1-233 &lt;MAR&gt;

A:Cross-references: GB:M26331; NID:9339763; PIDN:AAA6758.1; PID:9339764

A:Experimental source: U-937 cells

R:Takakura-Yamamoto, R.; Yamamoto, S.; Fukuda, S.; Kurimoto, M.

Eur. J. Biochem. 235, 431-437, 1996

A:Title: O-Glycosylated species of natural human tumor-necrosis factor-alpha.

A:Reference number: S62610; MUID:96202967; PMID:8631363

A:Accession: S62610

A:Molecule type: Protein

A:Residues: 77-99 &lt;TRAK&gt;

R:D'Alfonso, S.; Richiardi, P.M.  
 Immunogenetics 39, 150-154, 1994  
 A:Title: A polymorphic variation in a putative regulation box of the TNFA promoter re  
 A:Reference number: I54522; MUID:94102809; PMID:7903959  
 A:Accession: I54522

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-8 &lt;DAL&gt;

A:Cross-references: GB:S68530; NID:9544751

R:Stevenson, F.T.; Birstein, S.L.; Locksley, R.M.; Lovett, D.H.

J. Exp. Med. 176, 1053-1062, 1992

A:Title: Myristyl acylation of the tumor necrosis factor alpha precursor on specific

A:Reference number: A59163; MUID:93018820; PMID:1402651

A:Contents: annotation; identification of myristylated lysines

R:Aggarwal, B.B.; Kohr, W.J.; Hass, P.E.; Moffat, B.; Spencer, S.A.; Henzel, W.J.; Br

J. Biol. Chem. 260, 2345-2354, 1985

A:Title: Human tumor necrosis factor: production, purification, and characterization.

A:Reference number: A92511; MUID:85130974; PMID:3871770

A:Contents: annotation; disulfide bond

C:Comment: Secreted from mitogen-activated macrophages within 4-24 hours after induc

out detriment to normal cells. It can also act synergistically with interferon gamma

ut are produced by different cell types and have different induction kinetics.

C:Genetics: GDB:TNF; TNFA

A:Gene: GDB:TNF; TNFA

A:Cross-references: GDB:120441; OMIM:191160

A:Map position: 6p21.3-6p21.3

A:Introns: 62/3; 78/1; 94/1

C:Complex: homotrimer

C:Superfamily: tumor necrosis factor

C:Keywords: cytokine; cytotoxin; glycoprotein; homotrimer; lipoprotein; lymphokine; m

F:1-76/Domain: propeptide #status predicted &lt;PRO&gt;

F:77-233/Product: tumor necrosis factor #status experimental &lt;MAT&gt;

F:19,20/Binding site: myristate (lys) (covalent) #status experimental

F:81/Binding site: carbohydrate (Ser) (covalent) (partial) #status experimental

F:145-177/Disulfide bonds: #status experimental

Query Match 77.1%; Score 81; DB 1; Length 233;  
 Best Local Similarity 100.0%; Pred. No. 3.6e-05;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 3 QRETPGAEKAPMW 16  
 |||||||  
 Db 178 QRETPGAEKAPMW 191

RESULT 3  
 S22052  
 Tumor necrosis factor alpha precursor - baboon  
 C:Species: Papio sp. (baboon)  
 C:Date: 10-Sep-1999 #sequence, revision 10-Sep-1999 #text, change 04-Feb-2000  
 A:Accession: S22052

R:Sanjanwala, M.; Edwards, A.  
 submitted to the EMBL Data Library, September 1991  
 A:Description: Baboon Tumor Necrosis Factor Derived from Sequences of Genomic DNA.  
 A:Reference number: S22052  
 A:Accession: S22052

A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-233 <SAN>  
 A:Cross-references: EMBL:X62141; NID:938159; PIDN:CAA44068.1; PID:938160

C:Genetics:  
 A:Introns: 62/3; 78/1; 94/1  
 C:Superfamily: tumor necrosis factor

C:Keywords: glycoprotein; lipoprotein; myristylation; transmembrane protein  
 F:19,20/Binding site: myristate (lys) (covalent) #status predicted  
 F:81/Binding site: carbohydrate (Ser) (covalent) #status predicted  
 F:145-177/Disulfide bonds: #status predicted

Query Match 77.1%; Score 81; DB 1; Length 233;  
 Best Local Similarity 100.0%; Pred. No. 3.6e-05;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 QRETPGAEAKPMY 16  
 |||||  
 Db 178 QRETPGAEAKPMY 191

## RESULT 4

tumor necrosis factor alpha precursor - cat  
 S11688  
 C:Species: Felis silvestris catus (domestic cat)  
 C>Date: 21-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 04-Feb-2000  
 C:Accession: S11688  
 R:McGraw, R.A.; Coffee, B.W.; Otto, C.M.; Drews, R.T.; Rawlings, C.A.  
 Nucleic Acids Res. 18, 5563, 1990  
 A:Title: Gene sequence of feline tumor necrosis factor alpha.  
 A:Reference number: S11688; MUID:91016860; PMID:2216740  
 A:Accession: S11688  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-233 <MCG>  
 A:Cross-references: EMBL:X54000; NID:g1084; PIDN:CAA37948.1; PID:g295777  
 C:Genetics: 62/3; 78/1; 94/1  
 A:Introns:  
 C:Superfamily: tumor necrosis factor  
 C:Keywords: glycoprotein; lipoprotein; myristylation; transmembrane protein  
 F:19/20/Binding site: myristate (Lys) (covalent) #status predicted  
 F:81/Binding site: carbohydrate (Ser) (covalent) #status predicted  
 F:145-177/Disulfide bonds: #status predicted

## Query Match

Best Local Similarity 77.1%; Score 81; DB 2; Length 233;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 QRETPGAEAKPMY 16  
 |||||  
 Db 178 QRETPGAEAKPMY 191

## RESULT 5

tumor necrosis factor alpha precursor - bovine (fragment)  
 S52715  
 C:Species: Bos primigenius taurus (cattle)  
 C>Date: 19-May-1995 #sequence\_revision 21-Jul-1995 #text\_change 04-Feb-2000  
 C:Accession: S52715  
 R:Merrens, B.; Gaidulis, L.  
 Submitted to the EMBL Data Library, March 1995  
 A:Description: Cloning and sequence analysis of cDNAs encoding bovine CD40 ligand and bo  
 A:Reference number: S52715  
 A:Accession: S52715  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-185 <MER>  
 A:Cross-references: EMBL:Z48808; NID:g755701; PIDN:CAA88743.1; PID:g755702  
 C:Superfamily: tumor necrosis factor  
 C:Keywords: glycoprotein  
 F:33/Binding site: carbohydrate (Ser) (covalent) #status predicted  
 F:97-129/Disulfide bonds: #status predicted

## Query Match

Best Local Similarity 64.8%; Score 68; DB 2; Length 185;  
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 4 RETPEGAERAKPMY 16  
 |||||  
 Db 131 RETPEGAERAKPMY 143

## RESULT 6

tumor necrosis factor alpha precursor - bovine  
 S24642  
 C:Species: Bos primigenius taurus (cattle)  
 C>Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 04-Feb-2000  
 C:Accession: I46047; S24642  
 R:Cludts, I.; Cleuter, Y.; Kettmann, R.; Bury, A.; Droogmans, L.

Cytokine 5, 336-341, 1993  
 A:Title: Cloning and characterization of the tandemly arranged bovine lymphotoxin  
 A:Reference number: I46046; MUID:94083525; PMID:8260599  
 A:Accession: I46047  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-233 <CL2>  
 A:Cross-references: EMBL:Z14137; NID:g796; PIDN:CAA78511.1; PID:g798

C:Genetics:  
 A:Gene: TNFA  
 A:Introns: 62/3; 78/1; 94/1  
 C:Superfamily: tumor necrosis factor  
 C:Keywords: glycoprotein; lipoprotein; myristylation; transmembrane protein  
 F:20/Binding site: myristate (Lys) (covalent) #status predicted  
 F:81/Binding site: carbohydrate (Ser) (covalent) #status predicted  
 F:145-177/Disulfide bonds: #status predicted

## Query Match

Best Local Similarity 64.8%; Score 68; DB 1; Length 233;  
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 4 RETPEGAERAKPMY 16  
 |||||  
 Db 179 RETPEGAERAKPMY 191

## RESULT 7

tumor necrosis factor alpha precursor - sheep  
 JH0529  
 N:Alternate names: cachectin; TNF alpha  
 C:Species: Ovis orientalis aries; Ovis ammon aries (domestic sheep)  
 C>Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 04-Feb-2000  
 C:Accession: JH0529; S48118; S13114; S20661  
 R:Green, I.R.; Sargan, D.R.  
 Gene 109, 203-210, 1991  
 A:Title: Sequence of the cDNA encoding ovine tumor necrosis factor-alpha: problems  
 A:Reference number: JH0529; MUID:92112044; PMID:1765267  
 A:Accession: JH0529

A:Molecule type: mRNA  
 A:Residues: 1-234 <GRE>  
 A:Cross-references: EMBL:X55152; NID:g1405; PIDN:CAA38952.1; PID:g1406  
 A:Experimental source: alveolar macrophage  
 R:Nash, A.D.; Barclay, G.J.; Brandon, M.R.; Andrews, A.E.  
 Immunol. Cell Biol. 69, 273-283, 1991

A:Title: Molecular cloning, expression and characterization of ovine TNF-alpha.  
 A:Reference number: S48118; MUID:92155784; PMID:1786996  
 A:Accession: S48118

A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-234 <NAS>  
 A:Cross-references: EMBL:X56756; NID:g297806; PIDN:CAA40076.1; PID:g297807  
 R:Young, A.J.; Hay, J.B.; Chan, J.Y.C.  
 Nucleic Acids Res. 18, 6723, 1990

A:Title: Primary structure of ovine tumor necrosis factor alpha cDNA.  
 A:Reference number: S13114; MUID:91067496; PMID:2251151  
 A:Accession: S13114

A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-62, 64-234 <YOU>  
 A:Cross-references: EMBL:X55966; NID:g1403; PIDN:CAA39437.1; PID:g1404  
 A>Note: comparison with the introns of homologous sequences suggest that this is f.  
 C:Superfamily: tumor necrosis factor  
 C:Keywords: alternative splicing; cytokine; cytotoxin; glycoprotein; lipoprotein;  
 F:1-77/Domain: propeptide #status predicted <PRO>  
 F:78-234/Product: tumor necrosis factor alpha #status predicted <TRU>  
 F:20/Binding site: myristate (Lys) (covalent) #status predicted  
 F:82/Binding site: carbohydrate (Ser) (covalent) #status predicted  
 F:96/Binding site: carbohydrate (Asn) (covalent) #status predicted  
 F:146-178/Disulfide bonds: #status predicted

## Query Match

Best Local Similarity 62.9%; Score 66; DB 1; Length 234;  
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 4 RETPEGAELKPMY 16  
 Db 180 RETPEGAELKPMY 192

## RESULT 8

OMMSN

tumor necrosis factor alpha precursor - mouse  
 N:Alternate names: cachectin; TNF alpha

C:Species: Mus musculus (house mouse)

C:Date: 31-Mar-1988 #sequence,revision 31-Mar-1988 #extl,change 04-Feb-2000

C:Accession: A22908; S03791; A23203; A25164; A23127; A34251; I59058; A36696

R:Shirai, T.; Shimizu, N.; Shiojiri, S.; Horiuchi, S.; Ito, H.

DNA 7, 193-201, 1988

A:Title: Cloning and expression in Escherichia coli of the gene for mouse tumor necrosis

A:Reference number: A22908; MUID:88224564; PMID:2836146

A:Accession: A22908

A:Molecule type: DNA

A:Residues: 1-235 <SHI>

A:Cross-references: GB:M20155

R:Shakhov, A.N.; Nedospasov, S.A.

Bioorg. Khim. 13, 701-705, 1987

A:Title: Molecular cloning of the genes coding for tumor necrosis factors: complete nucl

A:Reference number: S03791; MUID:87298639; PMID:3040015

A:Accession: S03791

A:Molecule type: DNA

A:Residues: 1-235 <SHA>

A:Cross-references: GB:M38296; NID:9202086; PIDN:AAA0459.1; PID:9202087

A:Note: article in Russian with English abstract

R:Semon, D.; Kawashima, E.; Jongeneel, A.; Shakhov, A.N.; Nedospasov, S.A.

Nucleic Acids Res. 15, 9083-9084, 1987

A:Title: Nucleotide sequence of the murine TNF locus, including the TNF-alpha (tumor nec

A:Reference number: A93679; MUID:88067722; PMID:3684584

A:Accession: A27303

A:Molecule type: DNA

A:Residues: 1-235 <SEM>

A:Cross-references: GB:Y00467; NID:954830; PIDN:CAA66530.1; PID:954832

R:Penhale, D.; Hayflick, J.S.; Brinman, T.S.; Palladin, M.A.; Goeddel, D.V.

Proc. Natl. Acad. Sci. U.S.A. 82, 6060-6064, 1985

A:Title: Cloning and expression in Escherichia coli of the cDNA for murine tumor necrosis

A:Reference number: A25164; MUID:85298296; PMID:3898078

A:Accession: A25164

A:Molecule type: mRNA

A:Residues: 1-235 <PEN>

A:Cross-references: GB:M11731; NID:9202084; PIDN:AAA0458.1; PID:9202085

R:Franssen, L.; Muller, R.; Marmenout, A.; Tavernier, J.; Van der Heyden, J.; Kawashima,

Nucleic Acids Res. 13, 4417-4429, 1985

A:Title: Molecular cloning of mouse tumor necrosis factor cDNA and its eukaryotic expe

A:Reference number: A23127; MUID:85242112; PMID:2989794

A:Accession: A23127

A:Molecule type: mRNA

A:Residues: 1-235 <FRA>

A:Cross-references: GB:X02611; NID:954844; PIDN:CAA26457.1; PID:954845

R:Cash, K.; Beutler, B.

J. Biol. Chem. 264, 16256-16260, 1989

A:Title: Alternative cleavage of the cachectin/tumor necrosis factor propeptide results

A:Reference number: A34251; MUID:89380231; PMID:2777790

A:Accession: A34251

A:Molecule type: protein

A:Residues: 70-87 <CAS>

R:Caput, D.; Beutler, B.; Hartog, K.; Thayer, R.; Brown-Shmer, S.L.; Cerami, A.

Proc. Natl. Acad. Sci. U.S.A. 83, 1670-1674, 1986

A:Title: Identification of a common nucleotide sequence in the 3'-untranslated region of

A:Reference number: I59058; MUID:86149365; PMID:2419912

A:Accession: I59058

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-230; 'R', 232-235 <RES>

A:Cross-references: GB:M3049; NID:9202082; PIDN:AAA40457.1; PID:9202083

R:Sherry, B.; Jue, D.M.; Zentella, A.; Cerami, A.

Biochem. Biophys. Res. Commun. 173, 1072-1078, 1990

A:Title: Characterization of high molecular weight glycosylated forms of murine tumor ne

A:Reference number: A36696; MUID:91097531; PMID:2268312

A:Accession: A36696

A:Molecule type: protein

A:Residues: 80-85, 'X', 87-99 <SHE>

C:Genetics:

A:Introns: 62/3; 81/1; 97/1

A:Note: the first intron occurs in the 5'-untranslated region

C:Superfamily: tumor necrosis factor

C:Keywords: cytokine; cytotoxin; glycoprotein; lipoprotein; lymphokine; macrophage; m

F:80-235/Product: tumor necrosis factor #status experimental <MAT>

F:20/Binding site: myristate (Lys) (covalent) #status predicted

F:84/Binding site: carboxylate (Ser) (covalent) #status predicted

F:66/Binding site: carboxylate (Asn) (covalent) #status predicted

F:148-179/Disulfide bonds: #status predicted

Query Match 61.9%; Score 65; DB 1; Length 235;

Best Local Similarity 76.9%; Pred. No. 0.012;

Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 4 RETPEGAELKPMY 16

Db 181 KDPPEGAELKPMY 193

## RESULT 9

tumor necrosis factor alpha precursor - rat

N:Alternate names: cachectin; TNF alpha

C:Species: Rattus norvegicus (Norway rat)

C:Date: 07-Jun-1990 #sequence,revision 07-Jun-1990 #extl,change 04-Feb-2000

C:Accession: J00029; J00866; S21674

R:Shirai, T.; Shimizu, N.; Horiuchi, S.; Ito, H.

Agric. Biol. Chem. 53, 1733-1736, 1989

A:Title: Cloning and expression in Escherichia coli of the gene for rat tumor necrosi

A:Reference number: J00029

A:Accession: J00029

A:Molecule type: DNA

A:Residues: 1-235 <SHI>

R:Kwon, J.; Chung, I.Y.; Benveniste, E.N.

Gene 132, 227-236, 1993

A:Title: Cloning and sequence analysis of the rat tumor necrosis factor-encoding gene

A:Reference number: J00868; MUID:94040766; PMID:8224868

A:Accession: J00868

A:Molecule type: DNA

A:Residues: 1-235 <KWO>

A:Cross-references: GB:L00981; NID:9205253; PIDN:AAA16275.1; PID:9205254

R:Estler, H.C.; Grete, M.; Gausling, R.; Pavlovic, M.; Decker, K.

Biol. Chem. Hoppe-Seyler 373, 271-281, 1992

A:Title: Rat tumor necrosis factor-alpha. Transcription in rat Kupffer cells and in v

A:Reference number: S21674; MUID:92329007; PMID:1627266

A:Accession: S21674

A:Molecule type: mRNA

A:Residues: 1-38, 'P', 40-162, 'T', 164-201, 'S', 203-235 <EST>

A:Cross-references: GB:X65539; GB:S40199; NID:9395369; PIDN:CAA47146.1; PID:9395370

C:Comment: Tumor necrosis factor is secreted by macrophages in response to endotoxin

C:Genetics:

A:Gene: TNF-alpha

A:Introns: 62/3; 81/1; 97/1

C:Superfamily: tumor necrosis factor

C:Keywords: cytokine; cytotoxin; glycoprotein; lipoprotein; lymphokine; macrophage; m

F:80-235/Product: tumor necrosis factor #status predicted <MAT>

F:19,20/Binding site: myristate (Lys) (covalent) #status predicted

F:84/Binding site: carboxylate (Ser) (covalent) #status predicted

F:86/Binding site: carboxylate (Asn) (covalent) #status predicted

F:148-179/Disulfide bonds: #status predicted

Query Match 61.9%; Score 65; DB 2; Length 235;

Best Local Similarity 76.9%; Pred. No. 0.012;

Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 4 RETPEGAELKPMY 16

Db 181 KDPPEGAELKPMY 193

## RESULT 10

154490

tumor necrosis factor alpha precursor - white-footed mouse

C:Species: Peromyscus leucopus (white-footed mouse)

C:Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 04-Feb-2000

C:Accession: 154490

R:Crew, M.D.; Filipowski, M.E.

Immunogenetics 35, 351-353, 1992

A:Title: Sequence of the tumor necrosis factor/cachectin (TNF) gene from Peromyscus leu

A:Reference number: 154490; MUID:92218012; PMID:1348497

A:Accession: 154490

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-235 &lt;RES&gt;

A:Cross-references: GB:M59233; NID:g202506; PIDN:AAA0596.1; PID:g202507

C:Genetics:

A:Gene: P1TNF

A:Introns: 62/3; 81/1; 97/1

C:Superfamily: tumor necrosis factor

C:Keywords: glycoprotein; lipoprotein; myristylation

F:19,20/Binding site: myristate (Lys) (covalent) #status predicted

F:84/Binding site: carbohydrate (Ser) (covalent) #status predicted

Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 RETPEGAERKPMY 16

Db 181 RETPEGAERKPMY 193

## RESULT 11

506192

tumor necrosis factor alpha precursor - goat (fibrinogen)

N:Alternate names: cachectin; TNF alpha

C:Species: Capra aegagrus hircus (domestic goat)

C:Date: 28-Feb-1990 #sequence\_revision 28-Feb-1990 #text\_change 31-Jan-2000

C:Accession: 506192; S41867

R:Goldstein, I.M.; Henner, D.; Talhouk, A.

submitted to the EMBL Data Library, March 1989

A:Reference number: 506192

A:Accession: 506192

A:Molecule type: mRNA

A:Residues: 1-193 &lt;GOL&gt;

A:Cross-references: EMBL:X14828; NID:g992; PIDN:CAA32937.1; PID:g993

R:Rimstad, E.

submitted to the EMBL Data Library, January 1994

A:Reference number: S41867

A:Accession: S41867

A:Molecule type: mRNA

A:Status: preliminary

A:Residues: 36-38, 'S', 'A', '80-88, 'N', '90-114, 'Q', '116-123, 'D', '125-144, 'G', '145-173, 'L'

A:Cross-references: EMBL:X77317; NID:g452607; PIDN:CAA54523.1; PID:g452608

C:Superfamily: tumor necrosis factor

C:Keywords: cytokine; cytotoxin; glycoprotein; lymphokine; macrophage; membrane protein

F:42/Binding site: carbohydrate (Ser) (covalent) #status predicted

F:106-138/Disulfide bonds: #status predicted

Query Match 56.7%; Score 59.5; DB 2; Length 193;

Best Local Similarity 92.3%; Pred. No. 0.072;

Matches 12; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

OY 4 RETPEGAERKPMY 16

Db 140 RETPEGAERKPMY 151

## RESULT 12

J01344

tumor necrosis factor alpha precursor - horse

N:Alternate names: cachectin; TNF alpha

C:Species: Equus caballus (domestic horse)

C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 04-Feb-2000

C:Accession: J01344

R:Su, X.; Morris, D.D.; McGraw, R.A.

Gene 107, 319-321, 1991

A:Title: Cloning and characterization of gene TNF alpha encoding equine tumor nec

A:Reference number: J01344; MUID:92084125; PMID:1748301

A:Accession: J01344

A:Molecule type: DNA

A:Residues: 1-234 &lt;SUX&gt;

A:Cross-references: GB:M64087; NID:g164244; PIDN:AAA30959.1; PID:g164245

C:Comment: This protein is an important proximal mediator of endotoxemia.

C:Genetics:

A:Gene: TNF-alpha

A:Introns: 62/3; 79/1; 95/1

C:Superfamily: tumor necrosis factor

C:Keywords: cytokine; cytotoxin; glycoprotein; lipoprotein; lymphokine; macrophag

F:78-234/Product: tumor necrosis factor alpha #status predicted &lt;TUM&gt;

F:19,20/Binding site: myristate (Lys) (covalent) #status predicted

F:82/Binding site: carbohydrate (Ser) (covalent) #status predicted

F:146-178/Disulfide bonds: #status predicted

Query Match 56.2%; Score 59; DB 1; Length 234;

Best Local Similarity 83.3%; Pred. No. 0.1;

Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 5 RETPEGAERKPMY 16

Db 181 ESPQAEARPMY 192

## RESULT 13

D69373

immunogenic protein (bcsp31-3) homolog - Archaeoglobus fulgidus

C:Species: Archaeoglobus fulgidus

C:Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 17-Mar-2000

C:Accession: D69373

R:Rienk, H.P.; Claydon, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.;

.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirknes;

Glocke, A.; Zhou, L.; Overbeek, R.; Goeyne, J.D.; Weidman, J.F.; McDonald, L.

Nature 390, 364-370, 1997

A:Authors: Uterback, T.; Cotton, M.D.; Spriggs, T.; Artlach, P.; Kaine, B.P.; Syl

Smith, H.O.; Woese, C.R.; Venter, J.C.

A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing

A:Reference number: A69250; MUID:98049343; PMID:9389475

A:Accession: D69373

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-347 &lt;KLE&gt;

A:Cross-references: GB:AE001036; GB:AE000782; NID:g2689359; PIDN:AAB90255.1; PID:

C:Superfamily: immunogenic protein BCSP31

Query Match 47.1%; Score 49.5; DB 2; Length 347;

Best Local Similarity 50.0%; Pred. No. 4.7;

Matches 10; Conservative 0; Mismatches 5; Indels 5; Gaps 1;

OY 1 CGGRTPEGAERKPMY 15

Db 20 CAERKPEGAERKPMY 39

## RESULT 14

A25451

tumor necrosis factor alpha precursor - rabbit

N:Alternate names: cachectin; TNF alpha

C:Species: Oryctolagus cuniculus (domestic rabbit)

C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 04-Feb-2000

C:Accession: A25454; A25451; J50727

R:Ito, H.; Yamamoto, S.; Kuroda, S.; Sakamoto, H.; Kajihara, J.; Kiyota, T.; Hayas

DNA 5, 149-156, 1986

A:Title: Molecular cloning and expression in Escherichia coli of the cDNA coding f

A:Reference number: A25454; MUID:86219711; PMID:3519137



A:Accession: A25454  
 A:Molecule type: mRNA  
 A:Residues: 1-234 <IR2>  
 A:Cross-references: GB:M12845; NID:g165750; PIDN:AAA31486.1; PID:g165760  
 R:Ito, H.; Shirai, T.; Yamamoto, S.; Akira, M.; Kawahara, S.; Todd, C.W.; Wallace, R.B.  
 DNA 5, 157-165, 1986  
 A:Title: Molecular cloning of the gene encoding rabbit tumor necrosis factor.  
 A:Reference number: A25451; MUID:86219712; PMID:3519138  
 A:Accession: A25451  
 A:Molecule type: DNA  
 A:Residues: 1-234 <IR2>  
 A:Note: this sequence differs from that shown in having a Gln inserted between residues  
 R:Shakhov, A.N.; Kuprash, D.V.; Azizov, M.M.; Jongeneel, C.V.; Nedospasov, S.A.  
 Gene 95, 215-221, 1990  
 A:Title: Structural analysis of the rabbit TNF locus, containing the genes encoding TNF-  
 A:Reference number: JH0309; MUID:91065534; PMID:2249779  
 A:Accession: J50727  
 A:Status: nucleic acid sequence not shown; translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-62, 'Q', 63-234 <SH2>  
 A:Cross-references: GB:M60340; GB:M35326; NID:g165754; PIDN:AAA31484.1; PID:g165756  
 C:Genetics:  
 A:Introns: 62/3; 80/1, 96/1  
 C:Superfamily: tumor necrosis factor  
 C:Keywords: cytokine; cytotoxin; glycoprotein; lipoprotein; lymphokine; macrophage; memb  
 F:1-81/Domain: propeptide #status predicted <PRO>  
 F:82-234/Product: tumor necrosis factor #status predicted <MAT>  
 F:19,20/Binding site: myristate (Lys) (covalent) #status predicted  
 F:83/Binding site: carbohydrate (Ser) (covalent) #status predicted  
 F:147-178/Disulfide bonds: #status predicted

Query Match 46.7%; Score 49; DB 1; Length 234;

Best Local Similarity 69.2%; Pred. No. 3.9;

Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 4 RETPEGAEPKPY 16

Db 180 RETPEAEPMAY 192

# RESULT 15

AH2218  
 hypothetical protein alr3303 [imported] - Nostoc sp. (strain PCC 7120)

C:Species: Nostoc sp.

A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120

C:Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 30-Jun-2002

C:Accession: AH2218

R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriyuchi,  
 Nakazaki, N.; Shimpou, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.  
 DNA Res. 8, 205-213, 2001

A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana

A:Reference number: AB1807; MUID:21595285; PMID:11759840

A:Accession: AH2218

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-328 <KUR>

A:Cross-references: GB:BA000019; PIDN:BA075002.1; PID:g17132398; GSPDB:GN00179

A:Experimental source: strain PCC 7120

C:Genetics:

A:Gene: alr3303

Query Match 45.7%; Score 48; DB 2; Length 328;

Best Local Similarity 52.6%; Pred. No. 7.7;

Matches 10; Conservative 2; Mismatches 1; Indels 6; Gaps 2;

OY 1 CG--ORETPEGAEPKPYC 17

Db 261 CGIDKQRTPDGA----WYC 275

Search completed: April 4, 2003, 08:42:58  
 Job time : 13.3387 secs

GenCore version 5.1.4-p5-4578  
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OM protein - protein search, using sw model

Run on: April 4, 2003, 08:36:51 ; Search time 6.85484 Seconds

(without alignments)  
102.861 Million cell updates/sec

Title: US-09-779-703-4

Perfect score: 105

Sequence: 1 CGGRTPEGAFAKFWC 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

112892

Total number of hits satisfying chosen parameters:

112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	81	77.1	232	1	TNFA_PIG
2	81	77.1	233	1	TNFA_DELE
3	81	77.1	233	1	TNFA_FELCA
4	81	77.1	233	1	TNFA_HUMAN
5	81	77.1	233	1	TNFA_MACFA
6	81	77.1	233	1	TNFA_MACMU
7	81	77.1	233	1	TNFA_PAPHU
8	81	77.1	233	1	TNFA_PAPSP
9	81	77.1	233	1	TNFA_PAPTR
10	77	73.3	234	1	TNFA_CANFA
11	76	72.4	234	1	TNFA_CAFHI
12	73	69.5	234	1	TNFA_CAVPO
13	68	64.8	229	1	TNFA_CEREL
14	68	64.8	233	1	TNFA_BOVIN
15	66	62.9	234	1	TNFA_SHEEP
16	65	61.9	235	1	TNFA_MOUSE
17	65	61.9	235	1	TNFA_PERLE
18	65	61.9	235	1	TNFA_RAT
19	59	56.2	234	1	TNFA_HORSE
20	53	50.5	234	1	TNFA_MARMO
21	49	46.7	225	1	TNFA_RABIT
22	45	42.9	3038	1	TRIO_HUMAN
23	44	41.9	142	1	YFCC_CHRVI
24	44	41.9	842	1	ABCG_HUMAN
25	43	41.0	289	1	APAH_YERPE
26	43	41.0	733	1	MUPB_STRCM
27	43	41.0	879	1	LDLR_RAT
28	42	40.0	402	1	ARCA_MCTU
29	42	40.0	697	1	Y441_HUMAN
30	42	40.0	1047	1	POL_SIVAI
31	42	40.0	4544	1	LRPI_HUMAN
32	41	39.0	212	1	NOG2_BRANE
33	41	39.0	392	1	NYLB_FLASK

34	41	39.0	480	1	UGDH_SOYAN
35	41	39.0	710	1	PRM6_MYXNA
36	41	39.0	712	1	MOTB_RHINE
37	41	39.0	774	1	FECA_ECOLI
38	41	39.0	891	1	MUTS_RICPR
39	41	39.0	950	1	Y136_HUMAN
40	41	39.0	1696	1	PKCS_BRACL
41	41	39.0	2222	1	CCAE_RAT
42	41	39.0	2259	1	CCAE_RABIT
43	41	39.0	2272	1	CCAE_MOUSE
44	41	39.0	2312	1	CCAE_HUMAN
45	40	38.1	259	1	APAH_KLEAE

## ALIGNMENTS

RESULT 1

ID	TNFA_PIG	STANDARD:	PRT:	232 AA.
AC	P23563:			
DT	01-NOV-1991 (Rel. 20, Created)			
DT	01-NOV-1991 (Rel. 20, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor			
GN	1 ligand superfamily member 2) (Cachectin).			
OS	Sus scrofa (Pig).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.			
OX	NCBI_TaxID=9623;			
OX	(1)			
RN	SEQUENCE FROM N.A.			
RP	MEDLINE=91016861; PubMed=2216741;			
RA	Drews R.T., Coffee B.W., Prestwood A.K., McGraw R.A.;			
RT	"Gene sequence of porcine tumor necrosis factor alpha.";			
RL	Nucleic Acids Res. 18:5564-5564 (1990).			
RN	(2)			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Liver;			
RX	MEDLINE=91340150; PubMed=1874444;			
RA	Choi C.S., Molitor T.W., Iln G.F., Murtaugh M.P.;			
RT	"Complete nucleotide sequence of a cDNA encoding porcine tumor			
RL	necrosis factor alpha.";			
RN	Gene 102:171-178(1991).			
RP	(3)			
RC	SEQUENCE FROM N.A.			
RA	TISSUE=Macrophage;			
RT	Choi C.S., Molitor T.W., Iln G.F., Murtaugh M.P.;			
RL	"Complete nucleotide sequence of a cDNA encoding porcine tumor			
RN	necrosis factor alpha.";			
RP	Anlm. Biotechnol. 2:97-105(1991).			
RP	(4)			
RC	SEQUENCE FROM N.A.			
RA	STRAIN=Large white; TISSUE=Flbroblast;			
RT	MEDLINE=21108615; PubMed=11169259;			
RL	Chardon P., Rogel-Galliard C., Cattolico L., Duprat S., Valman M.,			
RA	Renard C.;			
RT	"Sequence of the swine major histocompatibility complex region			
RL	containing all non-classical class I genes.";			
RN	Tissue Antigens 57:55-65(2001).			
RP	(5)			
RC	SEQUENCE OF 44-232 FROM N.A.			
RA	MEDLINE=90034181; PubMed=2478420;			
RT	Pauli U., Beutler B., Peterhans E.;			
RL	"Porcine tumor necrosis factor alpha: cloning with the polymerase			
CC	chain reaction and determination of the nucleotide sequence.";			
CC	Gene 81:185-191(1989).			
CC	-I- FUNCTION: Cytochrome that binds to TNFRSF1A/TNFR1 and			
CC	TNFRSF1B/TNFR2. It is mainly secreted by macrophages and can			
CC	induce cell death of certain tumor cell lines. It is potent			
CC	pyrogen causing fever by direct action or by stimulation of			
CC	interleukin 1 secretion and is implicated in the induction of			

CC cachexia, under certain conditions it can stimulate cell  
 CC proliferation and induce cell differentiation.  
 CC -1- SUBUNIT: Homotrimer (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an  
 CC extracellular soluble form (By similarity).  
 CC -1- PTM: The soluble form derives from the membrane form by  
 CC proteolytic processing (By similarity).  
 CC -1- PTM: The membrane form, but not the soluble form, is  
 CC phosphorylated on serine residues. Dephosphorylation of the  
 CC membrane form occurs by binding to soluble TNFRSF1A/TNFR1 (By  
 CC similarity).  
 CC -1- DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF DISEASES, INCLUDING  
 CC CANCER AND INFECTION, AND IS CHARACTERIZED BY GENERAL ILL HEALTH  
 CC AND MALNUTRITION.  
 CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.  
 CC  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 CC EMBL; X54001; CAA37949.1; -  
 CC EMBL; X54859; CAA38639.1; -  
 CC EMBL; X57321; CAA40591.1; -  
 CC EMBL; AJ251914; CAB63852.1; -  
 CC EMBL; M29079; AAA31128.1; -  
 CC PIR; S12606; S12606.  
 CC PIR; S17290; S17290.  
 CC PIR; S18965; S18965.  
 CC HSSP; P01375; 4RSV.  
 CC InterPro: IPR003636; TNF\_abc.  
 CC InterPro: IPR00478; TNF\_family.  
 CC Pfam; PF00229; TNF\_1.  
 CC PRINTS; PR01234; TNECROSISFCT.  
 CC PRODOM; PD002012; TNF\_abc; 1.  
 CC SMART; SM00207; TNF\_1.  
 CC PROSITE; PS00251; TNF\_abc; 1.  
 CC PROSITE; PS50049; TNF\_2; 1.  
 CC CytoKine; CytoKine; Transmembrane; Phosphorylation; Signal-anchor.  
 CC CHAIN 1 232 TUMOR NECROSIS FACTOR, MEMBRANE FORM.  
 CC CHAIN 77 232 TUMOR NECROSIS FACTOR, SOLUBLE FORM.  
 CC DOMAIN 1 35 CYTOPLASMIC (POTENTIAL).  
 CC TRANSMEM 36 56 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)  
 CC (POTENTIAL).  
 CC DOMAIN 57 232 EXTRACELLULAR (POTENTIAL).  
 CC SITE 76 77 CLEAVAGE (BY ADAM17) (BY SIMILARITY).  
 CC MOD\_RES 2 2 PHOSPHORYLATION (BY CK1) (BY SIMILARITY).  
 CC DISULFID 144 176 BY SIMILARITY.  
 CC SEQUENCE 232 AA; 25254 MW; 65B28F702D99C8BE CRC64;  
 SO  
 Query Match 77.1%; Score 81; DB 1; Length 232;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-05;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 QRETPGAEAKPMY 16  
 Db 177 QRETPGAEAKPMY 190  
 TNFA\_DELLE  
 ID TNFA\_DELLE STANDARD; PRT; 233 AA.  
 AC 08WNR1;  
 DT 15-JUN-2002 (Rel. 41, Created)  
 DT 15-JUN-2002 (Rel. 41, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor  
 DE ligand superfamily member 2) (cachectin).  
 GN TNF OR TNFSF2 OR TNFA.  
 OS Delphinapterus leucas (beluga whale).

CC Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Cetartiodactyla; Cetacea; Odontoceti.  
 CC Monodontidae; Delphinapterus.  
 CC NCBI\_TaxID=9749;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX Pubmed=11768130;  
 RA Denis F., Archambault D.;  
 RT "Molecular cloning and characterization of beluga whale  
 RT (Delphinapterus leucas) interleukin-1beta and tumor necrosis  
 RT factor-alpha".  
 RL Can. J. Vet. Res. 65:233-240(2001).  
 CC -1- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and  
 CC TNFSF1B/TNFR. It is mainly secreted by macrophages and can  
 CC induce cell death of certain tumor cell lines. It is potent  
 CC pyrogen causing fever by direct action or by stimulation of  
 CC interleukin 1 secretion and is implicated in the induction of  
 CC cachexia, under certain conditions it can stimulate cell  
 CC proliferation and induce cell differentiation (By similarity).  
 CC -1- SUBUNIT: Homotrimer (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an  
 CC extracellular soluble form (By similarity).  
 CC -1- PTM: The soluble form derives from the membrane form by  
 CC proteolytic processing (By similarity).  
 CC -1- PTM: The membrane form, but not the soluble form, is  
 CC phosphorylated on serine residues. Dephosphorylation of the  
 CC membrane form occurs by binding to soluble TNFRSF1A/TNFR1 (By  
 CC similarity).  
 CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 CC EMBL; AF320323; AAL56946.1; -  
 CC InterPro: IPR003636; TNF\_abc.  
 CC InterPro: IPR00478; TNF\_family.  
 CC Pfam; PF00229; TNF\_1.  
 CC PRINTS; PR01234; TNECROSISFCT.  
 CC PRODOM; PD002012; TNF\_abc; 1.  
 CC SMART; SM00207; TNF\_1.  
 CC PROSITE; PS00251; TNF\_1.  
 CC PROSITE; PS50049; TNF\_2; 1.  
 CC CytoKine; CytoKine; Transmembrane; Glycoprotein; Phosphorylation;  
 CC Signal-anchor.  
 CC CHAIN 1 233 TUMOR NECROSIS FACTOR, MEMBRANE FORM.  
 CC CHAIN 78 233 TUMOR NECROSIS FACTOR, SOLUBLE FORM.  
 CC DOMAIN 1 35 CYTOPLASMIC (POTENTIAL).  
 CC TRANSMEM 36 56 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)  
 CC (POTENTIAL).  
 CC DOMAIN 57 233 EXTRACELLULAR (POTENTIAL).  
 CC SITE 77 78 CLEAVAGE (BY ADAM17) (BY SIMILARITY).  
 CC MOD\_RES 2 2 PHOSPHORYLATION (BY CK1) (BY SIMILARITY).  
 CC DISULFID 145 177 BY SIMILARITY.  
 CC CARBOHYD 95 95 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC SEQUENCE 233 AA; 25420 MW; 2DF37DCB28C9E961 CRC64;  
 SO  
 Query Match 77.1%; Score 81; DB 1; Length 233;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-05;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 QRETPGAEAKPMY 16  
 Db 178 QRETPGAEAKPMY 191  
 TNFA\_FEICA  
 ID TNFA\_FEICA STANDARD; PRT; 233 AA.  
 AC  
 DT  
 DT  
 DE  
 DE  
 GN  
 OS

AC P19101;  
 DT 01-NOV-1990 (Rel. 16, Created)  
 DT 01-NOV-1990 (Rel. 16, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor ligand superfamily member 2) (cachectin).  
 GN TNF OR TNFSF2 OR TNFA.  
 OS Fols silvestris catus (Cat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.  
 OX NCBI\_TaxID:9685;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-Blood;  
 RX MEDLINE=91016860; PubMed=2216740;  
 RA McGraw R.A., Coffee B.W., Otto C.M., Drews R.T., Rawlings C.A.;  
 RT "Gene sequence of feline tumor necrosis factor alpha."  
 RL Nucleic Acids Res. 18:5563-5563(1990).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-Bone marrow;  
 RA Daniel S.L., Brenner C.A., Legendre A.M., Solomon A., Rouse B.T.;  
 RL Submitted (xxx-1993) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and TNFRSF1B/TNFR. It is mainly secreted by macrophages and can induce cell death of certain tumor cell lines. It is potent pyrogen causing fever by direct action or by stimulation of interleukin 1 secretion and is implicated in the induction of cachexia. Under certain conditions it can stimulate cell proliferation and induce cell differentiation.  
 CC -1- SUBUNIT: Homotrimer (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an extracellular soluble form (By similarity).  
 CC -1- PFM: The soluble form derives from the membrane form by proteolytic processing (By similarity).  
 CC -1- PFM: The membrane form, but not the soluble form, is phosphorylated on serine residues. Dephosphorylation of the membrane form occurs by binding to soluble TNFRSF1A/TNFR1 (By similarity).  
 CC -1- DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF DISEASES, INCLUDING CANCER AND INFECTION, AND IS CHARACTERIZED BY GENERAL ILL HEALTH AND MALNUTRITION.  
 CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL: X54000; CAA37948.1;  
 DR EMBL: M92061; AAA30818.1;  
 DR PIR: S11688; S11688.  
 DR HSSP: P01375; 4TSV.  
 DR InterPro: IPR003636; TNF\_abc.  
 DR InterPro: IPR000478; TNF\_family.  
 DR Pfam: PF00229; TNF\_1.  
 DR PRINTS: PR01234; TNCRSISPT.  
 DR PRODOM: PD002012; TNF\_abc; 1.  
 DR SMART: SM00207; TNF\_1.  
 DR PROSITE: PS00251; TNF\_1; 1.  
 DR PROSITE: PS50049; TNF\_2; 1.  
 KW Cytokine; Cytotoxin; Transmembrane; Phosphorylation; Signal-anchor.  
 FT CHAIN 1 233  
 FT FT 233 TUMOR NECROSIS FACTOR, MEMBRANE FORM.  
 FT DOMAIN 1 35 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 36 56 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN) (POTENTIAL).  
 FT DOMAIN 57 233 EXTRACELLULAR (POTENTIAL).  
 FT SITE 76 77 CLEAVAGE (BY ADAM17) (BY SIMILARITY).  
 FT MOD\_RES 2 2 PHOSPHORYLATION (BY CK1) (BY SIMILARITY).

FT DISULFID 145 177 BY SIMILARITY.  
 FT CONFLICT 28 28 G -> R (IN REF. 2).  
 FT CONFLICT 104 104 R -> W (IN REF. 2).  
 FT CONFLICT 151 151 L -> H (IN REF. 2).  
 FT CONFLICT 155 155 A -> T (IN REF. 2).  
 FT CONFLICT 210 210 T -> A (IN REF. 2).  
 SQ SEQUENCE 233 AA; 25322 MW; 434D239567862506 CRC64;  
 Query Match 77.1%; Score 81; DB 1; Length 233;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-05;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 QRETPGCAKPKWY 16  
 Db 178 QRETPGCAKPKWY 191  
 |||||  
 RESULT 4  
 ID TNFA\_HUMAN STANDARD: PRT; 233 AA.  
 AC P01375;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor ligand superfamily member 2) (cachectin).  
 GN TNF OR TNFSF2 OR TNFA.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=87217060; PubMed=3555974;  
 RA Nedospasov S.A., Shakhov A.N., Turetskaya R.L., Mett V.A., Azizov M.M., Georgiev G.P., Korobko V.G., Dobrylin V.N., Filipov S.A., Bystron N.S., Boldyreva E.F., Chuvpilo S.A., Chumakov A.M., Shingarova L.N., Ovchinnikov Y.A.;  
 RT "Tandem arrangement of genes coding for tumor necrosis factor (TNF-alpha) and lymphotoxin (TNF-beta) in the human genome."  
 RL Cold Spring Harb. Symp. Quant. Biol. 51:611-624(1986).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=865086244; PubMed=6392892;  
 RA Pennica D., Nedwin G.E., Hayflick J.S., Seeburg P.H., Derynck R., Palladino M.A., Kohr W.J., Aggarwal B.B., Goeddel D.V.;  
 RT "Human tumour necrosis factor: precursor structure, expression and homology to lymphotoxin."  
 RL Nature 312:724-729(1984).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=865137898; PubMed=3883195;  
 RA Shirai T., Yamaguchi H., Ito H., Todd C.W., Wallace R.B.;  
 RT "Cloning and expression in Escherichia coli of the gene for human tumour necrosis factor."  
 RL Nature 313:803-806(1985).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=86016093; PubMed=2995927;  
 RA Nedwin G.E., Naylor S.L., Sakaguchi A.Y., Smith D.H., Jarrett-Nedwin J., Pennica D., Goeddel D.V., Gray P.W.;  
 RT "Human lymphotoxin and tumor necrosis factor genes: structure, homology and chromosomal localization."  
 RL Nucleic Acids Res. 13:6361-6373(1985).  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=85142190; PubMed=3856324;  
 RA Wang A.M., Creasey A.A., Ladner M.B., Lin L.S., Strickler J., van Arsdel J.N., Yamamoto R., Mark D.F.;  
 RT "Molecular cloning of the complementary DNA for human tumor necrosis factor."  
 RL Science 228:149-154(1985).  
 RN [6]

RP SEQUENCE FROM N.A.  
RX MEDLINE=86030296; PubMed=3932069;  
RA Marmenout A., Fransen L., Tavernier J., van der Heyden J., Tizard R.,  
RA Kawashima E., Shaw A., Johnson M.J., Semon D., Mueller R.,  
RA Ruysschaert M.R., van Vliet A., Fiers W.;  
RT "Molecular cloning and expression of human tumor necrosis factor and  
RT comparison with mouse tumor necrosis factor.";  
RL Eur. J. Biochem. 152:515-522(1985).  
RN [17]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=93272029; PubMed=8499947;  
RA Iris F.J.M., Bougueleret L., Prieur S., Caterina D., Primas G.,  
RA Perrot V., Jurka J., Rodriguez-Rome P., Claverie J.-M., Dausset J.,  
RA Cohen D.;  
RT "Dense Alu clustering and a potential new member of the NF kappa B  
RT family within a 90 kilobase HLA class III segment.";  
RL Nat. Genet. 3:137-145(1993).  
RN [18]  
RP SEQUENCE FROM N.A.  
RA Rowen L., Madan A., Qin S., Shaffer T., James R., Ratcliffe A.,  
RA Abbasi N., Dickhoff R., Loretz C., Madan A., Dors M., Young J.,  
RA Lasky S., Hood L.;  
RT "Sequence of the human major histocompatibility complex class III  
RT region.";  
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.  
RN [19]  
RP SEQUENCE FROM N.A.  
RA Shilina S., Tamiya G., Oka A., Inoko H.;  
RT "Homo sapiens 2,229,817bp genomic DNA of 6p21.3 HLA class I region.";  
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.  
RN [10]  
RP SEQUENCE FROM N.A.  
RA Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poel C.L., Yi Q.,  
RA Nickerson D.A.;  
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.  
RN [11]  
RP SEQUENCE FROM N.A.  
RC TISSUE-Blood:  
RA Strausberg R.;  
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.  
RN [12]  
RP PHOSPHORYLATION (MEMBRANE FORM).  
RX PubMed=8597870;  
RA Pocsik E., Duda E., Wallach D.;  
RT "Phosphorylation of the 26 kDa TNF precursor in monocytic cells and in  
RT transfectected HeLa cells.";  
RL J. Inflamm. 45:152-160(1995).  
RN [13]  
RP PHOSPHORYLATION BY CK1, AND DEPHOSPHORYLATION.  
RX PubMed=10205166;  
RA Watts A.D., Hunt N.H., Manigasekara Y., Bloomfield G., Wallach D.,  
RA Roufogalis B.D., Chaudhuri G.;  
RT "A casein kinase I motif present in the cytoplasmic domain of members  
RT of the tumor necrosis factor ligand family is implicated in 'reverse  
RT signalling'.";  
RL EMBO J. 18:2119-2126(1999).  
RN [14]  
RP MUTAGENESIS.  
RX MEDLINE=91184128; PubMed=2009860;  
RA Ostade X.V., Tavernier J., Prange T., Fiers W.;  
RT "Localization of the active site of human tumour necrosis factor  
RT (hTNF) by mutational analysis.";  
RL EMBO J. 10:827-836(1991).  
RN [15]  
RP MYRISTOYLATION.  
RX MEDLINE=93018820; PubMed=1402651;  
RA Stevenson F.T., Bursten S.L., Locksley R.M., Lovett D.H.;  
RT "Myristyl acylation of the tumor necrosis factor alpha precursor on  
RT specific lysine residues.";  
RL J. Exp. Med. 176:1053-1062(1992).  
RN [16]  
RP CLEAVAGE BY ADAM17.  
RX MEDLINE=97186575; PubMed=9034191;

RA Moss M.L., Jin S.-L.C., Milla M.E., Burkhardt W., Carter H.L.,  
RA Chen W.-J., Clay W.C., Didsbury J.R., Hassler D., Hoffman C.R.,  
RA Kost T.A., Lambert M.H., Leeslitzer M.A., McCalley P., McGeenan G.,  
RA Mitchell J., Moyer M., Pahel G., Rocque W., Overton L.K., Schoenen F.,  
RA Seaton T., Su J.-L., Warner J., Willard D., Becherer J.D.;  
RT "Cloning of a disintegrin metalloproteinase that processes precursor  
RT tumor necrosis factor-alpha.";  
RL Nature 385:733-736(1997).  
RN [17]  
RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).  
RX MEDLINE=89159409; PubMed=2922050;  
RA Jones E.Y., Stuart D.I., Walker N.P.;  
RT "Structure of tumour necrosis factor.";  
RL Nature 338:225-228(1989).  
RN [18]  
RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).  
RX MEDLINE=91193276; PubMed=1964681;  
RA Jones E.Y., Stuart D.I., Walker N.P.;  
RT "The structure of tumour necrosis factor -- implications for  
RT biological function.";  
RL J. Cell Sci. Suppl. 13:11-18(1990).  
RN [19]  
RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).  
RX MEDLINE=90008932; PubMed=2551905;  
RA Eck M.J., Sprang S.R.;  
RT "The structure of tumor necrosis factor-alpha at 2.6-A resolution.  
RT Implications for receptor binding.";  
RL J. Biol. Chem. 264:17595-17605(1989).  
RN [20]  
RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF MUTANT ARG-107.  
RX MEDLINE=98147459; PubMed=9488135;  
RA Reed C., Fu Z.Q., Wu J., Xue Y.N., Harrison R.W., Chen M.J.,  
RA Weber I.T.;  
RT "Crystal structure of TNF-alpha mutant R31D with greater affinity for  
RT receptor R1 compared with R2.";  
RL Protein Eng. 10:1101-1107(1997).  
RN [21]  
RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF MUTANT MS.  
RX MEDLINE=98113178; PubMed=9442056;  
RA Cha S.S., Kim J.S., Cho H.S., Shin N.K., Jeong W., Shin H.C.,  
RA Kim Y.J., Hahn J.H., Oh B.H.;  
RT "High resolution crystal structure of a human tumor necrosis factor-  
RT alpha mutant with low systemic toxicity.";  
RL J. Biol. Chem. 273:2153-2160(1998).  
RN [22]  
RP FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and  
CC TNFRSF1B/TNFR. It is mainly secreted by macrophages and can  
CC induce cell death of certain tumor cell lines. It is potent  
CC pyrogen causing fever by direct action or by stimulation of  
CC interleukin 1 secretion and is implicated in the induction of  
CC cachexia, under certain conditions it can stimulate cell  
CC proliferation and induce cell differentiation.  
CC -1- SUBUNIT: Homotrimer.  
CC -1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN  
CC EXTRACELLULAR SOLUBLE FORM.  
CC -1- PTR: THE SOLUBLE FORM DERIVES FROM THE MEMBRANE FORM BY  
CC PROTEOLYTIC PROCESSING.  
CC -1- PTM: The membrane form, but not the soluble form, is  
CC phosphorylated on serine residues. Dephosphorylation of the  
CC membrane form occurs by binding to soluble TNFRSF1A/TNFR1.  
CC -1- DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF DISEASES, INCLUDING  
CC CANCER AND INFECTION, AND IS CHARACTERIZED BY GENERAL ILL HEALTH  
CC AND MALNUTRITION.  
CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.  
CC -----  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
CC EMBL; X02910; CAA26669.1; -

Query Match 77.1%; Score 81; DB 1; Length 233;  
Best Local Similarity 100.0%; Pred. No. 1.5e-05;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QRETPGAGAKPMY 16  
Db 178 QRETPGAGAKPMY 191

RESULT 5  
TNFA\_MACFA STANDARD; PRT: 233 AA.

AC P79337;  
DT 15-JUL-1998 (Rel. 36, Created)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor  
ligand superfamily member 2) (cachectin).  
GN TNF OR TNFSF2 OR TNFA.  
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
OC Cercopithecinae; Macaca.  
OX NCBI\_TaxID=9541;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Lymphocytes;  
RA Tatsumi M.;  
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.  
CC -1- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and  
TNFRSF1B/TNFR. It is mainly secreted by macrophages and can  
induce cell death of certain tumor cell lines. It is potent  
pyrogen causing fever by direct action or by stimulation of  
interleukin 1 secretion and is implicated in the induction of  
cachexia. Under certain conditions it can stimulate cell  
proliferation and induce cell differentiation.  
CC -1- SUBUNIT: Homotrimer (By similarity).  
CC -1- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an  
extracellular soluble form (By similarity).  
CC -1- PTM: The soluble form derives from the membrane form by  
proteolytic processing (By similarity).  
CC -1- PTM: The membrane form, but not the soluble form, is  
phosphorylated on serine residues. Dephosphorylation of the  
membrane form occurs by binding to soluble TNFRSF1A/TNFR1 (By  
similarity).  
CC -1- DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF DISEASES, INCLUDING  
CANCER AND INFECTION, AND IS CHARACTERIZED BY GENERAL ILL HEALTH  
AND MALNUTRITION.  
CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.  
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or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
EMBL: AB000513; BAA19131.1; -  
DR HSSP: P01375; 4TSV  
DR InterPro: IPR003636; TNF\_abC.  
DR InterPro: IPR000478; TNF\_family.  
DR Pfam: PF00229; TNF\_1.  
DR PRINTS: PR01234; TNCRSISFCT.  
DR ProDom: PD002012; TNF\_abC\_1.  
DR SMART: SM00207; TNF\_1.  
DR PROSITE: PS00251; TNF\_1; 1.  
DR PROSITE: PS50049; TNF\_2; 1.  
KM Cytokine; Cytokoxin; Transmembrane; Phosphorylation; Signal-anchor.  
FT CHAIN 1 233 TUMOR NECROSIS FACTOR, MEMBRANE FORM.  
FT CHAIN 77 233 TUMOR NECROSIS FACTOR, SOLUBLE FORM.  
FT DOMAIN 1 35 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 36 56 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)  
FT DOMAIN 57 233 (POTENTIAL).  
FT SITE 76 77 EXTRACELLULAR (POTENTIAL).  
FT MOD\_RES 2 2 CLEAVAGE (BY ADAM17) (BY SIMILARITY).  
FT DISULFID 145 177 PHOSPHORYLATION (BY CK1) (BY SIMILARITY).  
SQ SEQUENCE 233 AA; 25558 MW; 6AB2C3AB132C217 CRC64;

Query Match 77.1%; Score 81; DB 1; Length 233;  
Best Local Similarity 100.0%; Pred. No. 1.5e-05;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QRETPGAGAKPMY 16  
Db 178 QRETPGAGAKPMY 191

RESULT 6  
TNFA\_MACMU STANDARD; PRT: 233 AA.

AC P48094;  
DT 01-FEB-1996 (Rel. 33, Created)  
DT 01-FEB-1996 (Rel. 33, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor  
ligand superfamily member 2) (cachectin).  
GN TNF OR TNFSF2 OR TNFA.  
OS Macaca mulatta (Rhesus macaque).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
OC Cercopithecinae; Macaca.  
OX NCBI\_TaxID=9544;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Villinger F.J., Brar S.S., Wayne A.E., Chikkala N., Ansari A.A.;  
RX MEDLINE=96003435; PubMed=7561102;  
RT "Comparative sequence analysis of cytokine genes from human and  
nonhuman primates."  
CC -1- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and  
TNFRSF1B/TNFR. It is mainly secreted by macrophages and can  
induce cell death of certain tumor cell lines. It is potent  
pyrogen causing fever by direct action or by stimulation of  
interleukin 1 secretion and is implicated in the induction of  
cachexia. Under certain conditions it can stimulate cell  
proliferation and induce cell differentiation.  
CC -1- SUBUNIT: Homotrimer (By similarity).  
CC -1- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an  
extracellular soluble form (By similarity).  
CC -1- PTM: The soluble form derives from the membrane form by  
proteolytic processing (By similarity).  
CC -1- PTM: The membrane form, but not the soluble form, is  
phosphorylated on serine residues. Dephosphorylation of the  
membrane form occurs by binding to soluble TNFRSF1A/TNFR1 (By  
similarity).  
CC -1- DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF DISEASES, INCLUDING  
CANCER AND INFECTION, AND IS CHARACTERIZED BY GENERAL ILL HEALTH  
AND MALNUTRITION.  
CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.  
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CC -----  
EMBL: U19850; AAA86712.1; -  
DR HSSP: P01375; 4TSV  
DR InterPro: IPR003636; TNF\_abC.  
DR InterPro: IPR000478; TNF\_family.  
DR Pfam: PF00229; TNF\_1.

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DR PRINTS: PRO1234; TNECROSISFCT.
DR Prodom; PD002012; TNF_abc; 1.
DR SMART: SM00207; TNF; 1.
DR PROSITE: PS00251; TNF_1; 1.
DR PROSITE: PS0049; TNF_2; 1.
KW Cytokine; Cytotoxin; Transmembrane; Phosphorylation; Signal-anchor.
FT CHAIN 1 233 TUMOR NECROSIS FACTOR, MEMBRANE FORM.
FT CHAIN 77 233 TUMOR NECROSIS FACTOR, SOLUBLE FORM.
FT DOMAIN 1 35 CYTOLASMIC (POTENTIAL).
FT TRANSMEM 36 56 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
(POTENTIAL).
FT DOMAIN 57 233 EXTRACELLULAR (POTENTIAL).
FT SITE 76 77 CLEAVAGE (BY ADAM17) (BY SIMILARITY).
FT MOD_RES 2 2 PHOSPHORYLATION (BY CK1) (BY SIMILARITY).
FT DISULFID 145 177 BY SIMILARITY.
SQ SEQUENCE 233 AA; 25630 MM; 96F6850595FD59 CRC64;

Query Match 77.1%; Score 81; DB 1; Length 233;
Best Local Similarity 100.0%; Pred. No. 1.5e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 3 QRETEPEGAEPKPY 16
Db 178 QRETEPEGAEPKPY 191

RESULT 7
TNFA_PAPHU STANDARD; PRT; 233 AA.
AC 077510;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DE 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tumor necrosis factor precursor (TNF-alpha) (tumor necrosis factor
ligand superfamily member 2) (Cachectin).
GN TNF OR TNFSF2 OR TNFA.
OS Papio hamadryas ursinus (Chacma baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoinae; Papio.
NCBI_TaxID=36229;
[1]
SEQUENCE FROM N.A.
MEDLINE=98147379; PubMed=9488055;
RA Haudek S.B., Redl H., Schlag G., Giroir B.P.;
RT "Complementary DNA (cDNA) sequence of baboon tumor necrosis factor
alpha."
RL Mol. Immunol. 34:1041-1042(1997).
CC -!- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and
TNFSF1B/TNFR. It is mainly secreted by macrophages and can
induce cell death of certain tumor cell lines. It is potent
pyrogen causing fever by direct action or by stimulation of
interleukin 1 secretion and is implicated in the induction of
cachexia. Under certain conditions it can stimulate cell
proliferation and induce cell differentiation.
CC -!- SUBUNIT: Homotrimer (By similarity).
CC -!- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an
extracellular soluble form (By similarity).
CC -!- PTM: The soluble form derives from the membrane form by
proteolytic processing (By similarity).
CC -!- PTM: The membrane form, but not the soluble form, is
phosphorylated on serine residues. Dephosphorylation of the
membrane form occurs by binding to soluble TNFRSF1A/TNFR1 (By
similarity).
CC -!- DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF DISEASES, INCLUDING
CANCER AND INFECTION, AND IS CHARACTERIZED BY GENERAL ILL HEALTH
AND MAINTENANCE.
CC -!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AF019663; AAC31675.1; -.
DR HSSP: P01375; ATSV.
DR InterPro: IPR003636; TNF_abc.
DR InterPro: IPR000478; TNF_family.
DR Pfam: PF00229; TNF; 1.
DR PRINTS: PRO1234; TNECROSISFCT.
DR Prodom; PD002012; TNF_abc; 1.
DR SMART: SM00207; TNF; 1.
DR PROSITE: PS00251; TNF_1; 1.
DR PROSITE: PS0049; TNF_2; 1.
KW Cytokine; Cytotoxin; Transmembrane; Phosphorylation; Signal-anchor.
FT CHAIN 1 233 TUMOR NECROSIS FACTOR, MEMBRANE FORM.
FT CHAIN 77 233 TUMOR NECROSIS FACTOR, SOLUBLE FORM.
FT DOMAIN 1 35 CYTOLASMIC (POTENTIAL).
FT TRANSMEM 36 56 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
(POTENTIAL).
FT DOMAIN 57 233 EXTRACELLULAR (POTENTIAL).
FT SITE 76 77 CLEAVAGE (BY ADAM17) (BY SIMILARITY).
FT MOD_RES 2 2 PHOSPHORYLATION (BY CK1) (BY SIMILARITY).
FT DISULFID 145 177 BY SIMILARITY.
SQ SEQUENCE 233 AA; 25658 MM; B940325058D4A03 CRC64;

Query Match 77.1%; Score 81; DB 1; Length 233;
Best Local Similarity 100.0%; Pred. No. 1.5e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 3 QRETEPEGAEPKPY 16
Db 178 QRETEPEGAEPKPY 191

RESULT 8
TNFA_PAPSP STANDARD; PRT; 233 AA.
AC P33620;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DE 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tumor necrosis factor precursor (TNF-alpha) (tumor necrosis factor
ligand superfamily member 2) (Cachectin).
GN TNF OR TNFSF2 OR TNFA.
OS Papio sp. (Baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoinae; Papio.
NCBI_TaxID=61183;
[1]
SEQUENCE FROM N.A.
RA Sanjanwala M., Edwards A.;
RL Submitted (SEP-1991) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and
TNFSF1B/TNFR. It is mainly secreted by macrophages and can
induce cell death of certain tumor cell lines. It is potent
pyrogen causing fever by direct action or by stimulation of
interleukin 1 secretion and is implicated in the induction of
cachexia. Under certain conditions it can stimulate cell
proliferation and induce cell differentiation.
CC -!- SUBUNIT: Homotrimer (By similarity).
CC -!- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an
extracellular soluble form (By similarity).
CC -!- PTM: The soluble form derives from the membrane form by
proteolytic processing (By similarity).
CC -!- PTM: The membrane form, but not the soluble form, is
phosphorylated on serine residues. Dephosphorylation of the
membrane form occurs by binding to soluble TNFRSF1A/TNFR1 (By
similarity).
CC -!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

DR EMBL: X62141; CAA44068.1; -  
 DR PIR: S22052; S22052.

DR HSSP: P01375; 1A8M.  
 DR InterPro: IPR003636; TNF-abc.  
 DR InterPro: IPR000478; TNF\_family.

DR Pfam: PF00229; TNF; 1.  
 DR PRINTS: PR01234; TNCRSISRCT.

DR PRODOM: PD002012; TNF-abc; 1.  
 DR SMART: SM00207; TNF; 1.

DR PROSITE: PS00251; TNF\_1; 1.  
 DR PROSITE: PS50049; TNF\_2; 1.

KW Cytochrome; Cytochrome; Transmembrane; Phosphorylation; Signal-anchor;  
 Myristate.

FT CHAIN 1 233 TUMOR NECROSIS FACTOR, MEMBRANE FORM.  
 FT DOMAIN 77 233 TUMOR NECROSIS FACTOR, SOLUBLE FORM.

FT TRANSMEM 36 56 CYTOPLASMIC (POTENTIAL).  
 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)

FT DOMAIN 57 233 (POTENTIAL).  
 EXTRACELLULAR (POTENTIAL).

FT SITE 76 77 CLEAVAGE (BY ADAM17) (BY SIMILARITY).  
 FT MOD\_RES 2 2 PHOSPHORYLATION (BY CK1) (BY SIMILARITY).

FT LIPID 19 19 MYRISTATE (BY SIMILARITY).  
 FT LIPID 20 20 MYRISTATE (BY SIMILARITY).

FT DISULFID 145 177 BY SIMILARITY.  
 SQ SEQUENCE 233 AA; 25557 MW; 455360B48DC74173 CRC64;

Query Match 77.1%; Score 81; DB 1; Length 233;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-05;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 QRETPGAEAKPMY 16  
 DB 178 QRETPGAEAKPMY 191

RESULT 9

TNFA\_TURTR STANDARD; PRT; 233 AA.

AC Q9BEA1;  
 DT 15-JUN-2002 (Rel. 41, Created)

DT 15-JUN-2002 (Rel. 41, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor  
 ligand superfamily member 2) (Cachectin).

GN TNF OR TNFSF2 OR TNFA.

OS Tursiops truncatus (Atlantic bottlenose dolphin).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Cetacea; Odontoceti; Delphinidae;

OC Tursiops.  
 NC NCB1\_TaxID=9739;

RN [1]  
 RP SEQUENCE FROM N.A.

RX PubMed-11587733;  
 RA SPOJ Y., Inoue Y., Sugisawa H., Ito T., Endo T., Sakai T.;

RT "Molecular cloning and functional characterization of bottlenose  
 RT dolphin (Tursiops truncatus) tumor necrosis factor alpha.";

RL Vet. Immunol. Immunopathol. 82:183-192(2001).

CC -1- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and  
 CC TNFRSF1B/TNFR2. It is mainly secreted by macrophages and can

CC induce cell death of certain tumor cell lines. It is potent  
 CC pyrogen causing fever by direct action or by stimulation of

CC interleukin 1 secretion and is implicated in the induction of  
 CC cachexia, Under certain conditions it can stimulate cell

CC proliferation and induce cell differentiation (By similarity).  
 CC -1- SUBUNIT: Homotrimer (By similarity).

CC -1- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an

CC extracellular soluble form (By similarity).

CC -1- PTM: The soluble form derives from the membrane form by  
 CC proteolytic processing (By similarity).

CC -1- PTM: The membrane form, but not the soluble form, is  
 CC phosphorylated on serine residues. Dephosphorylation of the

CC membrane form occurs by binding to soluble TNFRSF1A/TNFR1 (By  
 CC similarity).

CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.

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DR EMBL: AB049358; BAB39855.1; -

DR HSSP: P01375; 4TSV.

DR InterPro: IPR003636; TNF-abc.  
 DR InterPro: IPR000478; TNF\_family.

DR Pfam: PF00229; TNF; 1.  
 DR PRINTS: PR01234; TNCRSISRCT.

DR PRODOM: PD002012; TNF-abc; 1.  
 DR SMART: SM00207; TNF; 1.

DR PROSITE: PS00251; TNF\_1; 1.  
 DR PROSITE: PS50049; TNF\_2; 1.

KW Cytochrome; Cytochrome; Transmembrane; Glycoprotein; Phosphorylation;  
 Signal-anchor.

FT CHAIN 1 233 TUMOR NECROSIS FACTOR, MEMBRANE FORM.  
 FT DOMAIN 78 233 TUMOR NECROSIS FACTOR, SOLUBLE FORM.

FT TRANSMEM 36 56 CYTOPLASMIC (POTENTIAL).  
 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)

FT DOMAIN 57 233 (POTENTIAL).  
 EXTRACELLULAR (POTENTIAL).

FT SITE 77 78 CLEAVAGE (BY ADAM17) (BY SIMILARITY).  
 FT MOD\_RES 2 2 PHOSPHORYLATION (BY CK1) (BY SIMILARITY).

FT DISULFID 145 177 BY SIMILARITY.  
 FT CARBOHYD 95 95 N-LINKED (GLCNAC. . .) (POTENTIAL).

SQ SEQUENCE 233 AA; 25404 MW; 71CC39C699CC49D9 CRC64;

Query Match 77.1%; Score 81; DB 1; Length 233;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-05;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 QRETPGAEAKPMY 16  
 DB 178 QRETPGAEAKPMY 191

RESULT 10

TNFA\_CANFA STANDARD; PRT; 233 AA.

AC P51742; Q28339;  
 DT 01-OCT-1996 (Rel. 34, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor  
 DE ligand superfamily member 2) (Cachectin).

GN TNF OR TNFSF2 OR TNFA.

OS Canis familiaris (Dog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

OC NCB1\_TaxID=9615;

RN [1]  
 RP SEQUENCE FROM N.A.

RA Eilers W., Beernaert M.;

RT Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.

CC -1- ZUCKER K., LU P., FULLER L., ASTHANA D., ESQUENAZI V., MILLER J.;

CC "Cloning and expression of the cDNA for canine tumor necrosis  
 CC factor-alpha in E. coli.";



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RN  Lymphokine Res. 13:191-196(1994).
RL  [3]
RP  SEQUENCE OF 74-205 FROM N.A.
RA  STRAIN-Beagle; TISSUE=Blood;
RL  Gilmore W.H., Carter S.D., Bennett M., Barnes A., Kelly D.F.;
CC  Submitted (MAR-1996) to the EMBL/Genbank/DBJ databases.
CC  -1- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and
CC  TNFRSF1B/TNFR. It is mainly secreted by macrophages and can
CC  induce cell death of certain tumor cell lines. It is potent
CC  pyrogen causing fever by direct action or by stimulation of
CC  interleukin 1 secretion and is implicated in the induction of
CC  cachexia. Under certain conditions it can stimulate cell
CC  proliferation and induce cell differentiation.
CC  -1- SUBUNIT: Homotrimer (by similarity).
CC  -1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN
CC  EXTRACELLULAR SOLUBLE FORM (BY SIMILARITY).
CC  -1- PTM: THE SOLUBLE FORM DERIVES FROM THE MEMBRANE FORM BY
CC  PROTEOLYTIC PROCESSING (BY SIMILARITY).
CC  -1- PTM: The membrane form, but not the soluble form, is
CC  phosphorylated on serine residues. Dephosphorylation of the
CC  membrane form occurs by binding to soluble TNFRSF1A/TNFR1 (by
CC  similarity).
CC  -1- DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF DISEASES, INCLUDING
CC  CANCER AND INFECTION, AND IS CHARACTERIZED BY GENERAL ILL HEALTH
CC  AND MALNUTRITION.
CC  -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
CC  -----
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CC  -----
DR  EMBL; X94932; CAAG64403.1; -
DR  EMBL; S74068; AAB32391.1; -
DR  EMBL; Z70046; CAA93908.1; -
DR  HSSP: P01375; 4TSV
DR  InterPro: IPR0003636; TNF_abc.
DR  InterPro: IPR000478; TNF_family.
DR  Pfam: PF00229; TNF_1.
DR  PRINTS: PR01234; TNECROSISFCT.
DR  PRODOM: PD002012; TNF_abc; 1.
DR  SMART: SM00207; TNF_1.
DR  PROSITE; PS00251; TNF_1; 1.
DR  PROSITE; PS50049; TNF_2; 1.
KW  Cytokine; Cytotoxin; Transmembrane; Phosphorylation; Signal-anchor.
FT  CHAIN 1 233
FT  CHAIN 77 233
FT  DOMAIN 1 35
FT  DOMAIN 36 56
FT  TRANSMEM 36 56
FT  DOMAIN 57 233
FT  SITE 76 77
FT  MOD_RES 2 2
FT  DISULFID 145 177
FT  CONFLICT 59 60
FT  CONFLICT 66 66
FT  CONFLICT 74 74
FT  CONFLICT 111 111
FT  CONFLICT 116 116
FT  CONFLICT 134 135
SQ  SEQUENCE 233 AA; 25447 MW; 7B2588FBC8B25340 CRC64;
Query Match 73.3%; Score 77; DB 1; Length 233;
Best Local Similarity 92.9%; Score No. 6,2e-05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 3 QRETPGCAKPMY 16
DB 178 QRETPGCTAKPMY 191

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RESULT 11
ID  TNFA_CAPRI
AC  P13296; Q28320; Q9MY22;
DT  01-JAN-1990 (Rel. 13, Created)
DT  15-JUN-2002 (Rel. 41, Last sequence update)
DT  15-JUN-2002 (Rel. 41, Last annotation update)
DE  Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor
GN  ligand superfamily member 2) (cachectin).
OS  Capra hircus (Goat).
OC  Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC  Bovidae; Caprinae; Capra.
OX  NCBI_TaxID=9925;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  TISSUE=spleenocyte;
RA  Takakura H., Mori Y., Tatsumi M.;
RT  "Molecular cloning of caprine TNF-alpha cDNA and its expression in
RL  E.coli and insect cells."
RN  [2]
RP  Submitted (JUN-1996) to the EMBL/Genbank/DBJ databases.
RA  Goldstein I.M., Henner D., Talhouk A.;
RL  Submitted (MAR-1989) to the EMBL/Genbank/DBJ databases.
RN  [3]
RP  SEQUENCE OF 44-234 FROM N.A.
RC  TISSUE-Ovarian follicle;
RA  Wang B., Zhang Y.;
RT  "Goat ovarian TNF alpha cDNA sequence."
RL  Submitted (JUN-2000) to the EMBL/Genbank/DBJ databases.
RN  [4]
RP  SEQUENCE OF 75-234 FROM N.A.
RC  TISSUE=Blood;
RA  Rimstad E.;
RL  Submitted (JAN-1994) to the EMBL/Genbank/DBJ databases.
CC  -1- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and
CC  TNFRSF1B/TNFR. It is mainly secreted by macrophages and can
CC  induce cell death of certain tumor cell lines. It is potent
CC  pyrogen causing fever by direct action or by stimulation of
CC  interleukin 1 secretion and is implicated in the induction of
CC  cachexia, under certain conditions it can stimulate cell
CC  proliferation and induce cell differentiation.
CC  -1- SUBUNIT: Homotrimer (By similarity).
CC  -1- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an
CC  extracellular soluble form (by similarity).
CC  -1- PTM: The soluble form derives from the membrane form by
CC  proteolytic processing (by similarity).
CC  -1- PTM: The membrane form, but not the soluble form, is
CC  phosphorylated on serine residues. Dephosphorylation of the
CC  membrane form occurs by binding to soluble TNFRSF1A/TNFR1 (by
CC  similarity).
CC  -1- DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF DISEASES, INCLUDING
CC  CANCER AND INFECTION, AND IS CHARACTERIZED BY GENERAL ILL HEALTH
CC  AND MALNUTRITION.
CC  -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
CC  -1- frame shift in position 60.
CC  -----
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CC  entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC  or send an email to license@isb-sib.ch).
CC  -----
DR  EMBL; D86587; BAA13130.1; -
DR  EMBL; X14828; CAA32937.1; ALT_FRAME.
DR  EMBL; AF276985; AAB8741.1; -
DR  EMBL; X77317; CAA34523.1; -

```



```

CC -1- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and
CC TNFRSF1B/TNFR. It is mainly secreted by macrophages and can
CC induce cell death of certain tumor cell lines. It is potent
CC pyrogen causing fever by direct action or by stimulation of
CC interleukin 1 secretion and is implicated in the induction of
CC cachexia, under certain conditions it can stimulate cell
CC proliferation and induce cell differentiation.
CC -1- SUBUNIT: Homotrimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an
CC EXTRACELLULAR SOLUBLE FORM (By similarity).
CC -1- PTM: THE SOLUBLE FORM DERIVES FROM THE MEMBRANE FORM BY
CC PROTEOLYTIC PROCESSING (By similarity).
CC -1- DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF DISEASES, INCLUDING
CC CANCER AND INFECTION, AND IS CHARACTERIZED BY GENERAL ILL HEALTH
CC AND MALNUTRITION.
CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
CC -----
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CC -----
CC EMBL: U14683; AAA50759.1; -.
CC HSSP: P01375; 4TSV.
CC InterPro: IPR003636; TNF_abc.
CC InterPro: IPR000478; TNF_family.
CC DR Pfam: PF00229; TNF; 1.
CC DR ProDom: PD002012; TNF_abc; 1.
CC DR SMART: SM00207; TNF; 1.
CC DR PROSITE: PS00251; TNF_1; 1.
CC DR PROSITE: PS50049; TNF_2; 1.
CC KW Cytokine; Cytotoxin; Transmembrane; Signal-anchor.
CC FT NON_TER 1 1
CC FT CHAIN <1 229 TUMOR NECROSIS FACTOR, MEMBRANE FORM.
CC FT CHAIN 74 229 TUMOR NECROSIS FACTOR, SOLUBLE FORM.
CC FT DOMAIN <1 30 CYTOPLASMIC (POTENTIAL).
CC FT TRANSMEM 31 51 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
CC FT (POTENTIAL).
CC DOMAIN 52 229 EXTRACELLULAR (POTENTIAL).
CC SITE 72 73 CLEAVAGE (BY ADAM17) (BY SIMILARITY).
CC FT DISULFID 141 173 BY SIMILARITY.
CC SQ SEQUENCE 229 AA; 24987 MW; 16DE5F7AA5A7DB35 CRC64;

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Query Match 64.8%; Score 68; DB 1; Length 229;
Best Local Similarity 92.3%; Pred. No. 0.0016;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 4 RETPEGAFAKFWY 16
Db 175 RETPEMAEAKFWY 187

RESULT 14
TNFA_BOVIN STANDARD; PRT; 233 AA.
AC Q06599; O18779;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor
DE ligand superfamily member 2) (Cachectin).
GN TNF OR TNFSF2 OR TNFA.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94083525; PubMed=8260599;

```

```

RA Cludts I., Cleuter Y., Kettmann R., Burny A., Droogmans L.;
RA "Cloning and characterization of the tandemly arranged bovine
RA lymphotoxin and tumour necrosis factor-alpha genes.";
RA Cytokine 5:336-341(1993).
RN [2]
RP SEQUENCE FROM N.A.
RP STRAIN-Boran, and N'Dama;
RA Iraqi F.;
RA "bovine TNF-alpha gene.";
RL Submitted (JUL-1997) to the EMBL/Genbank/DBJ databases.
RN [3]
RP SEQUENCE OF 50-233 FROM N.A.
RP TISSUE=Blood;
RX MEDLINE=96006582; PubMed=7590981;
RA Mertens B.E.L.C., Murituki M., Gaigulis L.;
RA "Cloning of two members of the TNF-superfamily in cattle: CD40 ligand
RA and tumor necrosis factor alpha.";
RL Immunogenetics 42:430-431(1995).
CC -1- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and
CC TNFRSF1B/TNFR. It is mainly secreted by macrophages and can
CC induce cell death of certain tumor cell lines. It is potent
CC pyrogen causing fever by direct action or by stimulation of
CC interleukin 1 secretion and is implicated in the induction of
CC cachexia, under certain conditions it can stimulate cell
CC proliferation and induce cell differentiation.
CC -1- SUBUNIT: Homotrimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an
CC extracellular soluble form (By similarity).
CC -1- PTM: The soluble form derives from the membrane form by
CC proteolytic processing (By similarity).
CC -1- PTM: The membrane form, but not the soluble form, is
CC phosphorylated on serine residues. Dephosphorylation of the
CC membrane form occurs by binding to soluble TNFRSF1A/TNFR1 (By
CC similarity).
CC -1- DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF DISEASES, INCLUDING
CC CANCER AND INFECTION, AND IS CHARACTERIZED BY GENERAL ILL HEALTH
CC AND MALNUTRITION.
CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
CC -----
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CC -----
CC EMBL: Z14137; CAA78511.1; -.
CC DR EMBL: AF011926; AAB84086.1; -.
CC DR EMBL: AF011927; AAB84087.1; -.
CC DR EMBL: Z48808; CAA88743.1; -.
CC DR PIR: S24642; S24642.
CC DR HSSP: P01375; 4TSV.
CC DR InterPro: IPR003636; TNF_abc.
CC DR InterPro: IPR000478; TNF_family.
CC DR Pfam: PF00229; TNF; 1.
CC DR PRINTS: PR01234; TNECROSISFCT.
CC DR ProDom: PD002012; TNF_abc; 1.
CC DR SMART: SM00207; TNF; 1.
CC DR PROSITE: PS00251; TNF_1; 1.
CC DR PROSITE: PS50049; TNF_2; 1.
CC KW Cytokine; Cytotoxin; Transmembrane; Phosphorylation; Signal-anchor;
CC Polymorphism.
CC FT CHAIN 1 233
CC FT CHAIN 78 233 TUMOR NECROSIS FACTOR, MEMBRANE FORM.
CC FT DOMAIN 1 35 CYTOPLASMIC (POTENTIAL).
CC FT TRANSMEM 36 56 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
CC FT (POTENTIAL).
CC DOMAIN 57 233 EXTRACELLULAR (POTENTIAL).
CC SITE 77 78 CLEAVAGE (BY ADAM17) (BY SIMILARITY).
CC FT MOD_RES 2 2 PHOSPHORYLATION (BY CK1) (BY SIMILARITY).
CC FT DISULFID 145 177 BY SIMILARITY.
CC FT VARIANT 48 48 F -> C (IN STRAIN N'DAMA).

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FT CONFLICT 62 62 E -> EQ (IN REF. 3).  
 SO SEQUENCE 233 AA; 23439 MM; 8AF55C002A9763B0 CRC64;  
 Query Match 64.8%; Score 68; DB 1; Length 233;  
 Best Local Similarity 92.3%; Pred. No. 0.0016;  
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 RETPEGAERAKPMY 16  
 DB 179 RETPEGAERAKPMY 191

RESULT 15  
 TNFA\_SHEEP STANDARD; PRT; 234 AA.  
 ID TNFA\_SHEEP  
 AC P23383;  
 DT 01-NOV-1991 (Rel. 20, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor ligand superfamily member 2) (Cachectin).  
 GN TNF OR TNFSF2 OR TNFA.  
 OS Ovis aries (Sheep).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Caprinae; Ovis.  
 OC NCB1\_TaxID=9940;  
 OX 11  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Liver;  
 RA MEDLINE=91067496; PubMed=2251151;  
 RA Young A.J., Hay J.B., Chen J.Y.C.;  
 RT Primary structure of ovine tumor necrosis factor alpha cDNA.;  
 RL Nucleic Acids Res. 18:6723-6723(1990).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Alveolar macrophage;  
 RA MEDLINE=92112044; PubMed=1765267;  
 RA Green I.R., Sargan D.R.;  
 RT "Sequence of the cDNA encoding ovine tumor necrosis factor-alpha: problems with cloning by inverse PCR.";  
 RL Gene 109:203-210(1991).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=92155784; PubMed=1786996;  
 RA Andrews A.E., Nash A.D., Barcham G.J., Brandon M.R.;  
 RT "Molecular cloning, expression and characterization of ovine TNF alpha";  
 RL Immunol. Cell Biol. 69:273-283(1991).  
 RL -1- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and TNFRSF1B/TNFR. It is mainly secreted by macrophages and can induce cell death of certain tumor cell lines. It is potent pyrogen causing fever by direct action or by stimulation of interleukin 1 secretion and is implicated in the induction of cachexia, under certain conditions it can stimulate cell proliferation and induce cell differentiation.  
 CC -1- SUBUNIT: Homotrimer (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an extracellular soluble form (By similarity).  
 CC -1- PTM: The soluble form derives from the membrane form by proteolytic processing (By similarity).  
 CC -1- PTM: The membrane form, but not the soluble form, is phosphorylated on serine residues. Dephosphorylation of the membrane form occurs by binding to soluble TNFRSF1A/TNFR1 (By similarity).  
 CC -1- DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF DISEASES, INCLUDING CANCER AND INFECTION, AND IS CHARACTERIZED BY GENERAL ILL HEALTH AND MALNUTRITION.  
 CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.  
 CC -----  
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 CC -----  
 CC EMBL; X55966; CAA39437.1; -  
 DR EMBL; X55152; CAA38952.1; -  
 DR EMBL; X56756; CAA40076.1; -  
 DR EMBL; A19163; CAA01445.1; -  
 DR PIR; S13114; S13114.  
 DR PIR; S20661; S20661.  
 DR PIR; JH0529; JH0529.  
 DR HSSP; P01375; 4TSV.  
 DR InterPro; IPR003636; TNF-abc.  
 DR InterPro; IPR000478; TNF\_family.  
 DR Pfam; PF00229; TNF; 1.  
 DR PRINTS; PR01234; TNECROSISFCT.  
 DR Prodom; PD002012; TNF-abc; 1.  
 DR SMART; SM00207; TNF; 1.  
 DR PROSITE; PS00251; TNF\_1; 1.  
 DR PROSITE; PS50049; TNF\_2; 1.  
 DR Cytochrome; Cytochrome; Transmembrane; Glycoprotein; Phosphorylation;  
 KM Signal-anchor.  
 FT CHAIN 1 234 TUMOR NECROSIS FACTOR, MEMBRANE FORM.  
 FT SITE 77 78 TUMOR NECROSIS FACTOR, SOLUBLE FORM.  
 FT MOD\_RES 2 2 CYTOPLASMIC (POTENTIAL).  
 FT DISULFID 146 178 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)  
 FT CARBOHYD 96 96 (POTENTIAL).  
 FT CONFLICT 63 63 MISSING (IN REF. 1).  
 SQ SEQUENCE 234 AA; 25536 MM; 4BCF8CAB7956B88 CRC64;

QY 4 RETPEGAERAKPMY 16  
 DB 180 RETPEGAERAKPMY 192

Search completed: April 4, 2003, 08:40:27  
 Job time : 7.85484 secs

GenCore version 5.1.4-p5.4578  
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OM protein - protein search, using sw model

Run on: April 4, 2003, 08:37:16 ; Search time 24.6774 Seconds

(without alignments)  
141.944 Million cell updates/sec

Title: US-09-779-703-4

Sequence: 1 CGORETPEGAEAKPWYC 17

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

SPREMBL\_21:\*

- 1: SP\_archaea:\*
- 2: SP\_bacteria:\*
- 3: SP\_fungi:\*
- 4: SP\_human:\*
- 5: SP\_invertebrate:\*
- 6: SP\_mammal:\*
- 7: SP\_mhc:\*
- 8: SP\_organelle:\*
- 9: SP\_phage:\*
- 10: SP\_plant:\*
- 11: SP\_rodent:\*
- 12: SP\_virus:\*
- 13: SP Vertebrate:\*
- 14: SP\_unclassified:\*
- 15: SP\_virus:\*
- 16: SP\_bacteriap:\*
- 17: SP\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	81	77.1	66	4	Q9P1Q2
2	81	77.1	149	6	Q97543
3	81	77.1	217	6	Q9BEF4
4	81	77.1	232	4	Q9UIV3
5	78	74.3	216	6	Q9BEC4
6	76	72.4	157	4	Q43647
7	76	72.4	217	6	Q9BEG0
8	73	66.5	217	6	Q9BEG1
9	72	66.6	215	6	Q9BEE8
10	69	65.7	217	6	Q9BEC5
11	68	64.8	104	6	Q27978
12	65	61.9	156	11	Q91ZL4
13	65	61.9	217	11	Q9ERG6
14	65	61.9	235	6	Q9J126
15	63	60.0	138	11	Q9TGT6
16	63	60.0	149	6	Q97538

17	63	60.0	149	6	Q9TTC8	Q9TTC8 actus nigri
18	63	60.0	216	11	Q70332	Q70332 mesocricetu
19	61	58.1	235	11	Q9J127	Q9J127 rattus norv
20	59	56.2	234	6	Q9TRJ3	Q9TRJ3 equus cabal
21	55	52.4	216	6	Q9BEC9	Q9BEC9 ochotona pr
22	53	50.5	215	11	Q99ND1	Q99ND1 tamiasciuru
23	49.5	47.1	317	17	Q29274	Q29274 archaeglob
24	48	45.7	328	16	Q8RYR9	Q8RYR9 anabaena sp
25	47	44.8	286	5	Q16148	Q16148 schistosoma
26	47	44.8	711	16	Q9RVE5	Q9RVE5 delnococtus
27	47	44.8	778	4	Q8TAA0	Q8TAA0 homo sapien
28	46.5	44.3	733	16	Q9HTC5	Q9HTC5 pseudomonas
29	46	43.8	647	17	Q90YN2	Q90YN2 pyrococcus
30	46	43.8	729	12	Q91TW1	Q91TW1 tupaia herp
31	46	43.8	5147	4	Q9Y6V0	Q9Y6V0 homo sapien
32	45	42.9	312	10	Q8W4L7	Q8W4L7 arabidopsis
33	45	42.9	448	12	Q90421	Q90421 equine herp
34	45	42.9	466	3	Q9PEY5	Q9PEY5 neurospora
35	45	42.9	553	10	Q9SNB9	Q9SNB9 arabidopsis
36	45	42.9	879	5	Q76978	Q76978 sycon rapha
37	45	42.9	1386	4	Q75064	Q75064 homo sapien
38	44	41.9	77	13	Q8UW12	Q8UW12 xenopus lae
39	44	41.9	140	3	Q9Y8D2	Q9Y8D2 cochlidiobol
40	44	41.9	195	2	Q05339	Q05339 stigmatella
41	44	41.9	199	2	Q8RWC2	Q8RWC2 streptomyce
42	44	41.9	283	4	Q9HA06	Q9HA06 homo sapien
43	44	41.9	299	2	Q93A65	Q93A65 uncultured
44	44	41.9	406	2	Q8VPM0	Q8VPM0 micrococcus
45	44	41.9	419	9	Q38619	Q38619 xanthomonas

## ALIGNMENTS

## RESULT 1

ID	Q9P1Q2	PRELIMINARY:	PRT:	66 AA.
AC	Q9P1Q2	01-OCT-2000 (TREMBlrel. 15, Created)		
DT	01-OCT-2000 (TREMBlrel. 15, Last sequence update)			
DT	01-DEC-2001 (TREMBlrel. 19, Last annotation update)			
DE	APC1 protein (Fragment).			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=PROSTATE TUMOR;			
RA	Shao C., Yan W., Zhu F., Yue W., Chai Y., Zhao Z., Wang C.;			
RL	Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.			
DR	EMBL: AF098751; AAF71992.1; -			
DR	HSSP: P01375; 5TSW.			
DR	InterPro: IPR003636; TNF_abc.			
DR	InterPro: IPR000478; TNF_family.			
DR	Pfam: PF00229; TNF_1.			
DR	PRINTS: PR01234; TNFCROSISCT.			
DR	ProDom: PD002012; TNF_abc; 1.			
DR	ProStie: PSS0049; TNF_2; 1.			
FT	NON_TER			
SQ	SEQUENCE	66 AA; 7300 MW; C58DC35377E6D368 CRC64;		

Query Match Best local Similarity 100.0%; Pred. No. 2e-05;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QRETPGAEAKPWY 16  
Db 30 QRETPGAEAKPWY 43

RESULT 2  
Q97543

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ID 097543      PRELIMINARY;      PRT;      149 AA.
AC 097543:
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, last sequence update)
DT 01-OCT-2001 (TREMBlrel. 18, last annotation update)
DE Tumor necrosis factor alpha (Fragment).
GN TNF-ALPHA.
OS Actus nancyanae (Owl monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.
OX NCBI_TaxID=37293;
RN [1]
RP SEQUENCE FROM N.A.
RA Echeverry S.J., Hernandez E., Moreno A., Patarroyo M.E., Murillo L.A.;
RT "Identification, cloning and sequencing of different interleukin genes
RT in Aotus species."
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF014513; AAD01539.1; -
DR HSSP; P01375; 4TSV.
DR InterPro: IPR003636; TNF_family.
DR InterPro: IPR000478; TNF_family.
DR Pfam; PF00229; TNF; 1.
DR PRINTS; PR01234; TNECROSISFCT.
DR PRODOM; PD002012; TNF_abc; 1.
DR SMART; SM00207; TNF_abc; 1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS50049; TNF_2; 1.
FT NON_TER
FT 1
FT 149
SQ SEQUENCE 149 AA; 16466 MW; 3C2A6140778EFA8A CRC64;

Query Match      77.1%; Score 81; DB 6; Length 149;
Best Local Similarity 100.0%; Pred. No. 4.6e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 QRETPEGAERKPMY 16
    |||||
Db 95 QRETPEGAERKPMY 108

RESULT 3
Q9BEF4      PRELIMINARY;      PRT;      217 AA.
ID Q9BEF4
AC Q9BEF4:
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, last annotation update)
DE Tumor necrosis factor (Fragment).
GN TNFA.
OS Cabassous unicinctus (Southern naked-tailed armadillo).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Edentata; Dasypodidae; Cabassous.
OX NCBI_TaxID=48852;
RN [1]
RP SEQUENCE FROM N.A.
RA van Dijk M.A.M., de Jong W.W.;
RT "Indels indicate that rodents are monophyletic and lagomorphs are
RT their sister group."
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ286829; CAC28518.1; -
DR HSSP; P01375; 4TSV.
DR InterPro: IPR003636; TNF_abc.
DR InterPro: IPR000478; TNF_family.
DR Pfam; PF00229; TNF; 1.
DR PRINTS; PR01234; TNECROSISFCT.
DR PRODOM; PD002012; TNF_abc; 1.
DR SMART; SM00207; TNF_1; 1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS50049; TNF_2; 1.
FT NON_TER
FT 1
FT 217
SQ SEQUENCE 217 AA; 23742 MW; 83C591DD6883FDB6 CRC64;

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Query Match      77.1%; Score 81; DB 6; Length 217;
Best Local Similarity 100.0%; Pred. No. 6.9e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 QRETPEGAERKPMY 16
    |||||
Db 170 QRETPEGAERKPMY 183

RESULT 4
Q9UIV3      PRELIMINARY;      PRT;      232 AA.
ID Q9UIV3
AC Q9UIV3:
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, last annotation update)
DE Tumor necrosis factor.
GN TNF.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE-93272029; PubMed-8499947;
RX Iris F., Bougueleret L., Prieur S., Caterina D., Primas G., Perrot V.,
RA Jurka J., Rodriguez-Tome P., Claverie J., Cohen D., Dausset J.;
RT "Dense Alu clustering and a potential new member of the NRKpapp
RT family within a 90 kilobase HLA class III segment."
RL Nat. Genet. 3:137-145(1993).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE-96215741; PubMed-8629302;
RA Utans U., Quist W.C., McManus B.M., Wilson J.E., Arceci R.J.,
RA Wallace A.F., Russell M.E.;
RT "Allograft inflammatory factory-1. A cytokine-responsive macrophage
RT molecule expressed in transplanted human hearts."
RL Transplantation 61:1387-1392(1996).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE-96006565; PubMed-7590964;
RA Holzinger I., de Baey A., Messer G., Kick G., Zwiernia H.,
RA Weiss E.H.;
RT "Cloning and genomic characterization of LST1: a new gene in the human
RT TNF region."
RL Immunogenetics 42:315-322(1995).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE-93208881; PubMed-7916655;
RA Browning J.L., Ngam-ek A., Lawton P., Dewarins J., Tizard R.,
RA Chow E.P., Hession C., O'Brine-Greco B., Foley S.F., Ware C.F.;
RT "Lymphotoxin-beta: A new member of the TNF family that forms a
RL heteromeric complex with lymphotoxin on the cell surface."
RL Cell 72:847-856(1993).
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE-86016093; PubMed-2995927;
RA Nedwin G.E., Naylor S.L., Sakaguchi A.Y., Smith D., Jarrett-Nedwin J.,
RA Pennica D., Goeddel D.V., Gray P.W.;
RT "Human lymphotoxin and tumor necrosis factor genes: structure,
RL homology and chromosomal localization."
RL Nucleic Acids Res. 13:6361-6373(1985).
RN [6]
RP SEQUENCE FROM N.A.
RX MEDLINE-91086846; PubMed-1670638;
RA Messer G., Spengler U., Jung M.C., Honold G., Bloemer K., Page G.R.,
RA Rietmueller G., Weiss E.H.;
RT "Polymorphic Structure of the Tumor Necrosis Factor (TNF) Locus: An
RT Ncol Polymorphism in the First Intron of the Human TNF-beta Gene
RT Correlates with a Variant Amino Acid in Position 26 and a Reduced
RL Level of TNF-beta Production."
RL J. Exp. Med. 173:209-219(1991).
RN [7]

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RP SEQUENCE FROM N.A.
RX MEDLINE=91139175; PubMed=1671667;
RA Abraham L.J., Du D.C., Zahedi K., Dawkins R.L., Whitehead A.S.;
RT "Haploclypic polymorphisms of the TNF gene.";
RL Immunogenetics 33:50-53(1991).
RN [8]
RP SEQUENCE FROM N.A.
RX MEDLINE=94362679; PubMed=8081366;
RA Albertella M.R., Campbell D.R.;
RT "Characterization of a novel gene in the human major
histocompatibility complex that encodes a potential new member of the
I kappa B family of proteins.";
RL Hum. Mol. Genet. 3:793-799(1994).
RN [9]
RP SEQUENCE FROM N.A.
RX MEDLINE=95324911; PubMed=7601445;
RA Peelman L., Chardon P., Nunes M., Renard C., Gelfroin C., Vaiman M.,
Van zeveren A., Coppleters W., Van de Wehe A., Bouquet Y., Choy W.,
Strominger J., Spies T.;
RT "The BAT1 Gene in the MHC Encodes an Evolutionarily Conserved Putative
Nuclear RNA Helicase of the D-E-A-D Family.";
RL Genomics 26:210-218(1995).
RN [10]
RP SEQUENCE FROM N.A.
RX MEDLINE=20132445; PubMed=10668961;
RA Neville M.J., Campbell R.D.;
RT "Alternative splicing of the LST-1 gene located in the major
histocompatibility complex on human chromosome 6.";
RL DNA Seq. 8:155-160(1997).
RN [11]
RP SEQUENCE FROM N.A.
RX MEDLINE=98035883; PubMed=9367684;
RA de Baey A., Fellerhoff B., Maier S., Martinozzi S., Weidle U.,
Weiss E.H.;
RT "Complex expression pattern of the TNF region gene LST1 through
differential regulation, initiation, and alternative splicing.";
RL Genomics 45:591-600(1997).
RN [12]
RP SEQUENCE FROM N.A.
RX MEDLINE=98149985; PubMed=9480751;
RA Shima T., Tamiya G., Oka A., Yamagata T., Yamagata N., Kikkawa E.,
Goto K., Mizuki N., Watanabe K., Fukuzumi Y., Taguchi S., Sugawara C.,
Ono A., Chen L., Yamazaki M., Tashiro H., Ando A., Ikemura T.,
Kimura M., Inoko H.;
RT "Nucleotide sequencing analysis of the 146-kilobase segment around the
IKB1 and MICA genes at the centromeric end of the HLA class I
region.";
RL Genomics 47:372-382(1998).
DR EMBL: Y14768; CAA75070.1; -.
DR HSSP: P01375; 4TSV.
DR InterPro: IPR003636; TNF_abc.
DR InterPro: IPR000478; TNF_family.
DR Pfam: PF00229; TNF_1.
DR PRINTS: PR01234; TNECROSISFCT.
DR PRODOM: PD002012; TNF_abc; 1.
DR SMART: SM00207; TNF_1.
DR PROSITE: PS00251; TNF_1; 1.
DR PROSITE: PS50049; TNF_2; 1.
SQ SEQUENCE 232 AA; 25446 MW; E4D71B19C6AE0D03 CRC64;

Query Match 77.1%; Score 81; DB 4; Length 232;
Best Local Similarity 100.0%; Pred. No. 7.4e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 QRETPGAEAKPMY 16
DB 177 QRETPGAEAKPMY 190

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DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Tumor necrosis factor (Fragment).
GN TNFA.
OS Talpa europaea (European mole).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Insectivora; Talpidae; Talpa.
OX NCBI_TaxID=9375;
RN [1]
RP SEQUENCE FROM N.A.
RA van Dijk M.A.M., de Jong W.W.;
RT "Indels indicate that rodents are monophyletic and lagomorphs are
their sister group.";
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ286831; CAC28539.1; -.
DR HSSP: P01375; 1A8M.
DR InterPro: IPR003636; TNF_abc.
DR InterPro: IPR000478; TNF_family.
DR Pfam: PF00229; TNF_1.
DR PRINTS: PR01234; TNECROSISFCT.
DR PRODOM: PD002012; TNF_abc; 1.
DR SMART: SM00207; TNF_1.
DR PROSITE: PS00251; TNF_1; 1.
DR PROSITE: PS50049; TNF_2; 1.
FT NON_TER 1
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 216 AA; 23542 MW; FFFEF8DBBD27836 CRC64;

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Query Match 74.3%; Score 78; DB 6; Length 216;
Best Local Similarity 92.9%; Pred. No. 0.0002;
Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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OY 3 QRETPGAEAKPMY 16
DB 169 QRETPGAEAKPMY 182

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RESULT 6
OY 043647 PRELIMINARY; PRT; 157 AA.
AC 043647.
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Tumor necrosis factor alpha (Fragment).
GN TNFA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Jiang J.S., Kim B.E.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF043342; AAC03542.1; -.
DR HSSP: P01375; 1A8M.
DR InterPro: IPR003636; TNF_abc.
DR InterPro: IPR000478; TNF_family.
DR Pfam: PF00229; TNF_1.
DR PRINTS: PR01234; TNECROSISFCT.
DR PRODOM: PD002012; TNF_abc; 1.
DR SMART: SM00207; TNF_1.
DR PROSITE: PS00251; TNF_1; 1.
DR PROSITE: PS50049; TNF_2; 1.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 157 AA; 17380 MW; D1344822267E9F20 CRC64;

```

```

Query Match 72.4%; Score 76; DB 4; Length 157;
Best Local Similarity 92.9%; Pred. No. 0.0003;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 3 QRETPGAEAKPMY 16

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Db 102 QRETPGGAEPKWPY 115

## RESULT 7

Q9BEG0 PRELIMINARY; PRT; 217 AA.

AC Q9BEG0: 01-JUN-2001 (TREMBLrel. 17, Created)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
 DE Tumor necrosis factor (Fragment).  
 GN TNFA.  
 OS Cyclopes diactylus (silky anteater).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Edentata; Myrmecophagidae; Cyclopes.  
 OX NCBI\_TaxID=94074;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA van Dijk M.A.M., de Jong W.W.;  
 RT "Indels indicate that rodents are monophyletic and lagomorphs are their sister group."  
 RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AJ286828; CAC28514.1; -  
 DR HSSP; P01375; 1A8M.  
 DR InterPro; IPR003636; TNF\_abc.  
 DR InterPro; IPR000478; TNF\_family.  
 DR Pfam; PF00229; TNF\_1.  
 DR PRINTS; PR01234; TNECROSISFCT.  
 DR PRODOM; PD002012; TNF\_abc; 1.  
 DR SMART; SM00207; TNF\_1.  
 DR PROSITE; PS00251; TNF\_1; 1.  
 DR PROSITE; PS50049; TNF\_2; 1.  
 FT NON\_TER 1 1  
 FT NON\_TER 217 217  
 SQ SEQUENCE 217 AA; 23753 MW; F760B87F6C29EBB CRC64;

Query Match 72.4%; Score 76; DB 6; Length 217;  
 Best Local Similarity 92.9%; Pred. No. 0.00042;  
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 3 QRETPGGAEPKWPY 16  
 Db 170 QRETPGGAEPKWPY 183

RESULT 8  
 Q9BEG1 PRELIMINARY; PRT; 217 AA.

AC Q9BEG1: 01-JUN-2001 (TREMBLrel. 17, Created)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
 DE Tumor necrosis factor (Fragment).  
 GN TNFA.  
 OS Bradypus tridactylus (Pale-throated three-toed sloth).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Edentata; Bradypodidae; Bradypus.  
 OX NCBI\_TaxID=9354;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA van Dijk M.A.M., de Jong W.W.;  
 RT "Indels indicate that rodents are monophyletic and lagomorphs are their sister group."  
 RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AJ286827; CAC28513.1; -  
 DR HSSP; P01375; 1A8M.  
 DR InterPro; IPR003636; TNF\_abc.  
 DR InterPro; IPR000478; TNF\_family.  
 DR Pfam; PF00229; TNF\_1.  
 DR PRINTS; PR01234; TNECROSISFCT.  
 DR PRODOM; PD002012; TNF\_abc; 1.  
 DR SMART; SM00207; TNF\_1.  
 DR PROSITE; PS00251; TNF\_1; 1.  
 DR PROSITE; PS50049; TNF\_2; 1.  
 FT NON\_TER 1 1  
 FT NON\_TER 217 217  
 SQ SEQUENCE 215 AA; 23696 MW; 3E337E7E65F074EA CRC64;

DR PROSITE; PS00251; TNF\_1; 1.  
 DR PROSITE; PS50049; TNF\_2; 1.  
 FT NON\_TER 1 1  
 FT NON\_TER 217 217  
 SQ SEQUENCE 217 AA; 23655 MW; A7056710B6238074 CRC64;

Query Match 69.5%; Score 73; DB 6; Length 217;  
 Best Local Similarity 85.7%; Pred. No. 0.0012;  
 Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 3 QRETPGGAEPKWPY 16  
 Db 170 QRETPGGAEPKWPY 183

## RESULT 9

Q9BEE8 PRELIMINARY; PRT; 215 AA.

AC Q9BEE8: 01-JUN-2001 (TREMBLrel. 17, Created)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
 DE Tumor necrosis factor (Fragment).  
 GN TNFA.  
 OS Erinaceus europaeus (Western European hedgehog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Insectivora; Erinaceidae; Erinaceus.  
 OX NCBI\_TaxID=9365;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA van Dijk M.A.M., de Jong W.W.;  
 RT "Indels indicate that rodents are monophyletic and lagomorphs are their sister group."  
 RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AJ286830; CAC28522.1; -  
 DR HSSP; P01375; 4TGV.  
 DR InterPro; IPR003636; TNF\_abc.  
 DR InterPro; IPR000478; TNF\_family.  
 DR Pfam; PF00229; TNF\_1.  
 DR PRINTS; PR01234; TNECROSISFCT.  
 DR PRODOM; PD002012; TNF\_abc; 1.  
 DR SMART; SM00207; TNF\_1.  
 DR PROSITE; PS00251; TNF\_1; 1.  
 DR PROSITE; PS50049; TNF\_2; 1.  
 FT NON\_TER 1 1  
 FT NON\_TER 215 215  
 SQ SEQUENCE 215 AA; 23696 MW; 3E337E7E65F074EA CRC64;

Query Match 68.6%; Score 72; DB 6; Length 215;  
 Best Local Similarity 85.7%; Pred. No. 0.0018;  
 Matches 12; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 3 QRETPGGAEPKWPY 16  
 Db 168 QRETPGGAEPKWPY 181

RESULT 10  
 Q9BEC5 PRELIMINARY; PRT; 217 AA.

AC Q9BEC5: 01-JUN-2001 (TREMBLrel. 17, Created)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
 DE Tumor necrosis factor (Fragment).  
 GN TNFA.  
 OS Tenrec ecaudatus (tailless tenrec).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Insectivora; Tenrecidae; Tenrec.  
 OX NCBI\_TaxID=94439;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA van Dijk M.A.M., de Jong W.W.;



"Indels indicate that rodents are monophyletic and lagomorphs are their sister group." to the EMBL/GenBank/DBJ databases.

DR EMBL: AJ266826; CAC28538.1; -  
 DR HSSP: P01375; 4TSV.  
 DR InterPro: IPR003636; TNF\_abc.  
 DR InterPro: IPR00478; TNF\_family.  
 DR Pfam: PF00229; TNF; 1.  
 DR PRINTS: PR01234; TNECROSISFCT.  
 DR PRODOM: PD002012; TNF\_abc; 1.  
 DR SMART: SM00207; TNF; 1.  
 DR PROSITE: PS00251; TNF\_1; 1.  
 DR PROSITE: PS50049; TNF\_2; 1.  
 FT NON\_TER 1  
 FT SEQUENCE 217 AA; 23845 MW; 1C5013E9B777B54A CRC64;

Query Match  
 Best Local Similarity 84.6%; Score 69; DB 6; Length 217;  
 Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 4 RETPEGAERKPMY 16  
 DB 171 RETPEGAERKPMY 183

RESULT 11  
 ID 027978 PRELIMINARY; PRT; 104 AA.

DT 01-NOV-1996 (TREMBlrel. 01, Created)  
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
 DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
 OS TNFa (Fragment).  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=HOLSTEIN;  
 RA Dietz A.B., Nelbergs H.L., Kehli M.E.;  
 RT "Development of a Bovine TNFa single strand conformational  
 polymorphism."  
 RL Submitted (JUN-1994) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: U11040; AAA19573.1; -  
 DR HSSP: P01375; 4TSV.  
 DR InterPro: IPR003636; TNF\_abc.  
 DR InterPro: IPR00478; TNF\_family.  
 DR Pfam: PF00229; TNF; 1.  
 DR PRINTS: PR01234; TNECROSISFCT.  
 DR PRODOM: PD002012; TNF\_abc; 1.  
 DR SMART: SM00207; TNF; 1.  
 DR PROSITE: PS00251; TNF\_1; 1.  
 DR PROSITE: PS50049; TNF\_2; 1.  
 FT NON\_TER 1  
 FT SEQUENCE 104 AA; 11662 MW; BCE0A76D9FFA4BD CRC64;

Query Match  
 Best Local Similarity 92.3%; Score 68; DB 6; Length 104;  
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 4 RETPEGAERKPMY 16  
 DB 90 RETPEGAERKPMY 102

RESULT 12  
 ID 0912L4 PRELIMINARY; PRT; 156 AA.  
 AC 0912L4;

DT 01-DEC-2001 (TREMBlrel. 19, Created)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)  
 DE Tumor necrosis factor alpha (Fragment).  
 OS Sigmodon hispidus (Hispid cotton rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;  
 OC Sigmodon.  
 NCBI\_TaxID=42415;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Blanco J.C., Plehneva L.M., Prince G.A.;  
 RT "Sigmodon hispidus cytokines, chemokines and interferons."  
 RT Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF421384; AAL1818.1; -  
 DR InterPro: IPR003636; TNF\_abc.  
 DR InterPro: IPR00478; TNF\_family.  
 DR Pfam: PF00229; TNF; 1.  
 DR PRODOM: PD002012; TNF\_abc; 1.  
 DR PROSITE: PS00251; TNF\_1; UNKNOWN\_1.  
 DR PROSITE: PS50049; TNF\_2; 1.  
 FT NON\_TER 1  
 FT SEQUENCE 156 AA; 17303 MW; DC565F3BC3C826B4 CRC64;

Query Match  
 Best Local Similarity 76.9%; Score 65; DB 11; Length 156;  
 Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 4 RETPEGAERKPMY 16  
 DB 102 KETPGAEKPMY 114

RESULT 13  
 ID 09ER6 PRELIMINARY; PRT; 217 AA.  
 AC 09ER6;  
 DT 01-MAR-2001 (TREMBlrel. 16, Created)  
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)  
 DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
 DE Tumor necrosis factor alpha (Fragment).  
 OS Peromyscus maniculatus (Deer mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;  
 OC Peromyscus.  
 NCBI\_TaxID=10042;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=SPLEEN;  
 RA Herbst M.M., Schountz T.;  
 RT "Cloning of the deer mouse interferon gamma, interleukin-10 and tumor  
 necrosis factor genes."  
 RT Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF307013; AAG30264.1; -  
 DR HSSP: P06804; 2TNF.  
 DR InterPro: IPR003636; TNF\_abc.  
 DR InterPro: IPR00478; TNF\_family.  
 DR Pfam: PF00229; TNF; 1.  
 DR PRINTS: PR01234; TNECROSISFCT.  
 DR PRODOM: PD002012; TNF\_abc; 1.  
 DR SMART: SM00207; TNF; 1.  
 DR PROSITE: PS00251; TNF\_1; 1.  
 DR PROSITE: PS50049; TNF\_2; 1.  
 FT NON\_TER 1  
 FT SEQUENCE 217 AA; 23964 MW; D6F90C74C0B3021F CRC64;

Query Match  
 Best Local Similarity 76.9%; Score 65; DB 11; Length 217;  
 Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 4 RETPEGAERKPMY 16

Db 173 KETPEGSELKPMY 185

RESULT 14

09J126

ID 09J126 PRELIMINARY; PRT: 235 AA.

AC 09J126; PRELIMINARY; PRT: 235 AA.

DT 01-OCT-2000 (TREMBlrel. 15, Created)

DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)

DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)

DE TNF-alpha propeptide 3 (Fragment).

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI\_TaxID=10116;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=DARK AGOUTI;

RA Seidel M.F., Junier M.-P., Vetter H.;

RT "TNF-alpha polymorphism in rats with collagen-induced arthritis.";

RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF269160; AAF82568.1; -

DR HSSP; P06804; 2TNF.

DR InterPro; IPR003636; TNF\_abc.

DR InterPro; IPR000478; TNF\_family.

DR Pfam; PF00229; TNF; 1.

DR PRINTS; PR01234; TNECROSISFCT.

DR PRODOM; PD002012; TNF\_abc; 1.

DR SMART; SM00207; TNF; 1.

DR PROSITE; PS00251; TNF\_1; 1.

DR PROSITE; PS50049; TNF\_2; 1.

FT NON\_TER 235 235

SQ SEQUENCE 235 AA; 25789 MW; C801B92D049C2F2E CRC64;

Query Match 61.9%; Score 65; DB 11; Length 235;

Best Local Similarity 76.9%; Pred. No. 0.024;

Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 KETPEGAELKPMY 16

Db 181 KETPEGAELKPMY 193

RESULT 15

09TTG7

ID 09TTG7 PRELIMINARY; PRT: 138 AA.

AC 09TTG7; PRELIMINARY; PRT: 138 AA.

DT 01-MAY-2000 (TREMBlrel. 13, Created)

DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)

DT 01-OCT-2001 (TREMBlrel. 18, Last annotation update)

DE Tumor necrosis factor alpha (Fragment).

GN TNF-ALPHA.

OS Aotus lemurinus (Northern gray-necked night monkey).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.

OX NCBI\_TaxID=43147;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=L.A. Hernandez E., Echeverry S.J., Mendez J.A.,

RA Patirioy M.E.;

RT "Aotus lemurinus gene for TNF alpha.";

RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF097329; AAF21304.1; -

DR HSSP; P01375; 4NSV.

DR InterPro; IPR003636; TNF\_abc.

DR InterPro; IPR000478; TNF\_family.

DR Pfam; PF00229; TNF; 1.

DR PRINTS; PR01234; TNECROSISFCT.

DR PRODOM; PD002012; TNF\_abc; 1.

DR SMART; SM00207; TNF; 1.

DR PROSITE; PS00251; TNF\_1; 1.

DR PROSITE; PS50049; TNF\_2; 1.

FT NON\_TER 1 1

SQ SEQUENCE 138 AA; 15269 MW; 29275EAF4CD5068 CRC64;

Query Match 60.0%; Score 63; DB 6; Length 138;

Best Local Similarity 71.4%; Pred. No. 0.028;

Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 KETPEGAELKPMY 16

Db 95 KETPEGAELKPMY 108

Search completed: April 4, 2003, 08:42:07  
Job time : 26.6774 secs

GenCore version 5.1.4-p5\_4578  
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OM protein - protein search, using sw model

Run on: April 4, 2003, 08:37:56 ; Search time 10.9677 Seconds

(without alignments)  
45.606 Million cell updates/sec

Title: US-09-779-703-4

Perfect score: 105

Sequence: 1 CGORETEGAKRPMYC 17

Scoring table:

BLOSUM62

Searched: Gapop 10.0 , Gapext 0.5

262574 seqs, 29422922 residues

262574

## ALIGNMENTS

Total number of hits satisfying chosen parameters:

262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: /cgn2\_6/ptodata/1/1aa/5A.COMB.pep:\*  
2: /cgn2\_6/ptodata/1/1aa/5B.COMB.pep:\*  
3: /cgn2\_6/ptodata/1/1aa/5C.COMB.pep:\*  
4: /cgn2\_6/ptodata/1/1aa/5D.COMB.pep:\*  
5: /cgn2\_6/ptodata/1/1aa/5E.COMB.pep:\*  
6: /cgn2\_6/ptodata/1/1aa/5F.COMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	105	100.0	17	2	US-08-500-860A-25
2	88	83.8	17	2	US-08-500-860A-24
3	81	77.1	147	1	US-07-668-517-1
4	81	77.1	148	1	US-07-668-517-2
5	81	77.1	148	1	US-07-668-517-3
6	81	77.1	149	1	US-07-668-517-4
7	81	77.1	149	1	US-07-668-517-5
8	81	77.1	150	1	US-07-668-517-6
9	81	77.1	150	1	US-07-668-517-7
10	81	77.1	150	1	US-07-668-517-8
11	81	77.1	150	1	US-07-668-517-9
12	81	77.1	150	1	US-07-668-517-10
13	81	77.1	150	1	US-07-668-517-11
14	81	77.1	150	1	US-07-668-517-12
15	81	77.1	150	1	US-07-668-517-13
16	81	77.1	150	1	US-07-668-517-14
17	81	77.1	150	1	US-07-668-517-15
18	81	77.1	150	1	US-07-668-517-16
19	81	77.1	150	1	US-07-668-517-17
20	81	77.1	150	1	US-07-668-517-18
21	81	77.1	150	1	US-07-668-517-19
22	81	77.1	150	1	US-07-668-517-20
23	81	77.1	150	1	US-07-668-517-21
24	81	77.1	150	1	US-07-668-517-22
25	81	77.1	150	1	US-07-668-517-23
26	81	77.1	150	1	US-07-668-517-24
27	81	77.1	150	1	US-07-668-517-25

28	81	77.1	151	1	US-07-668-517-7	Sequence 7, Appl
29	81	77.1	151	1	US-07-668-517-18	Sequence 19, Appl
30	81	77.1	151	1	US-07-668-517-19	Sequence 18, Appl
31	81	77.1	151	1	US-07-668-517-20	Sequence 20, Appl
32	81	77.1	151	1	US-07-668-517-22	Sequence 22, Appl
33	81	77.1	151	1	US-07-668-517-23	Sequence 24, Appl
34	81	77.1	151	1	US-07-668-517-24	Sequence 25, Appl
35	81	77.1	151	1	US-07-668-517-25	Sequence 26, Appl
36	81	77.1	151	1	US-07-668-517-26	Sequence 27, Appl
37	81	77.1	151	1	US-07-668-517-27	Sequence 28, Appl
38	81	77.1	151	1	US-07-668-517-28	Sequence 29, Appl
39	81	77.1	151	1	US-07-668-517-30	Sequence 30, Appl
40	81	77.1	151	1	US-07-668-517-32	Sequence 32, Appl
41	81	77.1	151	1	US-07-668-517-36	Sequence 34, Appl
42	81	77.1	151	1	US-07-668-517-38	Sequence 36, Appl
43	81	77.1	151	1	US-07-668-517-41	Sequence 38, Appl
44	81	77.1	155	1	US-07-668-517-21	Sequence 21, Appl
45	81	77.1	155	1	US-07-668-517-21	Sequence 1, Appl

RESULT 1  
US-08-500-860A-25  
Sequence 25, Application US/08500860A  
Patent No. 5891679  
GENERAL INFORMATION:  
APPLICANT: LUCAS, RUDOLPH  
APPLICANT: DE BARSELIER, PATRICK  
APPLICANT: FRANSSEN, LUCIE  
APPLICANT: SABLO, ERWIN  
TITLE OF INVENTION: TNF-MOTILINS, A PROCESS FOR PREPARING THEM AND  
TITLE OF INVENTION: THEIR USE AS ACTIVE SUBSTANCES IN PHARMACEUTICAL COMPOS;  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: NIXON & VANDERHYTE P.C.  
STREET: 1100 NORTH GLEBE ROAD  
CITY: ARLINGTON  
STATE: VIRGINIA  
COUNTRY: U.S.A.  
ZIP: 22201-4714  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/500,860A  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: BYRNE, THOMAS E.  
REGISTRATION NUMBER: 32,205  
REFERENCE/DOCKET NUMBER: 1487-8  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703)816-4000  
TELEFAX: (703)816-4100  
TELEX: 200797 NIXN UR  
INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Binding-site  
LOCATION: 1  
OTHER INFORMATION: /note= "Biotin-Gly is coupled  
OTHER INFORMATION: to the N-terminus of the peptide"  
US-08-500-860A-25

Query Match 100.0%; Score 105; DB 2; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.8e-10;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGORETEPGAARAKPWC 17  
|||||  
Db 1 CGORETEPGAARAKPWC 17

## RESULT 2

US-08-500-860A-24  
Sequence 24, Application US/08500860A  
Patent No. 5891679  
GENERAL INFORMATION:  
APPLICANT: LUCAS, RUDOLPH  
APPLICANT: DE BAERSE, LUCIE  
APPLICANT: FRANKEN, PATRICK  
APPLICANT: SABON, ERWIN  
TITLE OF INVENTION: TNE-MUTINS, A PROCESS FOR PREPARING THEM AND  
TITLE OF INVENTION: THEIR USE AS ACTIVE SUBSTANCES IN PHARMACEUTICAL COMPOSITIONS  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: NIXON & VANDERHAYE P.C.  
STREET: 1100 NORTH GLEBE ROAD  
CITY: ARLINGTON  
STATE: VIRGINIA  
COUNTRY: U.S.A.  
ZIP: 22201-4714  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/500.860A  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: BYRNE, THOMAS E.  
REGISTRATION NUMBER: 32,205  
REFERENCE/DOCKET NUMBER: 1487-8  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703)816-4000  
TELEFAX: (703)816-4100  
TELEX: 200797 NIXN UR  
INFORMATION FOR SEQ ID NO: 24:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 1  
OTHER INFORMATION: /note= "Biotin-Gly is coupled  
US-08-500-860A-24 to the N-terminus of the peptide"

Query Match 83.8%; Score 88; DB 2; Length 17;  
Best Local Similarity 76.5%; Pred. No. 9e-08;  
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGORETEPGAARAKPWC 17  
||:|||||  
Db 1 CGPMDTEPGAELKPMWC 17

## RESULT 3

US-07-668-517-1  
Sequence 1, Application US/07668517  
Patent No. 5262309  
GENERAL INFORMATION:

APPLICANT: Satoshi NAKAMURA et al.  
TITLE OF INVENTION: No. 5262309e1 Physiologically Active  
TITLE OF INVENTION: Polypeptide, Recombinant Plasmid, Recombinant Microorganism  
TITLE OF INVENTION: Cell, Pharmaceutical Composition and Method of Recovering  
NUMBER OF SEQUENCES: 50  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wenderoth, Lind & Ponack  
STREET: 805 Fifteenth Street, N.W., #700  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005

## COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 5.25 inch, 500 Kb

COMPUTER: IBM Compatible

OPERATING SYSTEM: MS-DOS

SOFTWARE: DisplayWrite

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/668.517

FILING DATE: 19910322

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Matthew Jacob

REGISTRATION NUMBER: 25,154

REFERENCE/DOCKET NUMBER:

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-371-8850

TELEFAX: 202-371-8856

TELEX:

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 147 amino acids

TYPE: AMINO ACID

STRANDEDNESS: single

TOPOLOGY: linear

FEATURE:

NAME/KEY:

LOCATION:

IDENTIFICATION METHOD:

OTHER INFORMATION:

US-07-668-517-1

Query Match 77.1%; Score 81; DB 1; Length 147;  
Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ORETEPGAARAKPW 16  
|||||  
Db 92 ORETEPGAARAKPW 105

## RESULT 4

US-07-668-517-2  
Sequence 2, Application US/07668517  
Patent No. 5262309  
GENERAL INFORMATION:  
APPLICANT: Satoshi NAKAMURA et al.  
TITLE OF INVENTION: No. 5262309e1 Physiologically Active  
TITLE OF INVENTION: Polypeptide, Recombinant Plasmid, Recombinant Microorganism  
TITLE OF INVENTION: Cell, Pharmaceutical Composition and Method of Recovering  
NUMBER OF SEQUENCES: 50  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wenderoth, Lind & Ponack  
STREET: 805 Fifteenth Street, N.W., #700  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch, 500 Kb

RESULT 6  
 US-07-668-517-3  
 Sequence 3, Application US/07668517  
 Patent No. 5262309  
 GENERAL INFORMATION:  
 APPLICANT: Satoshi NAKAMURA et al.  
 TITLE OF INVENTION: No. 5262309el. Physiologically Active  
 TITLE OF INVENTION: Polypeptide, Recombinant Plasmid, Recombinant Microorganism  
 TITLE OF INVENTION: Cell, Pharmaceutical Composition and Method of Recovery  
 NUMBER OF SEQUENCES: 50  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Wenderoth, Lind & Ponack  
 STREET: 805 Fifteenth Street, N.W., #700  
 City: Washington  
 STATE: D.C.  
 COUNTRY: U.S.A.  
 Zip: 20005  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette, 5.25 inch, 500 KB  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: MS-DOS  
 SOFTWARE: DisplayWrite  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/07/668,517  
 FILING DATE: 19910322  
 CLASSIFICATION: 530  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER:  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Matthew JACOD  
 REGISTRATION NUMBER: 25,154  
 REFERENCE/DOCKET NUMBER:  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 202-371-8850  
 TELEFAX: 202-371-8856  
 TELEX:  
 INFORMATION FOR SEQ ID NO: 3:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 149 amino acids  
 TYPE: AMINO ACID  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 FEATURE:  
 NAME/KEY:  
 LOCATION:  
 IDENTIFICATION METHOD:

OTHER INFORMATION:  
US-07-668-517-3

Query Match 77.1%; Score 81; DB 1; Length 149;  
Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 ORETPGAEAKPMY 16  
|||||  
DB 94 ORETPGAEAKPMY 107

RESULT 7  
US-07-668-517-16

Sequence 16, Application US/07668517  
Patent No. 5262309  
GENERAL INFORMATION:  
APPLICANT: SATOSHI NAKAMURA et al.  
TITLE OF INVENTION: No. 5262309el Physiologically Active  
TITLE OF INVENTION: Polypeptide, Recombinant Plasmid, Recombinant Microorganism  
TITLE OF INVENTION: Cell, Pharmaceutical Composition and Method of Recovering  
NUMBER OF SEQUENCES: 50  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wenderoth, Lind & Ponack  
STREET: 805 Fifteenth Street, N.W., #700  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch, 500 KB  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: DisplayWrite  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/668,517  
FILING DATE: 19910322  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Matthew Jacob  
REGISTRATION NUMBER: 25,154  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-8850  
TELEFAX: 202-371-8856  
TELEX:  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 149 amino acids  
TYPE: AMINO ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY:  
LOCATION:  
IDENTIFICATION METHOD:  
OTHER INFORMATION:  
US-07-668-517-16

Query Match 77.1%; Score 81; DB 1; Length 149;  
Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 ORETPGAEAKPMY 16  
|||||  
DB 94 ORETPGAEAKPMY 107

RESULT 8  
US-07-668-517-4

Sequence 4, Application US/07668517  
Patent No. 5262309

GENERAL INFORMATION:  
APPLICANT: SATOSHI NAKAMURA et al.  
TITLE OF INVENTION: No. 5262309el Physiologically Active  
TITLE OF INVENTION: Polypeptide, Recombinant Plasmid, Recombinant Microorganism  
TITLE OF INVENTION: Cell, Pharmaceutical Composition and Method of Recovering  
NUMBER OF SEQUENCES: 50  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wenderoth, Lind & Ponack  
STREET: 805 Fifteenth Street, N.W., #700  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch, 500 KB  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: DisplayWrite  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/668,517  
FILING DATE: 19910322  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Matthew Jacob  
REGISTRATION NUMBER: 25,154  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-8850  
TELEFAX: 202-371-8856  
TELEX:  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 150 amino acids  
TYPE: AMINO ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY:  
LOCATION:  
IDENTIFICATION METHOD:  
OTHER INFORMATION:  
US-07-668-517-4

Query Match 77.1%; Score 81; DB 1; Length 150;  
Best Local Similarity 100.0%; Pred. No. 1.4e-05;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 ORETPGAEAKPMY 16  
|||||  
DB 95 ORETPGAEAKPMY 108

RESULT 9  
US-07-668-517-5

Sequence 5, Application US/07668517  
Patent No. 5262309  
GENERAL INFORMATION:  
APPLICANT: SATOSHI NAKAMURA et al.  
TITLE OF INVENTION: No. 5262309el Physiologically Active  
TITLE OF INVENTION: Polypeptide, Recombinant Plasmid, Recombinant Microorganism  
TITLE OF INVENTION: Cell, Pharmaceutical Composition and Method of Recovering  
NUMBER OF SEQUENCES: 50  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wenderoth, Lind & Ponack  
STREET: 805 Fifteenth Street, N.W., #700  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch, 500 KB  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: DisplayWrite  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/668,517  
FILING DATE: 19910322  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Matthew Jacob  
REGISTRATION NUMBER: 25,154  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-8850  
TELEFAX: 202-371-8856  
TELEX:  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 150 amino acids  
TYPE: AMINO ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY:  
LOCATION:  
IDENTIFICATION METHOD:  
OTHER INFORMATION:  
US-07-668-517-4

Query Match 77.1%; Score 81; DB 1; Length 150;  
Best Local Similarity 100.0%; Pred. No. 1.4e-05;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 ORETPGAEAKPMY 16  
|||||  
DB 95 ORETPGAEAKPMY 108

RESULT 9  
US-07-668-517-5

ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch, 500 Kb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Displaywrite  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/668,517  
FILING DATE: 19910322  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Matthew Jacob  
REGISTRATION NUMBER: 25,154  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-8850  
TELEFAX: 202-371-8856  
TELEX:  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 150 amino acids  
TYPE: AMINO ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY:  
LOCATION:  
IDENTIFICATION METHOD:  
OTHER INFORMATION:  
US-07-668-517-5

Query Match 77.1%; Score 81; DB 1; Length 150;  
Best Local Similarity 100.0%; Pred. No. 1.4e-05;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 ORETEGAEAKPWY 16  
|||||  
Db 95 ORETEGAEAKPWY 108

RESULT 10  
US-07-668-517-6  
Sequence 6, Application US/07668517  
Patent No. 5262309  
GENERAL INFORMATION:  
APPLICANT: Satoshi NAKAMURA et al.  
TITLE OF INVENTION: No. 5262309el Physiologically Active  
TITLE OF INVENTION: Polypeptide, Recombinant Plasmid, Recombinant Microorganism  
NUMBER OF SEQUENCES: 50  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wenderoth, Lind & Ponack  
STREET: 805 Fifteenth Street, N.W., #700  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch, 500 Kb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Displaywrite  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/668,517  
FILING DATE: 19910322  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:

NAME: Matthew Jacob  
REGISTRATION NUMBER: 25,154  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-8850  
TELEFAX: 202-371-8856  
TELEX:  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 150 amino acids  
TYPE: AMINO ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY:  
LOCATION:  
IDENTIFICATION METHOD:  
OTHER INFORMATION:  
US-07-668-517-6

Query Match 77.1%; Score 81; DB 1; Length 150;  
Best Local Similarity 100.0%; Pred. No. 1.4e-05;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 ORETEGAEAKPWY 16  
|||||  
Db 95 ORETEGAEAKPWY 108

RESULT 11  
US-07-668-517-8  
Sequence 8, Application US/07668517  
Patent No. 5262309  
GENERAL INFORMATION:  
APPLICANT: Satoshi NAKAMURA et al.  
TITLE OF INVENTION: No. 5262309el Physiologically Active  
TITLE OF INVENTION: Polypeptide, Recombinant Plasmid, Recombinant Microorganism  
NUMBER OF SEQUENCES: 50  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wenderoth, Lind & Ponack  
STREET: 805 Fifteenth Street, N.W., #700  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch, 500 Kb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Displaywrite  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/668,517  
FILING DATE: 19910322  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Matthew Jacob  
REGISTRATION NUMBER: 25,154  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-8850  
TELEFAX: 202-371-8856  
TELEX:  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 150 amino acids  
TYPE: AMINO ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:

NAME/KEY:  
LOCATION:  
IDENTIFICATION METHOD:  
OTHER INFORMATION:  
US-07-668-517-8

Query Match 77.1%; Score 81; DB 1; Length 150;  
Best Local Similarity 100.0%; Pred. No. 1.4e-05;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 QRETPGAEAKPMY 16  
DB 95 QRETPGAEAKPMY 108

RESULT 12  
US-07-668-517-9  
Sequence 9, Application US/07668517  
Patent No. 5262309  
GENERAL INFORMATION:  
APPLICANT: Satoshi NAKAMURA et al.  
TITLE OF INVENTION: No. 5262309el Physiologically Active  
TITLE OF INVENTION: Polypeptide, Recombinant Plasmid, Recombinant Microorganism  
TITLE OF INVENTION: Cell, Pharmaceutical Composition and Method of Recovering  
NUMBER OF SEQUENCES: 50  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wenderoth, Lind & Ponack  
STREET: 805 Fifteenth Street, N.W., #700  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch, 500 KB  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: DisplayWrite  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/668,517  
FILING DATE: 19910322  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Matthew Jacob  
REGISTRATION NUMBER: 25,154  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-8850  
TELEFAX: 202-371-8856  
TELEX:  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 150 amino acids  
TYPE: AMINO ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY:  
LOCATION:  
IDENTIFICATION METHOD:  
OTHER INFORMATION:  
US-07-668-517-9

Query Match 77.1%; Score 81; DB 1; Length 150;  
Best Local Similarity 100.0%; Pred. No. 1.4e-05;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 QRETPGAEAKPMY 16  
DB 95 QRETPGAEAKPMY 108

RESULT 13  
US-07-668-517-10  
Sequence 10, Application US/07668517  
Patent No. 5262309  
GENERAL INFORMATION:  
APPLICANT: Satoshi NAKAMURA et al.  
TITLE OF INVENTION: No. 5262309el Physiologically Active  
TITLE OF INVENTION: Polypeptide, Recombinant Plasmid, Recombinant Microorganism  
TITLE OF INVENTION: Cell, Pharmaceutical Composition and Method of Recovering  
NUMBER OF SEQUENCES: 50  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wenderoth, Lind & Ponack  
STREET: 805 Fifteenth Street, N.W., #700  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch, 500 KB  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: DisplayWrite  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/668,517  
FILING DATE: 19910322  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Matthew Jacob  
REGISTRATION NUMBER: 25,154  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-8850  
TELEFAX: 202-371-8856  
TELEX:  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 150 amino acids  
TYPE: AMINO ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY:  
LOCATION:  
IDENTIFICATION METHOD:  
OTHER INFORMATION:  
US-07-668-517-10

Query Match 77.1%; Score 81; DB 1; Length 150;  
Best Local Similarity 100.0%; Pred. No. 1.4e-05;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 QRETPGAEAKPMY 16  
DB 95 QRETPGAEAKPMY 108

RESULT 14  
US-07-668-517-11  
Sequence 11, Application US/07668517  
Patent No. 5262309  
GENERAL INFORMATION:  
APPLICANT: Satoshi NAKAMURA et al.  
TITLE OF INVENTION: No. 5262309el Physiologically Active  
TITLE OF INVENTION: Polypeptide, Recombinant Plasmid, Recombinant Microorganism  
TITLE OF INVENTION: Cell, Pharmaceutical Composition and Method of Recovering  
NUMBER OF SEQUENCES: 50  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wenderoth, Lind & Ponack  
STREET: 805 Fifteenth Street, N.W., #700



CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch, 500 Kb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: DisplayWrite  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/668,517  
FILING DATE: 19910322  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Matthew Jacob  
REGISTRATION NUMBER: 25,154  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-8850  
TELEFAX: 202-371-8856  
TELEX:  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 150 amino acids  
TYPE: AMINO ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY:  
LOCATION:  
IDENTIFICATION METHOD:  
OTHER INFORMATION:  
US-07-668-517-11

Query Match 77.1%; Score 81; DB 1; Length 150;  
Best Local Similarity 100.0%; Pred. No. 1.4e-05;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QRETEGAEAKPMY 16  
DB 95 QRETEGAEAKPMY 108

RESULT 15  
US-07-668-517-12  
Sequence 12, Application US/07668517  
Patent No. 5262309  
GENERAL INFORMATION:  
APPLICANT: Satoshi NAKAMURA et al.  
TITLE OF INVENTION: No. 5262309el Physiologically Active  
TITLE OF INVENTION: Polypeptide, Recombinant Plasmid, Recombinant Microorganism  
TITLE OF INVENTION: Cell, Pharmaceutical Composition and Method of Recovering  
NUMBER OF SEQUENCES: 50  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wenderoth, Lind & Ponack  
STREET: 805 Fifteenth Street, N.W., #700  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch, 500 Kb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: DisplayWrite  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/668,517  
FILING DATE: 19910322  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:

APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Matthew Jacob  
REGISTRATION NUMBER: 25,154  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-8850  
TELEFAX: 202-371-8856  
TELEX:  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 150 amino acids  
TYPE: AMINO ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY:  
LOCATION:  
IDENTIFICATION METHOD:  
OTHER INFORMATION:  
US-07-668-517-12

Query Match 77.1%; Score 81; DB 1; Length 150;  
Best Local Similarity 100.0%; Pred. No. 1.4e-05;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QRETEGAEAKPMY 16  
DB 95 QRETEGAEAKPMY 108

Search completed: April 4, 2003, 08:43:41  
Job time : 10.9677 secs

GenCore version 5.1.4.p5\_4578  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 4, 2003, 08:42:11 ; Search time 10.6935 Seconds  
(without alignments)  
97.191 Million cell updates/sec

Title: US-09-779-703-4

Perfect score: 105  
1 CCGRTPEGAERKPYC 17

Sequence: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 248812 segs, 61136040 residues

Total number of hits satisfying chosen parameters: 248812

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

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Published Applications AA:\*  
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2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep:\*  
3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep:\*  
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14: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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2	81	77.1	130	US-10-116-378-28	Sequence 28, Appl
3	81	77.1	152	US-09-779-050A-24	Sequence 24, Appl
4	81	77.1	157	US-09-903-327A-7	Sequence 7, Appl
5	81	77.1	157	US-10-043-432-1	Sequence 1, Appl
6	81	77.1	157	US-09-756-301A-1	Sequence 1, Appl
7	81	77.1	157	US-09-927-703-1	Sequence 1, Appl
8	81	77.1	157	US-09-854-280-19	Sequence 19, Appl
9	81	77.1	157	US-09-934-465-13	Sequence 13, Appl
10	81	77.1	157	US-09-766-535A-1	Sequence 1, Appl
11	81	77.1	157	US-09-854-208-19	Sequence 19, Appl
12	81	77.1	157	US-09-756-161A-1	Sequence 1, Appl
13	81	77.1	157	US-10-010-229-1	Sequence 1, Appl
14	81	77.1	157	US-10-043-450-1	Sequence 1, Appl
15	81	77.1	157	US-10-044-534-1	Sequence 1, Appl
16	81	77.1	164	US-09-798-789-2	Sequence 2, Appl
17	81	77.1	164	US-09-981-289-2	Sequence 2, Appl
18	81	77.1	193	US-10-145-014-3	Sequence 3, Appl
19	81	77.1	193	US-09-982-308-3	Sequence 3, Appl

20	81	77.1	233	8	US-08-971-317A-5	Sequence 5, Appl
21	81	77.1	233	9	US-10-136-511-3	Sequence 3, Appl
22	81	77.1	233	9	US-10-145-014-22	Sequence 22, Appl
23	81	77.1	233	9	US-09-131-237-3	Sequence 3, Appl
24	81	77.1	233	9	US-10-174-654-9	Sequence 9, Appl
25	81	77.1	233	9	US-10-151-882-42	Sequence 42, Appl
26	81	77.1	233	10	US-09-193-663-5	Sequence 5, Appl
27	81	77.1	233	10	US-09-878-919-5	Sequence 5, Appl
28	81	77.1	233	10	US-09-782-960-43	Sequence 43, Appl
29	81	77.1	233	10	US-09-840-707A-14	Sequence 14, Appl
30	81	77.1	233	10	US-09-246-129B-3	Sequence 3, Appl
31	81	77.1	233	10	US-09-345-790-3	Sequence 3, Appl
32	81	77.1	233	10	US-09-929-493-3	Sequence 3, Appl
33	81	77.1	233	10	US-09-899-059-3	Sequence 3, Appl
34	81	77.1	233	12	US-10-082-260-5	Sequence 5, Appl
35	81	77.1	233	12	US-10-012-452-10	Sequence 10, Appl
36	81	77.1	597	9	US-09-903-327A-11	Sequence 11, Appl
37	65	61.9	151	9	US-09-779-050A-40	Sequence 40, Appl
38	65	61.9	235	9	US-10-017-910-8	Sequence 8, Appl
39	65	61.9	268	9	US-10-185-425-6	Sequence 6, Appl
40	54	51.4	104	10	US-09-911-777-5	Sequence 5, Appl
41	49	46.7	235	9	US-09-131-237-7	Sequence 7, Appl
42	49	46.7	235	10	US-09-246-129B-7	Sequence 7, Appl
43	49	46.7	235	10	US-09-899-059-7	Sequence 7, Appl
44	49	46.7	235	12	US-10-012-452-14	Sequence 14, Appl
45	48	45.7	749	10	US-09-899-569A-2	Sequence 2, Appl

#### ALIGNMENTS

RESULT 1  
US-09-877-156-25  
; Sequence 25, Application US/09877156  
; Patent No. US20020055625A1  
; GENERAL INFORMATION:  
; APPLICANT: Catherine Tribouley  
; TITLE OF INVENTION: NEW MEMBERS OF TNF AND TNFR FAMILIES  
; FILE REFERENCE: 1408.003/200130.439C1  
; CURRENT FILING DATE: 2001-06-08  
; PRIOR APPLICATION NUMBER: US 09/286,529  
; PRIOR FILING DATE: 1998-04-05  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 25  
; LENGTH: 150  
; TYPE: PRT  
; ORGANISM: Homo sapien  
; US-09-877-156-25  
Query Match 77.1%; Score 81; DB 10; Length 150;  
Best Local Similarity 100.0%; Pred. No. 5.5e-05;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Db 95 QRETPGAEKPY 108  
OY 3 QRETPGAEKPY 16  
|||||  
Db 95 QRETPGAEKPY 108  
RESULT 2  
US-10-116-378-28  
; Sequence 28, Application US/10116378  
; Patent No. US2002015093A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Gurney, Austin  
; APPLICANT: Maisters, Scot A.  
; APPLICANT: Pitti, Robert M.  
; APPLICANT: Wood, William  
; TITLE OF INVENTION: NOVEL TUMOR NECROSIS FACTOR RECEPTOR HOMOLOG AND  
; TITLE OF INVENTION: NUCLEIC

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; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P1206R1
; CURRENT APPLICATION NUMBER: US/10/116,378
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/247,225
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/074,087
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-09
; NUMBER OF SEQ ID NOS: 31
; SEQ ID NO 28
; LENGTH: 150
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-116-378-28

Query Match
Best Local Similarity 77.1%; Score 81; DB 12; Length 150;
Best Local Similarity 100.0%; Pred. No. 5.5e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QRETEGAEAKPMY 16
Db 95 QRETEGAEAKPMY 108

RESULT 3
US-09-779-050A-24
; Sequence 24, Application US/09779050A
; Patent No. US20020160416A1
; GENERAL INFORMATION:
; APPLICANT: BOYLE, WILLIAM
; APPLICANT: HSU, HAILING
; TITLE OF INVENTION: RECEPTOR FROM TNF FAMILY
; FILE REFERENCE: A-570B
; CURRENT APPLICATION NUMBER: US/09/779,050A
; CURRENT FILING DATE: 2001-02-12
; PRIOR APPLICATION NUMBER: 60/181,800
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 24
; LENGTH: 152
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-779-050A-24

Query Match
Best Local Similarity 77.1%; Score 81; DB 9; Length 152;
Best Local Similarity 100.0%; Pred. No. 5.6e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QRETEGAEAKPMY 16
Db 97 QRETEGAEAKPMY 110

RESULT 4
US-09-903-327A-7
; Sequence 7, Application US/09903327A
; Patent No. US2002016433A1
; GENERAL INFORMATION:
; APPLICANT: Nemerov, Glen R.
; APPLICANT: Li, Ectung
; TITLE OF INVENTION: BIOFUNCTIONAL MOLECULES AND VECTORS COMPLEXED THEREWITH FOR TARGET
; TITLE OF INVENTION: GENE
; FILE REFERENCE: 22908-1228
; CURRENT APPLICATION NUMBER: US/09/903,327A
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 09/613,017
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 157
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; TYPE: PRT
; ORGANISM: Human
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (0)...(0)
; OTHER INFORMATION: Tumor necrosis factor-alpha (TNF alpha, mature
; OTHER INFORMATION: peptide)
; US-09-903-327A-7

Query Match
Best Local Similarity 77.1%; Score 81; DB 9; Length 157;
Best Local Similarity 100.0%; Pred. No. 5.8e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QRETEGAEAKPMY 16
Db 102 QRETEGAEAKPMY 115

RESULT 5
US-10-043-432-1
; Sequence 1, Application US/10043432
; Publication No. US20030054004A1
; GENERAL INFORMATION:
; APPLICANT: Le, Junming
; APPLICANT: Vilcek, Jan
; APPLICANT: Daddona, Peter
; APPLICANT: Ghayeb, John
; APPLICANT: Knight, David M.
; APPLICANT: Siegel, Scott
; TITLE OF INVENTION: Anti-TNF Antibodies and Peptides of
; TITLE OF INVENTION: Human Tumor Necrosis Factor
; FILE REFERENCE: 09/5.1005-013
; CURRENT APPLICATION NUMBER: US/10/043,432
; CURRENT FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: 09/927,703
; PRIOR FILING DATE: 2001-06-10
; PRIOR APPLICATION NUMBER: U.S. 09/756,398
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: U.S. 09/133,119
; PRIOR FILING DATE: 1998-08-12
; PRIOR APPLICATION NUMBER: U.S. 08/570,674
; PRIOR FILING DATE: 1995-12-11
; PRIOR APPLICATION NUMBER: U.S. 08/324,799
; PRIOR FILING DATE: 1994-10-18
; PRIOR APPLICATION NUMBER: U.S. 08/192,102
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/192,861
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/192,093
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/010,406
; PRIOR FILING DATE: 1993-01-29
; PRIOR APPLICATION NUMBER: U.S. 08/013,413
; PRIOR FILING DATE: 1993-02-02
; PRIOR APPLICATION NUMBER: U.S. 07/943,852
; PRIOR FILING DATE: 1992-09-11
; PRIOR APPLICATION NUMBER: U.S. 07/853,606
; PRIOR FILING DATE: 1992-03-18
; PRIOR APPLICATION NUMBER: U.S. 07/670,827
; PRIOR FILING DATE: 1991-03-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 157
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-043-432-1

Query Match
Best Local Similarity 77.1%; Score 81; DB 9; Length 157;
Best Local Similarity 100.0%; Pred. No. 5.8e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QRETEGAEAKPMY 16
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DB 102 QRETPGAEAKPMY 115

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RESULT 6
US-09-756-301A-1
; Sequence 1, Application US/09756301A
; Patent No. US20010027249A1
; GENERAL INFORMATION:
; APPLICANT: Le, Junming
; APPLICANT: Vilcek, Jan
; APPLICANT: Daddona, Peter
; APPLICANT: Ghayeb, John
; APPLICANT: Knight, David M.
; APPLICANT: Siegel, Scott
; TITLE OF INVENTION: Anti-TNF Antibodies and Peptides of
; FILE REFERENCE: 0975.1005-008
; CURRENT APPLICATION NUMBER: US/09/756.301A
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: U.S. 09/133,119
; PRIOR FILING DATE: 1998-08-12
; PRIOR APPLICATION NUMBER: U.S. 08/570,674
; PRIOR FILING DATE: 1995-12-11
; PRIOR APPLICATION NUMBER: U.S. 08/324,799
; PRIOR FILING DATE: 1994-10-18
; PRIOR APPLICATION NUMBER: U.S. 08/192,102
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/192,861
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/192,093
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/010,406
; PRIOR FILING DATE: 1993-01-29
; PRIOR APPLICATION NUMBER: U.S. 08/013,413
; PRIOR FILING DATE: 1993-02-02
; PRIOR APPLICATION NUMBER: U.S. 07/943,852
; PRIOR FILING DATE: 1992-09-11
; PRIOR APPLICATION NUMBER: U.S. 07/853,606
; PRIOR FILING DATE: 1992-03-18
; PRIOR APPLICATION NUMBER: U.S. 07/670,827
; PRIOR FILING DATE: 1991-03-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 157
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-756-301A-1

Query Match 77.1%; Score 81; DB 10; Length 157;
Best Local Similarity 100.0%; Pred. No. 5.8e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QRETPGAEAKPMY 16
DB 102 QRETPGAEAKPMY 115

RESULT 7
US-09-927-703-1
; Sequence 1, Application US/09927703
; Patent No. US20020022720A1
; GENERAL INFORMATION:
; APPLICANT: Le, Junming
; APPLICANT: Vilcek, Jan
; APPLICANT: Daddona, Peter
; APPLICANT: Ghayeb, John
; APPLICANT: Knight, David M.
; APPLICANT: Siegel, Scott
; TITLE OF INVENTION: Anti-TNF Antibodies and Peptides of
; FILE REFERENCE: 0975.1005-013
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;; CURRENT APPLICATION NUMBER: US/09/927,703
;; CURRENT FILING DATE: 2001-08-10
;; PRIOR APPLICATION NUMBER: U.S. 09/756,398
;; PRIOR FILING DATE: 2001-01-08
;; PRIOR APPLICATION NUMBER: U.S. 09/133,119
;; PRIOR FILING DATE: 1998-08-12
;; PRIOR APPLICATION NUMBER: U.S. 08/570,674
;; PRIOR FILING DATE: 1995-12-11
;; PRIOR APPLICATION NUMBER: U.S. 08/324,799
;; PRIOR FILING DATE: 1994-10-18
;; PRIOR APPLICATION NUMBER: U.S. 08/192,102
;; PRIOR FILING DATE: 1994-02-04
;; PRIOR APPLICATION NUMBER: U.S. 08/192,861
;; PRIOR FILING DATE: 1994-02-04
;; PRIOR APPLICATION NUMBER: U.S. 08/192,093
;; PRIOR FILING DATE: 1993-01-29
;; PRIOR APPLICATION NUMBER: U.S. 08/010,406
;; PRIOR FILING DATE: 1993-02-02
;; PRIOR APPLICATION NUMBER: U.S. 07/943,852
;; PRIOR FILING DATE: 1992-09-11
;; PRIOR APPLICATION NUMBER: U.S. 07/853,606
;; PRIOR FILING DATE: 1992-03-18
;; PRIOR APPLICATION NUMBER: U.S. 07/670,827
;; NUMBER OF SEQ ID NOS: 19
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 1
;; LENGTH: 157
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-927-703-1
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Query Match 77.1%; Score 81; DB 10; Length 157;  
Best Local Similarity 100.0%; Pred. No. 5.8e-05;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QRETPGAEAKPMY 16  
DB 102 QRETPGAEAKPMY 115

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RESULT 8
US-09-854-280-19
; Sequence 19, Application US/09854280
; Patent No. US20020052027A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Jian
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Gurney, Austin
; APPLICANT: Li, Hanzhong
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF
; FILE REFERENCE: P1381R1C2
; CURRENT APPLICATION NUMBER: US/09/854,280
; CURRENT FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: US 09/311,832
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: US 60/085,579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: US 60/113,621
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 26
; SEQ ID NO 19
; LENGTH: 157
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-280-19

Query Match 77.1%; Score 81; DB 10; Length 157;
Best Local Similarity 100.0%; Pred. No. 5.8e-05;
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Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 3 QRETPGAEAKPWY 16  
Db 102 QRETPGAEAKPWY 115

## RESULT 9

US-09-934-465-13  
; Sequence 13, Application US/09934465  
; Patent No. US2002010223A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; TITLE OF INVENTION: APO-2 LIGAND  
; FILE REFERENCE: 11669,22US03  
; CURRENT APPLICATION NUMBER: US/09/934,465  
; CURRENT FILING DATE: 2001-08-21  
; PRIOR APPLICATION NUMBER: 08/584,031  
; PRIOR FILING DATE: 1996-01-09  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: Patentl Ver. 2.0  
; SEQ ID NO 13  
; LENGTH: 157  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-934-465-13

Query Match 77.1%; Score 81; DB 10; Length 157;  
Best Local Similarity 100.0%; Pred. No. 5.8e-05;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QRETPGAEAKPWY 16  
Db 102 QRETPGAEAKPWY 115

## RESULT 10

US-09-766-535A-1  
; Sequence 1, Application US/09766535A  
; Patent No. US20020106372A1  
; GENERAL INFORMATION:  
; APPLICANT: Le, Junming  
; APPLICANT: Vilcek, Jan  
; APPLICANT: Daddona, Peter  
; APPLICANT: Ghayeb, John  
; APPLICANT: Knight, David M.  
; APPLICANT: Siegel, Scott  
; TITLE OF INVENTION: Anti-TNF Antibodies and Peptides of  
; TITLE OF INVENTION: Human Tumor Necrosis Factor  
; FILE REFERENCE: 0975,1005-010  
; CURRENT APPLICATION NUMBER: US/09/766,535A  
; CURRENT FILING DATE: 2001-01-18  
; PRIOR APPLICATION NUMBER: U.S. 09/133,119  
; PRIOR FILING DATE: 1998-08-12  
; PRIOR APPLICATION NUMBER: U.S. 08/570,674  
; PRIOR FILING DATE: 1995-12-11  
; PRIOR APPLICATION NUMBER: U.S. 08/324,799  
; PRIOR FILING DATE: 1994-10-18  
; PRIOR APPLICATION NUMBER: U.S. 08/192,102  
; PRIOR FILING DATE: 1994-02-04  
; PRIOR APPLICATION NUMBER: U.S. 08/192,861  
; PRIOR FILING DATE: 1994-02-04  
; PRIOR APPLICATION NUMBER: U.S. 08/192,093  
; PRIOR FILING DATE: 1994-02-04  
; PRIOR APPLICATION NUMBER: U.S. 08/010,406  
; PRIOR FILING DATE: 1993-01-29  
; PRIOR APPLICATION NUMBER: U.S. 08/013,413  
; PRIOR FILING DATE: 1993-02-02  
; PRIOR APPLICATION NUMBER: U.S. 07/943,852  
; PRIOR FILING DATE: 1992-09-11  
; PRIOR APPLICATION NUMBER: U.S. 07/853,606  
; PRIOR FILING DATE: 1992-03-18  
; PRIOR APPLICATION NUMBER: U.S. 07/670,827

; PRIOR FILING DATE: 1991-03-18  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 157  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-766-535A-1

Query Match 77.1%; Score 81; DB 10; Length 157;  
Best Local Similarity 100.0%; Pred. No. 5.8e-05;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QRETPGAEAKPWY 16  
Db 102 QRETPGAEAKPWY 115

## RESULT 11

US-09-854-208-19  
; Sequence 19, Application US/09854208  
; Patent No. US20020106743A1  
; GENERAL INFORMATION:  
; APPLICANT: Chen, Jian  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Gurney, Austin  
; APPLICANT: Li, Hanzhong  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USRS  
; FILE REFERENCE: P1381-R1  
; CURRENT APPLICATION NUMBER: US/09/854,208  
; CURRENT FILING DATE: 2001-05-10  
; PRIOR APPLICATION NUMBER: US/09/311,832  
; PRIOR FILING DATE: 1999-05-14  
; PRIOR APPLICATION NUMBER: US 60/085,579  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: US 60/113,621  
; PRIOR FILING DATE: 1998-12-23  
; NUMBER OF SEQ ID NOS: 26  
; SEQ ID NO 19  
; LENGTH: 157  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-854-208-19

Query Match 77.1%; Score 81; DB 10; Length 157;  
Best Local Similarity 100.0%; Pred. No. 5.8e-05;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QRETPGAEAKPWY 16  
Db 102 QRETPGAEAKPWY 115

## RESULT 12

US-09-756-161A-1  
; Sequence 1, Application US/09756161A  
; Patent No. US20020132307A1  
; GENERAL INFORMATION:  
; APPLICANT: Le, Junming  
; APPLICANT: Vilcek, Jan  
; APPLICANT: Daddona, Peter  
; APPLICANT: Ghayeb, John  
; APPLICANT: Knight, David M.  
; APPLICANT: Siegel, Scott  
; TITLE OF INVENTION: Anti-TNF Antibodies and Peptides of  
; TITLE OF INVENTION: Human Tumor Necrosis Factor  
; FILE REFERENCE: 0975,1005-007  
; CURRENT APPLICATION NUMBER: US/09/756,161A  
; CURRENT FILING DATE: 2001-01-08  
; PRIOR APPLICATION NUMBER: U.S. 09/133,119

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;; PRIOR FILING DATE: 1998-08-12
;; PRIOR APPLICATION NUMBER: U.S. 08/570,674
;; PRIOR FILING DATE: 1995-12-11
;; PRIOR APPLICATION NUMBER: U.S. 08/324,799
;; PRIOR FILING DATE: 1994-10-18
;; PRIOR APPLICATION NUMBER: U.S. 08/192,102
;; PRIOR FILING DATE: 1994-02-04
;; PRIOR APPLICATION NUMBER: U.S. 08/192,861
;; PRIOR FILING DATE: 1994-02-04
;; PRIOR APPLICATION NUMBER: U.S. 08/192,093
;; PRIOR FILING DATE: 1994-02-04
;; PRIOR APPLICATION NUMBER: U.S. 08/010,406
;; PRIOR FILING DATE: 1993-01-29
;; PRIOR APPLICATION NUMBER: U.S. 08/013,413
;; PRIOR FILING DATE: 1993-02-02
;; PRIOR APPLICATION NUMBER: U.S. 07/943,852
;; PRIOR FILING DATE: 1992-09-11
;; PRIOR APPLICATION NUMBER: U.S. 07/853,606
;; PRIOR FILING DATE: 1992-03-18
;; PRIOR APPLICATION NUMBER: U.S. 07/670,827
;; NUMBER OF SEQ ID NOS: 19
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO: 1
;; LENGTH: 157
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-756-161A-1
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Query Match
Best Local Similarity 77.1%; Score 81; DB 10; Length 157;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
OY 3 QRETPGAEAKPMY 16
Db 102 QRETPGAEAKPMY 115
```

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RESULT 13
US-10-010-229-1
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;; Sequence 1, Application US/10010229
;; Patent No. US2002014805A1
;; GENERAL INFORMATION:
;; APPLICANT: Le, Junming
;; APPLICANT: Vilcek, Jan
;; APPLICANT: Daddona, Peter
;; APPLICANT: Ghirayeb, John
;; APPLICANT: Knight, David M.
;; APPLICANT: Siegel, Scott
;; TITLE OF INVENTION: Anti-TNF Antibodies and Peptides of
;; FILE REFERENCE: 0975.1005-013
;; CURRENT APPLICATION NUMBER: US/10/010,229
;; PRIOR FILING DATE: 2001-12-07
;; PRIOR APPLICATION NUMBER: US/09/927,703
;; NUMBER OF SEQ ID NOS: 19
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO: 1
;; LENGTH: 157
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-010-229-1
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Query Match
Best Local Similarity 77.1%; Score 81; DB 12; Length 157;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
OY 3 QRETPGAEAKPMY 16
Db 102 QRETPGAEAKPMY 115
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RESULT 14
US-10-043-450-1
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;; Sequence 1, Application US/10043450
;; Patent No. US2002014196A1
;; GENERAL INFORMATION:
;; APPLICANT: Le, Junming
;; APPLICANT: Vilcek, Jan
;; APPLICANT: Daddona, Peter
;; APPLICANT: Ghirayeb, John
;; APPLICANT: Knight, David M.
;; APPLICANT: Siegel, Scott
;; TITLE OF INVENTION: Anti-TNF Antibodies and Peptides of
;; FILE REFERENCE: 0975.1005-013
;; CURRENT APPLICATION NUMBER: US/10/043,450
;; PRIOR FILING DATE: 2002-01-10
;; PRIOR APPLICATION NUMBER: 09/927,703
;; PRIOR FILING DATE: 2001-08-10
;; PRIOR APPLICATION NUMBER: U.S. 09/756,398
;; PRIOR FILING DATE: 2001-01-08
;; PRIOR APPLICATION NUMBER: U.S. 09/133,119
;; PRIOR FILING DATE: 1998-08-12
;; PRIOR APPLICATION NUMBER: U.S. 08/570,674
;; PRIOR FILING DATE: 1995-12-11
;; PRIOR APPLICATION NUMBER: U.S. 08/324,799
;; PRIOR FILING DATE: 1994-10-18
;; PRIOR APPLICATION NUMBER: U.S. 08/192,102
;; PRIOR FILING DATE: 1994-02-04
;; PRIOR APPLICATION NUMBER: U.S. 08/192,861
;; PRIOR FILING DATE: 1994-02-04
;; PRIOR APPLICATION NUMBER: U.S. 08/192,093
;; PRIOR FILING DATE: 1994-02-04
;; PRIOR APPLICATION NUMBER: U.S. 08/010,406
;; PRIOR FILING DATE: 1993-01-29
;; PRIOR APPLICATION NUMBER: U.S. 08/013,413
;; PRIOR FILING DATE: 1993-02-02
;; PRIOR APPLICATION NUMBER: U.S. 07/943,852
;; PRIOR FILING DATE: 1992-09-11
;; PRIOR APPLICATION NUMBER: U.S. 07/853,606
;; PRIOR FILING DATE: 1992-03-18
;; PRIOR APPLICATION NUMBER: U.S. 07/670,827
;; NUMBER OF SEQ ID NOS: 19
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO: 1
;; LENGTH: 157
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-043-450-1
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Query Match
Best Local Similarity 77.1%; Score 81; DB 12; Length 157;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY 3 QRETPGAEAKPMY 16
Db 102 QRETPGAEAKPMY 115
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RESULT 15
US-10-044-534-1
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;; Sequence 1, Application US/10044534
;; Patent No. US20020146419A1
;; GENERAL INFORMATION:
;; APPLICANT: Le, Junming
;; APPLICANT: Vilcek, Jan
;; APPLICANT: Daddona, Peter
;; APPLICANT: Ghirayeb, John
;; APPLICANT: Knight, David M.
;; APPLICANT: Siegel, Scott
;; TITLE OF INVENTION: Anti-TNF Antibodies and Peptides of
;; FILE REFERENCE: 0975.1005-013
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; CURRENT APPLICATION NUMBER: US/10/044,534
; CURRENT FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: 09/927,703
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: U.S. 09/756,398
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: U.S. 09/133,119
; PRIOR FILING DATE: 1998-08-12
; PRIOR APPLICATION NUMBER: U.S. 08/570,674
; PRIOR FILING DATE: 1995-12-11
; PRIOR APPLICATION NUMBER: U.S. 08/324,799
; PRIOR FILING DATE: 1994-10-18
; PRIOR APPLICATION NUMBER: U.S. 08/192,102
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/192,861
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/192,093
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/010,406
; PRIOR FILING DATE: 1993-01-29
; PRIOR APPLICATION NUMBER: U.S. 08/013,413
; PRIOR FILING DATE: 1993-02-02
; PRIOR APPLICATION NUMBER: U.S. 07/943,852
; PRIOR FILING DATE: 1992-09-11
; PRIOR APPLICATION NUMBER: U.S. 07/853,606
; PRIOR FILING DATE: 1992-03-18
; PRIOR APPLICATION NUMBER: U.S. 07/670,827
; PRIOR FILING DATE: 1991-03-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 157
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-044-534-1

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Query Match          77.1%; Score 81; DB 12; Length 157;
Best Local Similarity 100.0%; Pred. No. 5.8e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY      3 ORETPEGAEAKPMY 16
        |||||||||
Db      102 ORETPEGAEAKPMY 115

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GenCore version 5.1.4.p5.4578  
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OM protein - protein search, using sw model

Run on: April 4, 2003, 08:36:10 ; Search time 31.5323 seconds

(without alignments)  
71.839 Million cell updates/sec

Title: US-09-779-703-5

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Gap 10.0, Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	108	100.0	17	15	AA60232
2	108	100.0	17	21	AA82197
3	108	100.0	19	21	AA82198
4	91	84.3	19	21	AA82199
5	88	81.5	17	15	AA60233
6	88	81.5	17	21	AA82196
7	84	77.8	14	21	AA82195
8	84	77.8	154	8	AA60557
9	84	77.8	156	7	AA60526
10	84	77.8	156	14	AA81861

11	84	77.8	156	14	AA81862	Murine TNF-alpha m
12	84	77.8	156	15	AA60244	Mouse-alpha. Mus
13	84	77.8	157	7	AA60527	Sequence of tumour
14	84	77.8	157	14	AA838077	Non-human TNF-alpha
15	84	77.8	170	8	AA60558	Tumour necrosis fac
16	84	77.8	233	10	AA60424	Human tumour necro
17	84	77.8	235	7	AA60530	Sequence of tumour
18	84	77.8	235	11	AA805328	Rat tumour necrosi
19	84	77.8	235	11	AA805996	Rat tumour necrosi
20	84	77.8	235	17	AA88589	Mouse tumour necro
21	84	77.8	235	21	AA88596	Murine tumour necr
22	84	77.8	235	23	AAU10546	Rat tumour necrosi
23	84	77.8	268	22	AA86310	Fusion construct T
24	72	66.7	155	21	AA808283	Antitumour peptide
25	69	63.9	157	10	AA691633	Antitumour peptide
26	65	60.2	14	21	AA82194	Polypeptide derive
27	65	60.2	17	11	AA805469	Tumour necrosis fa
28	65	60.2	25	11	AA805513	Tumour necrosis fa
29	65	60.2	140	16	AA872456	Tumour necrosis fa
30	65	60.2	145	9	AA82043	Sequence of new tu
31	65	60.2	147	9	AA81853	Sequence of modifi
32	65	60.2	147	22	AA667245	Human tumour necro
33	65	60.2	147	22	AA671982	C-terminal region
34	65	60.2	149	10	AA691635	Polypeptide derive
35	65	60.2	149	11	AA805612	Antitumour peptide
36	65	60.2	150	8	AA670528	Synthetic tumour n
37	65	60.2	150	8	AA671245	TNF-derived polype
38	65	60.2	150	9	AA82136	Modified tumour ne
39	65	60.2	150	9	AA82190	TNF analogue. AA
40	65	60.2	150	9	AA82303	TNF analogue. AA
41	65	60.2	150	9	AA81066	Sequence of new ph
42	65	60.2	150	9	AA81068	Sequence of new ph
43	65	60.2	150	10	AA695660	Anti-tumour active
44	65	60.2	150	11	AA805286	New polypeptide w
45	65	60.2	150	11	AA808151	Polypeptide with a

#### ALIGNMENTS

RESULT 1	AA60232	standard: peptide; 17 AA.
ID	AA60232;	
AC	16-MAR-1995	(first entry)
XX	mtNF-alpha tip.	
XX	TNF-alpha; tumor necrosis factor-alpha; tip peptide; mutein; cancer;	
KW	sepsis; inflammation; cytokine; metastasis; lectin; adhesion;	
KW	mutagenesis; trypanoside.	
XX	Synthetic.	
OS		
XX	Key	Location/Qualifiers
FH	Misc-difference 1	/note="N-terminal biotin Gly-Gly"
FT		
XX	WO9418325-A.	
XX	18-AUG-1994.	
PD		
XX	02-FEB-1994;	94WO-EP00286.
PF		
XX	03-FEB-1993;	93EP-0400262.
PR		
XX	(INNO-) INNOGENETICS NV SA.	
PA		
XX	De Baetselier P, Franssen L, Lucas R, Sablon E;	
PI		
XX	WPI; 1994-279746/34.	
DR		



XX New tumour necrosis factor -alpha muteins, antibodies and  
 PT antisense peptide(s) - used in the treatment of diseases and  
 PT conditions associated with the in vivo activities of TNF-A eg  
 PT cancer, sepsis, inflammation, etc  
 XX  
 PS Disclosure; Page 61; 132pp; English.  
 CC The TNF-alpha tip peptides given in AAR60232-42 were modified with  
 CC N-terminal biotin-Gly-Gly moieties and were used to demonstrate  
 CC that the tip region of mouse and human TNF-alpha contains the  
 CC trypanosomal and lectin-like activities of the molecule and is  
 CC is involved in TNF-induced lethal shock.  
 XX  
 SO Sequence 17 AA:  
 Query Match 100.0%; Score 108; DB 15; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 5.1e-09;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CGPKDTPGAGELKPMWC 17  
 DB 1 CGPKDTPGAGELKPMWC 17  
 RESULT 2  
 AAY82197  
 ID AAY82197 standard; peptide; 17 AA.  
 XX  
 AC AAY82197;  
 XX  
 DT 08-JUN-2000 (first entry)  
 XX  
 DE Tumour necrosis factor alpha derived circularised peptide #2.  
 XX  
 KW Tumour necrosis factor alpha; TNF-alpha; human; mouse; oedema;  
 KM proinflammatory; pulmonary oedema; cyclic.  
 XX  
 OS Mus sp.  
 XX  
 FH Key Location/Qualifiers  
 FT Disulfide-bond 1..17  
 XX  
 PN WO200009149-A1.  
 XX  
 PD 24-FEB-2000.  
 XX  
 PF 10-AUG-1999; 99WO-EP05806.  
 XX  
 PR 14-AUG-1998; 98EP-0870180.  
 PR 18-SEP-1998; 98EP-0870198.  
 PR 21-OCT-1998; 98EP-0870222.  
 XX  
 PA (INNO-) INNOGENETICS NV.  
 XX  
 PI Lucas R, De Baetselier P, Pugin J, Bloc A, Franssen L;  
 DR WPI; 2000-282855/24.  
 XX  
 PT Use of peptides derived from human or mouse tissue necrosis  
 PT factor-alpha (TNF-alpha), and comprising 7-17 contiguous amino acids,  
 PT for preventing or treating oedema  
 XX  
 PS Claim 8; Page 16; 26pp; English.  
 CC The present invention describes the use of peptides comprising a chain  
 CC of 7-17 contiguous amino acids derived from the Ser100-Glu116 region  
 CC of human tumour necrosis factor-alpha (TNF-alpha), or Ser99-Glu115  
 CC region of mouse TNF-alpha, for treating oedema. The peptides form  
 CC pharmaceutical compositions for treating oedema, especially pulmonary  
 CC oedema. The peptides are non-toxic, whilst retaining the oedema  
 CC resorption-inducing capacity as TNF. The present sequence represents  
 CC a specifically claimed TNF-alpha circularised peptide from the present

CC invention.  
 XX  
 SO Sequence 17 AA:  
 Query Match 100.0%; Score 108; DB 21; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 5.1e-09;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CGPKDTPGAGELKPMWC 17  
 DB 1 CGPKDTPGAGELKPMWC 17  
 RESULT 3  
 AAY82198  
 ID AAY82198 standard; peptide; 19 AA.  
 XX  
 AC AAY82198;  
 XX  
 DT 08-JUN-2000 (first entry)  
 XX  
 DE Murine TNF derived peptide long tip peptide 99-115 (LTIP).  
 XX  
 KW Tumour necrosis factor alpha; TNF-alpha; human; mouse; oedema;  
 KM proinflammatory; pulmonary oedema.  
 XX  
 OS Mus sp.  
 XX  
 PN WO200009149-A1.  
 XX  
 PD 24-FEB-2000.  
 XX  
 PF 10-AUG-1999; 99WO-EP05806.  
 XX  
 PR 14-AUG-1998; 98EP-0870180.  
 PR 18-SEP-1998; 98EP-0870198.  
 PR 21-OCT-1998; 98EP-0870222.  
 XX  
 PA (INNO-) INNOGENETICS NV.  
 XX  
 PI Lucas R, De Baetselier P, Pugin J, Bloc A, Franssen L;  
 DR WPI; 2000-282855/24.  
 XX  
 PD Use of peptides derived from human or mouse tissue necrosis  
 PT factor-alpha (TNF-alpha), and comprising 7-17 contiguous amino acids,  
 PT for preventing or treating oedema  
 XX  
 PS Example 1; Page 7; 26pp; English.  
 XX  
 CC The present invention describes the use of peptides comprising a chain  
 CC of 7-17 contiguous amino acids derived from the Ser100-Glu116 region  
 CC of human tumour necrosis factor-alpha (TNF-alpha), or Ser99-Glu115  
 CC region of mouse TNF-alpha, for treating oedema. The peptides form  
 CC pharmaceutical compositions for treating oedema, especially pulmonary  
 CC oedema. The peptides are non-toxic, whilst retaining the oedema  
 CC resorption-inducing capacity as TNF. The present sequence represents  
 CC a murine TNF derived peptide used in an example from the present  
 CC invention.  
 XX  
 SO Sequence 19 AA:  
 Query Match 100.0%; Score 108; DB 21; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 5.7e-09;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CGPKDTPGAGELKPMWC 17  
 DB 3 CGPKDTPGAGELKPMWC 19  
 RESULT 4  
 AAY82199

ID AAY82199 standard; peptide; 19 AA.  
 XX  
 AC AAY82199;  
 XX  
 DT 08-JUN-2000 (first entry)  
 XX  
 DE Murine TNF derived peptide mutated tip peptide 99-115 (mutTip).  
 XX  
 KM Tumour necrosis factor alpha; TNF-alpha; human; mouse; oedema;  
 KM proinflammatory; pulmonary oedema.  
 XX  
 OS Mus sp.  
 OS Synthetic.  
 PN WO200009149-A1.  
 XX  
 PD 24-FEB-2000.  
 XX  
 PF 10-AUG-1999; 99WO-EP05806.  
 XX  
 PR 14-AUG-1998; 98EP-0870180.  
 PR 18-SEP-1998; 98EP-0870198.  
 PR 21-OCT-1998; 98EP-0870222.  
 XX  
 PA (INNO-) INNOGENETICS NV.  
 XX  
 PI Lucas R, De Baetselier P, Pugin J, Bloc A, Franssen L;  
 DR WPI: 2000-282855/24.  
 XX  
 PT Use of peptides derived from human or mouse tissue necrosis  
 PT factor-alpha (TNF-alpha), and comprising 7-17 contiguous amino acids,  
 PT for preventing or treating oedema  
 XX  
 PS Example 1; Page 8; 26pp; English.  
 XX  
 CC The present invention describes the use of peptides comprising a chain  
 CC of 7-17 contiguous amino acids derived from the Ser100-Glu116 region  
 CC of human tumour necrosis factor-alpha (TNF-alpha), or Ser99-Glu115  
 CC region of mouse TNF-alpha, for treating oedema. The peptides form  
 CC pharmaceutical compositions for treating oedema. The peptides form  
 CC oedema. The peptides are non-toxic, whilst retaining the oedema  
 CC resorption-inducing capacity as TNF. The present sequence represents  
 CC a murine TNF derived peptide used in an example from the present  
 CC invention.  
 XX  
 SQ Sequence 19 AA;  
 XX  
 Query Match 84.3%; Score 91; DB 21; Length 19;  
 Best Local Similarity 82.4%; Pred. No. 1.7e-06;  
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 OY 1 CGKDPPEGAELKPYWC 17  
 ||||| |||||  
 DB 3 CGKDPAPGALAPKPYWC 19  
 ||||| |||||  
 RESULT 5  
 AAR60233  
 ID AAR60233 standard; peptide; 17 AA.  
 XX  
 AC AAR60233;  
 XX  
 DT 16-MAR-1995 (first entry)  
 XX  
 DE hTNF-alpha tip.  
 XX  
 KM TNF-alpha; tumor necrosis factor-alpha; tip peptide; mutin; cancer;  
 KM sepsis; inflammation; cytokine; metastasis; lectin; adhesion;  
 KM mutagenesis; trypanoside.  
 XX  
 OS Synthetic.

FH Key Location/Qualifiers  
 FT Misc-difference 1 /note="N-terminal biotin Gly-Gly"  
 FT  
 XX  
 PN WO9418325-A.  
 XX  
 PD 18-AUG-1994.  
 XX  
 PF 02-FEB-1994; 94WO-EP00286.  
 XX  
 PR 03-FEB-1993; 93EP-0400262.  
 XX  
 PA (INNO-) INNOGENETICS NV SA.  
 XX  
 PI De Baetselier P, Franssen L, Lucas R, Sablon E;  
 DR WPI: 1994-279746/34.  
 XX  
 PT New tumour necrosis factor -alpha muteins, antibodies and  
 PT antisense peptide(s) - used in the treatment of diseases and  
 PT conditions associated with the in vivo activities of TNF-A eg  
 PT cancer, sepsis, inflammation, etc  
 XX  
 PS Disclosure; Page 61; 132pp; English.  
 XX  
 CC The TNF-alpha tip peptides given in AAR60232-42 were modified with  
 CC N-terminal biotin-Gly-Gly moieties and were used to demonstrate  
 CC that the tip region of mouse and human TNF-alpha contains the  
 CC trypanosomal and lectin-like activities of the molecule and is  
 CC involved in TNF-induced lethal shock.  
 XX  
 SQ Sequence 17 AA;  
 XX  
 Query Match 81.5%; Score 88; DB 15; Length 17;  
 Best Local Similarity 76.5%; Pred. No. 4.2e-06;  
 Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
 OY 1 CGKDPPEGAELKPYWC 17  
 ||:||||| |||||  
 DB 1 CGQRETPPEGAELKPYWC 17  
 ||:||||| |||||  
 RESULT 6  
 AAY82196  
 ID AAY82196 standard; peptide; 17 AA.  
 XX  
 AC AAY82196;  
 XX  
 DT 08-JUN-2000 (first entry)  
 XX  
 DE Tumour necrosis factor alpha derived circularised peptide #1.  
 XX  
 KM Tumour necrosis factor alpha; TNF-alpha; human; mouse; oedema;  
 KM proinflammatory; pulmonary oedema; cyclic.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Disulfide-bond 1..17  
 FT  
 XX  
 PN WO200009149-A1.  
 XX  
 PD 24-FEB-2000.  
 XX  
 PF 10-AUG-1999; 99WO-EP05806.  
 XX  
 PR 14-AUG-1998; 98EP-0870180.  
 PR 18-SEP-1998; 98EP-0870198.  
 PR 21-OCT-1998; 98EP-0870222.  
 XX  
 PA (INNO-) INNOGENETICS NV.  
 XX  
 PI Lucas R, De Baetselier P, Pugin J, Bloc A, Franssen L;

XX DR WPI: 2000-282855/24.  
 XX PT Use of peptides derived from human or mouse tissue necrosis  
 XX factor-alpha (TNF-alpha), and comprising 7-17 contiguous amino acids,  
 PT for preventing or treating oedema  
 XX PS Claim 8; Page 16; 26pp; English.  
 CC The present invention describes the use of peptides comprising a chain  
 CC of 7-17 contiguous amino acids derived from the Ser100-Glu116 region  
 CC of human tumour necrosis factor-alpha (TNF-alpha), or Ser99-Glu115  
 CC region of mouse TNF-alpha, for treating oedema. The peptides form  
 CC pharmaceutical compositions for treating oedema, especially pulmonary  
 CC oedema. The peptides are non-toxic, whilst retaining the oedema  
 CC resorption-inducing capacity as TNF. The present sequence represents  
 CC a specifically claimed TNF-alpha circularised peptide from the present  
 CC invention.  
 XX SQ Sequence 17 AA;  
 Query Match 81.5%; Score 88; DB 21; Length 17;  
 Best Local Similarity 76.5%; Pred. No. 4.2e-06;  
 Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
 OY 1 CGPKDTPGAGELKPMYC 17  
 DB 1 CGQRETPGAGAKPMYC 17  
 RESULT 7  
 ID AAY82195  
 AC AAY82195 standard; peptide; 14 AA.  
 XX AAY82195;  
 DT 08-JUN-2000 (first entry)  
 XX  
 DE Tumour necrosis factor alpha derived peptide #2.  
 XX  
 KW Tumour necrosis factor alpha; TNF-alpha; human; mouse; oedema;  
 KW proinflammatory; pulmonary oedema.  
 XX  
 OS Mus sp.  
 XX  
 PN WO200009149-A1.  
 XX  
 PD 24-FEB-2000.  
 XX  
 PF 10-AUG-1999; 99WO-EP05806.  
 XX  
 PR 14-AUG-1998; 98EP-0870180.  
 PR 18-SEP-1998; 98EP-0870198.  
 PR 21-OCT-1998; 98EP-0870222.  
 XX  
 PA (INNO-) INNOGENETICS NV.  
 PI Lucas R, De Baetselier P, Pugin J, Bloc A, Franssen L;  
 XX WPI: 2000-282855/24.  
 DR  
 XX  
 PT Use of peptides derived from human or mouse tissue necrosis  
 PT factor-alpha (TNF-alpha), and comprising 7-17 contiguous amino acids,  
 PT for preventing or treating oedema  
 XX PS Claim 5; Page 16; 26pp; English.  
 CC The present invention describes the use of peptides comprising a chain  
 CC of 7-17 contiguous amino acids derived from the Ser100-Glu116 region  
 CC of human tumour necrosis factor-alpha (TNF-alpha), or Ser99-Glu115  
 CC region of mouse TNF-alpha, for treating oedema. The peptides form  
 CC pharmaceutical compositions for treating oedema, especially pulmonary  
 CC oedema. The peptides are non-toxic, whilst retaining the oedema

CC resorption-inducing capacity as TNF. The present sequence represents  
 CC a specifically claimed TNF-alpha peptide from the present invention.  
 XX SQ Sequence 14 AA;  
 Query Match 77.8%; Score 84; DB 21; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 3 PKDTPGAGELKPMY 16  
 DB 1 PKDTPGAGELKPMY 14  
 RESULT 8  
 ID AAP70557  
 AC AAP70557 standard; protein; 154 AA.  
 XX AAP70557;  
 DT 26-FEB-1991 (first entry)  
 XX  
 DE Tumour necrosis factor.  
 XX  
 KW TNF; antitumor.  
 XX  
 PN JP62135493-A.  
 XX  
 PD 18-JUN-1987.  
 XX  
 PF 06-DEC-1985; 85JP-0275392.  
 XX  
 PR 06-DEC-1985; 85JP-0275392.  
 XX  
 PA (TANA) TANABE SEIYAKU KK.  
 XX  
 DR WPI: 1987-209318/30.  
 XX  
 PT Anticancer factor - expressed by specified amino acid sequence.  
 XX  
 PS Disclosure; Page 12; 12pp; Japanese.  
 XX  
 CC The sequence encodes tumor necrosis factor which is an antitumor  
 CC agent and a lymphokine. The sequence may optionally have up to 16  
 CC additional AA as the N-terminal.  
 CC See also AAP70558.  
 XX  
 SQ Sequence 154 AA;  
 Query Match 77.8%; Score 84; DB 8; Length 154;  
 Best Local Similarity 100.0%; Pred. No. 0.00014;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 3 PKDTPGAGELKPMY 16  
 DB 99 PKDTPGAGELKPMY 112  
 RESULT 9  
 ID AAP60526  
 AC AAP60526 standard; protein; 156 AA.  
 XX AAP60526;  
 DT 07-AUG-1991 (first entry)  
 XX  
 DE Sequence of tumour necrosis factor (TNF).  
 XX  
 KW Anticancer agent; antitumor; antimalarial; tumour necrosis factor.  
 XX  
 PN WO8603751-A.  
 XX  
 PD 03-JUL-1986.

XX PF 19-DEC-1985; 85WO-EP00721.  
 XX PR 09-OCT-1985; 85US-0785947.  
 XX PR 21-DEC-1984; 84US-0684595.  
 XX PR 09-OCT-1986; 86WO-US02133.  
 XX PA (BIOJ) BIOGEN NV.  
 XX PA (FIER) FIER W C.  
 XX PA (ALIE) ALLET B.  
 XX PA (BIOG) BIOGEN INC.  
 XX PI Fiers WC, Franssen LM, Tavernier JHL, Marmenout ALM;  
 XX PI VanderHeyden J, Allet B, Washima EH;  
 XX DR WPI: 1986-182891/28.  
 XX DR N-PSDB; AAN60440.  
 XX PT Mammalian tumour necrosis factors - produced by culturing  
 XX PT pro-karyotic hosts transformed with recombinant DNA  
 XX PS Claim 12; Page 66-67; 93pp; English.  
 XX CC TNF-like polypeptides and compns. are produced by the fermentation  
 XX CC of host cells transformed with at least one DNA sequence which codes  
 XX CC for a mammalian TNF-like polypeptide operatively linked to an  
 XX CC expression control sequence in the transformed host.  
 XX SQ Sequence 156 AA;  
 Query Match 77.8%; Score 84; DB 7; Length 156;  
 Best Local Similarity 100.0%; Pred. No. 0.00014;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 PKDPEGAELKPMY 16  
 DB 101 PKDPEGAELKPMY 114  
 RESULT 10  
 AAR41861  
 ID AAR41861 standard; protein; 156 AA.  
 AC AAR41861;  
 XX  
 XX 29-MAR-1994 (first entry)  
 DE Rat TNF-alpha mutein with modified channel-forming activity.  
 XX Tumour Necrosis Factor alpha; TNF-a; target membrane permeability;  
 KW TNF trimer; ion channel; mutein.  
 XX  
 OS Rattus rattus.  
 XX  
 FH Key  
 FT Misc-difference 11 Location/Qualifiers  
 FT /label= Glu, Arg, Cys, Asp, Gln, Asn, Ser, Thr  
 FT or His  
 FT /note= "wild-type channel residue is Lys"  
 FT Misc-difference 57  
 FT /label= Trp, Ser, Thr, Ala, Met, Cys, Phe or Tyr  
 FT /note= "wild-type channel residue is Leu"  
 FT Misc-difference 59  
 FT /label= Trp, Ser, Thr, Ala, Met, Cys or Phe  
 FT /note= "wild-type channel residue is Tyr"  
 FT Misc-difference 97  
 FT /label= Arg, Cys, Glu, Asp, Gln, Asn, Ser, Thr  
 FT or His  
 FT /note= "wild-type channel residue is Lys"  
 FT /label= Arg, Cys, Asp, Gln, Asn, Ser, Thr, Glu  
 FT or His  
 FT /note= "wild-type channel residue is Lys"  
 FT /label= Arg, Cys, Asp, Gln, Asn, Ser, Thr, Glu  
 FT or His  
 FT /note= "wild-type channel residue is Lys"

FT Misc-difference 115  
 FT /label= Lys, Arg, Cys, Asp, Gln, Asn, Ser, His  
 FT or Thr  
 FT /note= "wild-type channel residue is Glu"  
 FT Misc-difference 118  
 FT /label= Trp, Phe, Ser, Thr, Ala, Met or Cys  
 FT /note= "wild-type channel residue is Tyr"  
 FT Misc-difference 120  
 FT /label= Ala, Val, Ser or Thr  
 FT /note= "wild-type channel residue is Gly"  
 FT Misc-difference 154  
 FT /label= Trp, Ser, Thr, Ala, Met, Cys, Phe or Tyr  
 FT /note= "wild-type channel residue is Ile"  
 FT Misc-difference 156  
 FT /label= Trp, Ser, Thr, Ala, Cys or Tyr  
 FT /note= "wild-type channel residue is Leu"  
 W09318148-A.  
 PD 16-SEP-1993.  
 XX  
 XX 12-MAR-1993; 93WO-US02475.  
 XX  
 XX 12-MAR-1992; 92US-0852625.  
 XX  
 XX (WISN) WISNIESKI B J.  
 XX  
 XX WISNIESKI BJ;  
 XX  
 XX WPI: 1993-303462/38.  
 XX  
 XX  
 XX Producing modified tumour necrosis factor alpha - useful for  
 XX regulating tumour necrosis factor channel activity e.g.  
 XX increasing permeability  
 XX  
 XX Claim 6; Page 37-38 and 51-53; 72pp; English.  
 XX  
 XX The sequence of rat TNF-alpha disclosed in Agric.Biol.Chem 53:  
 XX 1733-1736 (1989) is given in the specification. A modified version  
 XX of this sequence is claimed in which at least one of the channel  
 XX residues is substituted (see Features Table). The resulting  
 XX TNF-alpha mutein has modified channel activity compared to wild-type.  
 XX SQ Sequence 156 AA;  
 Query Match 77.8%; Score 84; DB 14; Length 156;  
 Best Local Similarity 100.0%; Pred. No. 0.00014;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 PKDPEGAELKPMY 16  
 DB 101 PKDPEGAELKPMY 114  
 RESULT 11  
 AAR41862  
 ID AAR41862 standard; protein; 156 AA.  
 AC AAR41862;  
 XX  
 XX 29-MAR-1994 (first entry)  
 DE Murine TNF-alpha mutein with modified channel-forming activity.  
 XX Tumour Necrosis Factor alpha; TNF-a; target membrane permeability;  
 KW TNF trimer; ion channel; mutein.  
 XX  
 OS Mus musculus.  
 XX  
 FH Key  
 FT Misc-difference 11 Location/Qualifiers  
 FT /label= Glu, Arg, Cys, Asp, Gln, Asn, Ser, Thr  
 FT or His



CC Inducing capacity; reduced metastasis promoting activity; and/or  
 CC increased half-life. Mutens of the human TNF (given in AAR60243)  
 CC were also produced.  
 XX  
 SQ Sequence 156 AA;

Query Match 77.8%; Score 84; DB 15; Length 156;  
 Best Local Similarity 100.0%; Pred. No. 0.00014;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 PKDTPGAELEKPMY 16  
 DB 101 PKDTPGAELEKPMY 114  
 |||||

## RESULT 13

AAP60527  
 ID AAR60527 standard; Protein; 157 AA.

AC AAP60527;

DT 07-AUG-1991 (first entry)

DE Sequence of tumour necrosis factor (TNF).

KW Anticancer agent; antitumour; antimetastatic; tumour necrosis factor.

PN W08603751-A.

PD 03-JUL-1986.

PF 19-DEC-1985; 85WO-EP00721.

PR 09-OCT-1985; 85US-0785847.

PR 21-DEC-1984; 84US-0684595.

PR 09-OCT-1986; 86WO-US02133.

XX (BIOJ) BIOGEN NV.

PA (FIER) FIERIS W C.

PA (ALIE) ALLET B.

PA (BIOG) BIOGEN INC.

PI Fiers WC, Franssen LM, Tavernier JHL, Marmenout ALM;

PI Vanderheyden J, Allet B, Washima EH;

DR WPI: 1986-182891/28.

DR N-PSDB; AAN60439.

XX Mammalian tumour necrosis factors - produced by culturing

PT pro-karyotic hosts transformed with recombinant DNA

PS Claim 12; Page 67; 93pp; English.

CC TNF-like polypeptides and compans. are produced by the fermentation

CC of host cells transformed with at least one DNA sequence which codes

CC for a mammalian TNF-like polypeptide operatively linked to an

CC expression control sequence in the transformed host.

XX Sequence 157 AA;

SO Query Match 77.8%; Score 84; DB 7; Length 157;

Best Local Similarity 100.0%; Pred. No. 0.00014;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 PKDTPGAELEKPMY 16

DB 102 PKDTPGAELEKPMY 115

|||||

RESULT 14

AAR38077

ID AAR38077 standard; protein; 157 AA.

XX

AC AAR38077;

XX 14-OCT-1993 (first entry)

DE Non-human TNF-alpha.

KW Withdrawal symptom; tumour necrosis factor; narcotic; nicotine;

XX morphine; thymosin; alcohol.

XX Synthetic.

XX Key

FT MISC-difference 73

XX Location/Qualifiers

PN JP05117161-A.

XX 14-MAY-1993.

PD 23-OCT-1991; 91JP-0337489.

PF 23-OCT-1991; 91JP-0337489.

PR 23-OCT-1991; 91JP-0337489.

XX (MIZU) MIZUNO D.

PA (SOMA/) SOMA G.

XX WPI: 1993-191442/24.

DR Drugs for treating alcohol, morphine narcotics or nicotine

XX withdrawal symptoms - contg. tumour necrosis factor-alpha.

PT thymosin tumour necrosis factor fused cpd. or murine tumour

PT necrosis factor-alpha prep. from macrophage of human or animal

XX Disclosure; Page 2-3; 5pp; Japanese.

XX Drugs acting on withdrawal symptoms contain TNF, esp. TNF-alpha

CC (AAR38069 and AAR38077), rTNF-S-AM1 (AAR38070), rTNF-S-AM2 (AAR38071),

CC thymosin-beta4-TNF fused cpd. (AAR38072-76).

CC The drugs are effective in treatment of withdrawal symptoms caused

CC by habitual use of alcohol, morphine narcotics or nicotine in humans

CC or animals (e.g. swine, dog, cat, chicken). The drugs may be

CC administered as TNF at a dose of 10ng-10mg orally or 5ng-1mg i.v.

CC or 50ng-50mg percutaneously a day for a human adult. In animals,

CC the drugs may be administered according to the human dosage (1/60

CC per kg body wt.).

XX Sequence 157 AA;

SO Query Match 77.8%; Score 84; DB 14; Length 157;

Best Local Similarity 100.0%; Pred. No. 0.00014;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 PKDTPGAELEKPMY 16

DB 102 PKDTPGAELEKPMY 115

|||||

RESULT 15

AAP70558

ID AAP70558 standard; protein; 170 AA.

XX AAP70558;

AC 26-FEB-1991 (first entry)

DT Tumor necrosis factor.

DE TNF; antitumor.

XX JP62135493-A.

XX 18-JUN-1987.

XX

PF 06-DEC-1985; 85JP-0275392.  
XX  
PR 06-DEC-1985; 85JP-0275392.  
XX  
PA (TANA ) TANABE SEIYAKU KK.  
XX  
DR WPI; 1987-209318/30.  
DR N-PSDB; AAN70891.  
XX  
PT Anticancer factor - expressed by specified amino acid sequence.  
XX  
PS Disclosure; Page 12; 12pp; Japanese.  
XX  
CC The sequence encodes tumor necrosis factor which is an antitumor  
CC agent and a lymphokine. This sequence is the same as that in  
CC AAF70557 but has 16 extra amino acids at the N-terminal.  
XX  
SQ Sequence 170 AA;

Query Match 77.8%; Score 84; DB 8; Length 170;  
Best Local Similarity 100.0%; Pred. No. 0.00015;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PKDPEGAELKPMY 16  
|||||  
Db 115 PKDPEGAELKPMY 128

Search completed: April 4, 2003, 08:39:55  
Job time : 31.5323 secs

GenCore version 5.1.4.p5.4578  
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OM protein - protein search, using sw model

Run on: April 4, 2003, 08:37:36 ; Search time 12.3387 Seconds  
(Without alignments) 132.452 Million cell updates/sec

Title: US-09-779-703-5

Sequence: 1 CGPKDTPGCAELKPMYC 17

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_73:\*

1: p1r1:\*

2: p1r2:\*

3: p1r3:\*

4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	84	77.8	235	1 QWMSN	tumor necrosis fac
2	84	77.8	235	2 JUD0029	tumor necrosis fac
3	77	71.3	235	2 I54490	tumor necrosis fac
4	65	60.2	232	1 S12606	tumor necrosis fac
5	65	60.2	233	1 QWUN	tumor necrosis fac
6	65	60.2	233	1 S22052	tumor necrosis fac
7	65	60.2	233	2 S11688	tumor necrosis fac
8	57	52.8	185	2 S52715	tumor necrosis fac
9	57	52.8	233	1 S24642	tumor necrosis fac
10	55	50.9	234	1 JH0529	tumor necrosis fac
11	51	47.2	234	1 J01344	tumor necrosis fac
12	50	46.3	289	2 AH0060	tumor necrosis fac
13	49	45.4	407	2 T36669	bis(5'-nucleosyl)-
14	48.5	44.9	193	2 S06192	probable transpos
15	48.5	44.9	193	2 S06192	tumor necrosis fac
16	48	44.4	1649	2 D69373	immunogenic protei
17	47	43.5	1236	1 C86822	hypothetical prote
18	47	43.5	1236	1 VHMVME	structural polyp
19	47	43.5	1236	1 VHMVME	structural polyp
20	47	43.5	1241	1 VHMVME	structural polyp
21	47	43.5	1242	2 S26373	genome polyp
22	47	43.5	1242	2 S72350	structural polyp
23	46.5	43.1	543	2 A56605	structural polyp
24	46	42.6	501	2 G96570	hypothetical prote
25	46	42.6	711	2 B84748	similar to M10 pro
26	45	41.7	258	2 F75440	Methylmalonyl-CoA
27	45	41.7	258	2 S75950	hypothetical prote
28	45	41.7	469	2 T48783	related to SGT1 pr
29	45	41.7	593	1 S52984	catechol oxidase (
			684	1 TVHUSN	transforming prote

30	45	41.7	713	2 G98286	methylmalonyl-CoA
31	45	41.7	713	2 A82997	methylmalonyl-CoA
32	45	41.7	759	2 T11631	Na+/H+-exchanging
33	44.5	41.2	747	2 T23607	hypothetical prote
34	44	40.7	198	2 I46002	CAMP beta chain -
35	44	40.7	494	2 AD3255	1-sorbose dehydrog
36	44	40.7	557	2 H96590	hypothetical prote
37	44	40.7	649	2 T46500	hypothetical prote
38	43.5	40.3	275	2 AH0335	probable penicilli
39	43.5	40.3	322	2 C70344	hypothetical prote
40	43.5	40.3	733	2 F82965	hypothetical prote
41	43	39.8	142	2 A47169	hypothetical prote
42	43	39.8	237	2 T25152	membrane-bound mul
43	43	39.8	259	2 R42379	hypothetical prote
44	43	39.8	269	2 AF1737	bis(5'-nucleosyl)-
45	43	39.8	748	1 S08680	amino acid ABC tra
					methylmalonyl-CoA

## ALIGNMENTS

RESULT 1  
QWMSN  
tumor necrosis factor alpha precursor - mouse  
N:Alternate names: cachectin; TNF alpha  
C:Species: Mus musculus (house mouse)  
C:Date: 31-Mar-1988 #sequence, revision 31-Mar-1988 #text, change 04-Feb-2000  
C:Accession: A22908; S03791; A27303; A25164; A23127; A34251; I59058; A36696  
R:Shiral, T.; Shimizu, N.; Shiojiri, S.; Horiguchi, S.; Ito, H.  
DNA 7, 193-201, 1988  
A:Title: Cloning and expression in Escherichia coli of the gene for mouse tumor ne  
A:Reference number: A22908; MUID:88224564; PMID:2836146  
A:Accession: A22908  
A:Molecule type: DNA  
A:Residues: 1-235 <SHI>  
A:Cross-references: GB:M20155  
R:Shakhov, A.N.; Nedospasov, S.A.  
Bloorg. Khim. 13, 701-705, 1987  
A:Title: Molecular cloning of the genes coding for tumor necrosis factors: complet  
A:Reference number: S03791; MUID:87298639; PMID:3040015  
A:Accession: S03791  
A:Molecule type: DNA  
A:Residues: 1-235 <SHA>  
A:Cross-references: GB:M38296; NID:q202086; PIDN:AAA0459.1; PID:q202087  
R:Semon, D.; Haylick, J.S.; Bringham, T.S.; Palladino, M.A.; Goeddel, D.V.  
Nucleic Acids Res. 15, 9083-9084, 1987  
A:Title: Nucleotide sequence of the murine TNF locus, including the TNF-alpha (tunc  
A:Reference number: A93679; MUID:88067722; PMID:3684584  
A:Accession: A27303  
A:Molecule type: DNA  
A:Residues: 1-235 <SEM>  
A:Cross-references: GB:Y00467; NID:q54830; PIDN:CAA68530.1; PID:q54832  
R:Penick, D.; Haylick, J.S.; Bringham, T.S.; Palladino, M.A.; Goeddel, D.V.  
Proc. Natl. Acad. Sci. U.S.A. 82, 6060-6064, 1985  
A:Title: Cloning and expression in Escherichia coli of the cDNA for murine tumor ne  
A:Reference number: A25164; MUID:85298296; PMID:3698078  
A:Accession: A25164  
A:Molecule type: mRNA  
A:Residues: 1-235 <PEN>  
A:Cross-references: GB:M11731; NID:q202084; PIDN:AAA0458.1; PID:q202085  
R:Fransen, L.; Muller, R.; Marmont, A.; Tavernier, J.; van der Heyden, J.; Kawash  
Nucleic Acids Res. 13, 4417-4429, 1985  
A:Title: Molecular cloning of mouse tumour necrosis factor cDNA and its eukaryotic  
A:Reference number: A23127; MUID:85242112; PMID:2989794  
A:Accession: A23127  
A:Molecule type: mRNA  
A:Residues: 1-235 <FRA>  
A:Cross-references: GB:X02611; NID:q54844; PIDN:CAA26457.1; PID:q54845  
R:Cseh, K.; Beutler, B.  
J. Biol. Chem. 264, 16256-16260, 1989  
A:Title: Alternative cleavage of the cachectin/tumor necrosis factor propeptide res  
A:Reference number: A34251; MUID:89380231; PMID:2777790



A:Accession: A34251  
A:Molecule type: Protein  
A:Residues: 70-87 <CSE>  
R:Caput, D.; Beutler, B.; Hartog, K.; Thayer, R.; Brown-Shimer, S.L.; Cerami, A.  
Proc. Natl. Acad. Sci. U.S.A. 83, 1670-1674, 1986  
A:Title: Identification of a common nucleotide sequence in the 3'-untranslated region of  
A:Reference number: 159058; MUID:86149365; PMID:2419912  
A:Accession: 159058  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-230, 'R', 232-235 <RES>  
A:Cross-references: GB:M13049; NID:g202082; PIDN:AAA40457.1; PID:g202083  
R:Sherry, B.; Jue, D.M.; Zentella, A.; Cerami, A.  
Biochem. Biophys. Res. Commun. 173, 1072-1078, 1990  
A:Title: Characterization of high molecular weight glycosylated forms of murine tumor ne  
A:Reference number: A36696; MUID:91097531; PMID:2268312  
A:Accession: A36696  
A:Molecule type: Protein  
A:Residues: 80-85, 'X', 87-99 <SHE>  
C:Genetics:  
A:Introns: 62/3; 81/1; 97/1  
A:Note: the first intron occurs in the 5'-untranslated region  
C:Superfamily: tumor necrosis factor  
C:Keywords: cytokine; cytotoxin; glycoprotein; lipoprotein; lymphokine; macrophage; memb  
F:80-235/Product: tumor necrosis factor #status experimental <MAT>  
F:20/Binding site: myristate (Lys) (covalent) #status predicted  
F:84/Binding site: carbohydrate (Ser) (covalent) #status predicted  
F:86/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F:148-179/Disulfide bonds: #status predicted

Query Match 77.8%; Score 84; DB 1; Length 235;  
Best Local Similarity 100.0%; Pred. No. 2,4e-05;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 PKDPEGAELKPMY 16  
|||||  
Db 180 PKDPEGAELKPMY 193

## RESULT 2

tumor necrosis factor alpha precursor - rat  
N:Alternate names: cachectin; TNF alpha  
C:Species: Rattus norvegicus (Norway rat)  
C>Date: 07-Jun-1990 #sequence, revision 07-Jun-1990 #text, change 04-Feb-2000  
C:Accession: J00029; J00866; S21674  
R:Shiral, T.; Shimizu, N.; Horiguchi, S.; Ito, H.  
Agric. Biol. Chem. 53, 1733-1736, 1989  
A:Title: Cloning and expression in Escherichia coli of the gene for rat tumor necrosis f  
A:Reference number: J00029  
A:Accession: J00029  
A:Molecule type: DNA  
A:Residues: 1-235 <SHI>  
R:Kwon, J.; Chung, I.Y.; Benveniste, E.N.  
Gene 132, 227-236, 1993  
A:Title: Cloning and sequence analysis of the rat tumor necrosis factor-encoding genes.  
A:Reference number: J00866; MUID:94040766; PMID:8224868  
A:Accession: J00868  
A:Molecule type: DNA  
A:Residues: 1-235 <KMO>  
A:Cross-references: GB:I00981; NID:g205253; PIDN:AAA16275.1; PID:g205254  
R:Estler, H.C.; Grewe, M.; Gausling, R.; Pavlovic, M.; Decker, K.  
Biol. Chem. Hoppe-Seyler 373, 271-281, 1992  
A:Title: Rat tumor necrosis factor-alpha. Transcription in rat Kupffer cells and in vitr  
A:Reference number: S21674; MUID:92329007; PMID:1627266  
A:Accession: S21674  
A:Molecule type: mRNA  
A:Residues: 1-38, 'P', 40-162, 'T', 164-201, 'S', 203-225 <EST>  
A:Cross-references: GB:X6539; GB:S40199; NID:g395369; PIDN:CAA7146.1; PID:g395370  
C:Comment: Tumor necrosis factor is secreted by macrophages in response to endotoxin and  
C:Genetics:  
A:Gene: TNF-alpha  
A:Introns: 62/3; 81/1; 97/1

C:Superfamily: tumor necrosis factor  
C:Keywords: cytokine; cytotoxin; glycoprotein; lipoprotein; lymphokine; macrophage; m  
F:80-235/Product: tumor necrosis factor #status predicted <MAT>  
F:19-20/Binding site: myristate (Lys) (covalent) #status predicted  
F:84/Binding site: carbohydrate (Ser) (covalent) #status predicted  
F:86/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F:148-179/Disulfide bonds: #status predicted

Query Match 77.8%; Score 84; DB 2; Length 235;  
Best Local Similarity 100.0%; Pred. No. 2,4e-05;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 PKDPEGAELKPMY 16  
|||||  
Db 180 PKDPEGAELKPMY 193

## RESULT 3

tumor necrosis factor alpha precursor - white-footed mouse  
C:Species: Peromyscus leucopus (white-footed mouse)  
C>Date: 02-Aug-1996 #sequence, revision 02-Aug-1996 #text, change 04-Feb-2000  
C:Accession: 154490  
R:Crew, M.D.; Filipowsky, M.E.  
Immunogenetics 35, 351-353, 1992  
A:Title: Sequence of the tumor necrosis factor/cachectin (TNF) gene from Peromyscus 1  
A:Reference number: 154490; MUID:92218012; PMID:1348497  
A:Accession: 154490  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-235 <RES>  
A:Cross-references: GB:M59233; NID:g202506; PIDN:AAA40596.1; PID:g202507  
C:Genetics:  
A:Gene: P1TNF  
A:Introns: 62/3; 81/1; 97/1  
C:Superfamily: tumor necrosis factor  
C:Keywords: glycoprotein; lipoprotein; myristylation  
F:19-20/Binding site: myristate (Lys) (covalent) #status predicted  
F:84/Binding site: carbohydrate (Ser) (covalent) #status predicted

Query Match 71.3%; Score 77; DB 2; Length 235;  
Best Local Similarity 85.7%; Pred. No. 0.00028;  
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 3 PKDPEGAELKPMY 16  
|||||  
Db 180 PKDPEGAELKPMY 193

## RESULT 4

tumor necrosis factor alpha precursor - pig  
C:Species: Sus scrofa domestica (domestic pig)  
C>Date: 10-Sep-1999 #sequence, revision 10-Sep-1999 #text, change 04-Feb-2000  
C:Accession: S12606; S17290; S18965; I46659  
R:Drews, R.T.; Coffee, B.W.; Prestwood, A.K.; McGraw, R.A.  
Nucleic Acids Res. 18, 5564, 1990  
A:Title: Gene sequence of porcine tumor necrosis factor alpha.  
A:Reference number: S12606; MUID:91016861; PMID:2216741  
A:Accession: S12606  
A:Molecule type: DNA  
A:Residues: 1-232 <DRE>  
A:Cross-references: EMBL:X54001; NID:g2135; PIDN:CAA37949.1; PID:g2136  
R:Kühnert, P.; Wüethrich, C.; Peterhans, E.; Pauli, U.  
Gene 102, 171-178, 1991  
A:Title: The porcine tumor necrosis factor-encoding genes: sequence and comparative a  
A:Reference number: S17289; MUID:91340150; PMID:1874444  
A:Accession: S17290  
A:Molecule type: DNA  
A:Residues: 1-232 <KUH>  
A:Cross-references: EMBL:X54859; NID:g2132; PIDN:CAA38639.1; PID:g2134  
A:Note: the authors translated the codon GAG for residue 202 as Gly  
R:Choi, C.S.; Mollitor, T.W.; Lin, G.F.; Murtough, M.P.

Submitted to the EMBL Data Library, January 1991

A:Description: Complete nucleotide sequence of a cDNA encoding porcine tumor necrosis factor

A:Reference number: S18965

A:Accession: S18965

A:Molecule type: mRNA

A:Residues: 1-232 <CHO>

A:Cross-references: EMBL:X57321; NID:g2137; PIDN:CAA0591.1; PID:g2138

R:Pauli, U.; Beutler, B.; Peterhans, E.

Gene 81, 185-191, 1989

A:Title: Porcine tumor necrosis factor alpha: Cloning with the polymerase chain reaction

A:Reference number: 146659; MUID:90034181; PMID:2478420

A:Accession: 146659

A:Molecule type: translated from GB/EMBL/DBJ

A:Residues: 44-232 <PAU>

A:Cross-references: GB:M29079; NID:g164694; PIDN:AAA31128.1; PID:g164695

C:Genetics:

A:Introns: 62/3; 78/1; 93/1

C:Superfamily: tumor necrosis factor

C:Keywords: cytokine; cytotoxic; glycoprotein; lipoprotein; lymphokine; macrophage; myr

F:1-77/Domain: propeptide #status predicted <PRO>

F:78-232/Product: tumor necrosis factor alpha #status predicted <MAT>

F:19,20/Binding site: myristate (lys) (covalent) #status predicted

F:81/Binding site: carbohydrate (Ser) (covalent) #status predicted

F:144-176/Disulfide bonds: #status predicted

Query Match

Best Local Similarity 60.2%; Score 65; DB 1; Length 232;

Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

DB 178 RETPGEAKPMY 190

OMHUN

tumor necrosis factor alpha precursor [validated] - human

N:Alternate names: cachectin; TNFA

C:Species: Homo sapiens (man)

C>Date: 28-Aug-1985 #sequence revision 28-Aug-1985 #text change 08-Dec-2000

R:Nedwin, G.E.; Naylor, S.L.; Sakaguchi, A.Y.; Smith, D.; Jarrett-Nedwin, J.; Pennica, D.

Nucleic Acids Res. 13, 6361-6373, 1985

A:Title: Human lymphokine and tumor necrosis factor genes: structure, homology and chro

A:Reference number: A93585; MUID:86016093; PMID:2995927

A:Accession: A93585

A:Molecule type: DNA

A:Residues: 1-233 <MED>

A:Cross-references: GB:X02910; GB:X02159; NID:g37209; PIDN:CAA26669.1; PID:g37210

R:Rittis, F.J.M.; Bouquelarel, L.; Prieur, S.; Caterina, D.; Primas, G.; Perrot, V.; Jurke

Nature Genet. 3, 137-145, 1993

A:Title: Dense Alu clustering and a potential new member of the NF-kappaB family within a

A:Reference number: S36152; MUID:93272029; PMID:8499947

A:Accession: S36152

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-233 <IRI>

A:Cross-references: EMBL:Z15026; NID:g37211; PIDN:CAA78745.1; PID:g37212

R:Pennica, D.; Nedwin, G.E.; Hayflick, J.S.; Seeburg, P.H.; Derynck, R.; Palladino, M.A.

Nature 312, 724-729, 1984

A:Title: Human tumor necrosis factor: precursor structure, expression and homology to

A:Reference number: A93351; MUID:85086244; PMID:6392892

A:Accession: A93351

A:Molecule type: mRNA

A:Residues: 1-233 <PEN>

A:Cross-references: GB:X02910; GB:X02159; NID:g37209; PIDN:CAA26669.1; PID:g37210

R:Wang, A.M.; Creasey, A.A.; Ladner, M.B.; Lin, L.S.; Strickler, J.; Van Arsdel, J.N.;

Science 228, 149-154, 1985

A:Title: Molecular cloning of the complementary DNA for human tumor necrosis factor.

A:Reference number: A44189; MUID:85142190; PMID:3856324

A:Accession: A44189

A:Molecule type: mRNA

A:Residues: 1-62, 'S', '64-233 <MAN>

A:Cross-references: GB:M10988; NID:g339737; PIDN:AAA61198.1; PID:g339738

R:Fukuda, S.; Ando, S.; Sanou, O.; Tanai, M.; Fujii, M.; Masaki, N.; Nakamura, K.

Lymphokine Res. 7, 175-185, 1988

A:Title: Simultaneous production of natural human tumor necrosis factor-alpha, -bet

A:Reference number: A61478; MUID:88301617; PMID:2841543

A:Accession: B61478

A:Molecule type: protein

A:Residues: 83-102, 109-119, 121-128, 'X', 130-131, 142-144, 'X', 146, 'XXX', 150-152, 159-1

R:Marmenout, A.; Fransen, L.; Tavernier, J.; Van Der Heyden, J.; Tizad, R.; Kawash

Eur. J. Biochem. 152, 515-522, 1985

A:Title: Molecular cloning and expression of human tumor necrosis factor and compar

A:Reference number: 153311; MUID:86030296; PMID:3932069

A:Accession: 153311

A:Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-233 <MAN>

A:Cross-references: GB:M26331; NID:g339763; PIDN:AAA36758.1; PID:g339764

R:Experimental source: U-937 cells

R:Takakura-Yamamoto, R.; Yamamoto, S.; Fukuda, S.; Kurimoto, M.

Eur. J. Biochem. 235, 431-437, 1996

A:Title: O-Glycosylated species of natural human tumor necrosis factor-alpha.

A:Reference number: 562610; MUID:96202967; PMID:8631363

A:Accession: 562610

A:Molecule type: protein

A:Residues: 77-99 <TRK>

R:D'Alfonso, S.; Richiardi, P.M.

Immunogenetics 39, 150-154, 1994

A:Title: A polymorphic variation in a putative regulation box of the TNFA promoter 1

A:Reference number: 154522; MUID:94102809; PMID:7903959

A:Accession: 154522

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-8 <DAL>

A:Cross-references: GB:S68530; NID:g544751

R:Stevenson, F.T.; Burssten, S.L.; Locksley, R.M.; Lovett, D.H.

J. Exp. Med. 176, 1053-1062, 1992

A:Title: Myristyl acylation of the tumor necrosis factor alpha precursor on specific

A:Reference number: A59163; MUID:93018820; PMID:1402651

A:Accession: A59163

A:Contents: annotation; identification of myristylated lysines

J. Biol. Chem. 260, 2345-2354, 1985

A:Title: Human tumor necrosis factor. Production, purification, and characterization

A:Reference number: A92511; MUID:85130974; PMID:3871770

A:Accession: A92511

A:Contents: annotation; disulfide bond

C:Comment: Secreted from mitogen-activated macrophages within 4-24 hours after induc

tion; TNF-alpha and -beta (lymphotoxin) are the products of different genes clo

ut are produced by different cell types and have different induction kinetics.

A:Gene: GDB:TNF; TNFA

A:Map position: 6p21.3-6p21.3

A:Introns: 62/3; 78/1; 94/1

C:Complex: homotrimer

C:Superfamily: tumor necrosis factor

C:Keywords: cytokine; cytotoxic; glycoprotein; homotrimer; lipoprotein; lymphokine; m

F:1-76/Domain: propeptide #status predicted <PRO>

F:77-233/Product: tumor necrosis factor #status predicted <MAT>

F:19,20/Binding site: myristate (lys) (covalent) #status experimental

F:81/Binding site: carbohydrate (Ser) (covalent) (partial) #status experimental

F:145-177/Disulfide bonds: #status experimental

Query Match

Best Local Similarity 60.2%; Score 65; DB 1; Length 233;

Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

DB 179 RETPGEAKPMY 191

## RESULT 6

S22052 tumor necrosis factor alpha precursor - baboon

C:Species: Papio sp. (baboon)

C&gt;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 04-Feb-2000

C:Accession: S22052

R:Sanjanwala, M.; Edwards, A.

submitted to the EMBL Data Library, September 1991

A:Description: Baboon Tumor Necrosis Factor Derived from Sequences of Genomic DNA.

A:Reference number: S22052

A:Accession: S22052

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-233 &lt;SAN&gt;

A:Cross-references: EMBL:X62141; NID:g38159; PIDN:CAA44068.1; PID:g38160

C:Genetics:

A:Introns: 62/3; 78/1; 94/1

C:Superfamily: tumor necrosis factor

C:Keywords: glycoprotein; lipoprotein; myristylation; transmembrane protein

F:19/20/Binding site: myristate (Lys) (covalent) #status predicted

F:81/Binding site: carbohydrate (Ser) (covalent) #status predicted

F:145-177/Disulfide bonds: #status predicted

Query Match 60.2%; Score 65; DB 1; Length 233;

Best Local Similarity 76.9%; Pred. No. 0.019;

Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 KDPGGAELKPMY 16

Db 179 RETPEGAELKPMY 191

## RESULT 7

S11688 tumor necrosis factor alpha precursor - cat

C:Species: Felis silvestris catus (domestic cat)

C&gt;Date: 21-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 04-Feb-2000

C:Accession: S11688

R:McGraw, R.A.; Coffee, B.W.; Otto, C.M.; Drews, R.T.; Rawlings, C.A.

Nucleic Acids Res. 18, 5563, 1990

A:Title: Gene sequence of feline tumor necrosis factor alpha.

A:Reference number: S11688; MUID:91016860; PMID:2216740

A:Accession: S11688

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-233 &lt;MCG&gt;

A:Cross-references: EMBL:X54000; NID:g1084; PIDN:CAA37948.1; PID:g295777

C:Genetics: 62/3; 78/1; 94/1

C:Superfamily: tumor necrosis factor

C:Keywords: glycoprotein; lipoprotein; myristylation; transmembrane protein

F:19/20/Binding site: myristate (Lys) (covalent) #status predicted

F:81/Binding site: carbohydrate (Ser) (covalent) #status predicted

F:145-177/Disulfide bonds: #status predicted

Query Match 60.2%; Score 65; DB 2; Length 233;

Best Local Similarity 76.9%; Pred. No. 0.019;

Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 KDPGGAELKPMY 16

Db 179 RETPEGAELKPMY 191

## RESULT 8

S52715

tumor necrosis factor alpha precursor - bovine (fragment)

C:Species: Bos primigenius taurus (cattle)

C&gt;Date: 19-May-1995 #sequence\_revision 21-Jul-1995 #text\_change 04-Feb-2000

C:Accession: S52715

R:Wenters, B.; Gaidulis, L.

submitted to the EMBL Data Library, March 1995

A:Description: Cloning and sequence analysis of cDNAs encoding bovine CD40 ligand and

A:Reference number: S52715

A:Accession: S52715

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-185 &lt;MER&gt;

A:Cross-references: EMBL:Z48808; NID:g755701; PIDN:CAA88743.1; PID:g755702

C:Superfamily: tumor necrosis factor

C:Keywords: glycoprotein

F:33/Binding site: carbohydrate (Ser) (covalent) #status predicted

F:97-129/Disulfide bonds: #status predicted

Query Match 52.8%; Score 57; DB 2; Length 185;

Best Local Similarity 69.2%; Pred. No. 0.26;

Matches 9; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 4 KDPGGAELKPMY 16

Db 131 RETPEGAELKPMY 143

## RESULT 9

S24642 tumor necrosis factor alpha precursor - bovine

C:Species: Bos primigenius taurus (cattle)

C&gt;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 04-Feb-2000

C:Accession: S24642

R:Cludts, I.; Cleuter, Y.; Kettmann, R.; Burny, A.; Droogmans, L.

Cytokine 5, 336-341, 1993

A:Title: Cloning and characterization of the tandemly arranged bovine lymphotoxin and

A:Reference number: S24642; MUID:94083525; PMID:8260599

A:Accession: S24642

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-233 &lt;CLD&gt;

A:Cross-references: EMBL:Z14137; NID:g796; PIDN:CAA78511.1; PID:g798

C:Genetics:

A:Gene: TNFA

A:Introns: 62/3; 78/1; 94/1

C:Superfamily: tumor necrosis factor

C:Keywords: glycoprotein; lipoprotein; myristylation; transmembrane protein

F:81/Binding site: myristate (Lys) (covalent) #status predicted

F:81/Binding site: carbohydrate (Ser) (covalent) #status predicted

F:145-177/Disulfide bonds: #status predicted

Query Match 52.8%; Score 57; DB 1; Length 233;

Best Local Similarity 69.2%; Pred. No. 0.33;

Matches 9; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 4 KDPGGAELKPMY 16

Db 179 RETPEGAELKPMY 191

## RESULT 10

JH0529 tumor necrosis factor alpha precursor - sheep

N:Alternate names: cachectin; TNF alpha

C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)

C&gt;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 04-Feb-2000

C:Accession: JH0529; S48118; S13114; S20661

R:Green, I.R.; Sargan, D.R.

Gene 109, 203-210, 1991

A:Title: Sequence of the cDNA encoding ovine tumor necrosis factor-alpha: problems w/

A:Reference number: JH0529; MUID:92112044; PMID:1765267

A:Accession: JH0529

A:Molecule type: mRNA

A:Residues: 1-234 &lt;GRE&gt;

A:Cross-references: EMBL:X55152; NID:g1405; PIDN:CAA38952.1; PID:g1406

A:Experimental source: alveolar macrophage

R:Nash, A.D.; Barham, G.J.; Brandon, M.R.; Andrews, A.E.

Immunol. Cell Biol. 69, 273-283, 1991

A:Title: Molecular cloning, expression and characterization of ovine TNF-alpha.

A:Reference number: S48118; MUID:92155784; PMID:1786996  
 A:Accession: S48118  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-234 <MAS>  
 A:Cross-references: EMBL:X56756; NID:g297806; PIDN:CAA40076.1; PID:g297807  
 R:Young, A.J.; Hay, J.B.; Chan, J.Y.C.  
 Nucleic Acids Res. 18, 6723, 1990  
 A:Title: Primary structure of ovine tumor necrosis factor alpha cDNA.  
 A:Reference number: S13114; MUID:91067496; PMID:2251151  
 A:Accession: S13114  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-62,64-234 <YOUN>  
 A:Cross-references: EMBL:X55966; NID:g1403; PIDN:CAA39437.1; PID:g1404  
 A:Note: comparison with the introns of homologous sequences suggest that this is probably  
 C:Superfamily: tumor necrosis factor  
 C:Keywords: alternative splicing; cytokine; cytotoxin; glycoprotein; lipoprotein; lymph  
 F:1-77/Domain: propeptide #status predicted <PRO>  
 F:78-234/Product: tumor necrosis factor alpha #status predicted <TUM>  
 F:20/Binding site: myristate (Lys) (covalent) #status predicted  
 F:82/Binding site: carbohydrate (Ser) (covalent) #status predicted  
 F:96/Binding site: carbohydrate (Asp) (covalent) #status predicted  
 F:146-178/Disulfide bonds: #status predicted

Query Match 50.9%; Score 55; DB 1; Length 234;  
 Best Local Similarity 69.2%; Pred. No. 0.66;  
 Matches 9; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 4 KDTPEGAELEKPMY 16  
 Db 180 RETLEGAELEKPMY 192

RESULT 11  
 J01344  
 tumor necrosis factor alpha precursor - horse

N:Alternate names: cachectin; TNF alpha  
 C:Species: Equus caballus (domestic horse)  
 C>Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 04-Feb-2000  
 C:Accession: J01344  
 R:Su, X.; Morris, D.D.; McGraw, R.A.  
 Gene 107, 319-321, 1991  
 A:Title: Cloning and characterization of gene TNF alpha encoding equine tumor necrosis f  
 A:Reference number: J01344; MUID:92084125; PMID:1748301  
 A:Accession: J01344  
 A:Molecule type: DNA  
 A:Residues: 1-234 <SUXX>  
 A:Cross-references: GB:M64087; NID:g164244; PIDN:AAA30959.1; PID:g164245  
 C:Comment: This protein is an important proximal mediator of endotoxemia.  
 C:Genetics:  
 A:Gene: TNF-alpha  
 A:Introns: 62/3; 79/1; 95/1  
 C:Superfamily: tumor necrosis factor  
 C:Keywords: cytokine; cytotoxin; glycoprotein; lipoprotein; lymphokine; macrophage; men  
 F:78-234/Product: tumor necrosis factor alpha #status predicted <TUM>  
 F:19,20/Binding site: myristate (Lys) (covalent) #status predicted  
 F:82/Binding site: carbohydrate (Ser) (covalent) #status predicted  
 F:146-178/Disulfide bonds: #status predicted

Query Match 47.2%; Score 51; DB 1; Length 234;  
 Best Local Similarity 66.7%; Pred. No. 2.7;  
 Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 5 DTPEGAELKPMY 16  
 Db 181 ESPEGAELKPMY 192

RESULT 12  
 AH0060  
 bis(5'-nucleosyl)-tetrachosphatase (symmetrical) (EC 3.6.1.41) [imported] - Yersinia pes  
 C:Species: Yersinia pestis

C>Date: 02-Nov-2001 #sequence\_revision 02-Nov-2001 #text\_change 11-Jan-2002  
 C:Accession: AH0060  
 R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice  
 deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan  
 11, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Bar  
 Nature 413, 523-527, 2001  
 A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.  
 A:Reference number: AB0001; MUID:21470413; PMID:11586360  
 A:Accession: AH0060  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-289 <KUR>  
 A:Cross-references: GB:AL590842; PIDN:CAC89347.1; PID:g15978584; GSPDB:GN00175  
 C:Genetics:  
 A:Gene: ap4H  
 C:Superfamily: bis(5'-nucleosyl)-tetrachosphatase (symmetrical); phosphoesterase c  
 C:Keywords: hydrolase

Query Match 46.3%; Score 50; DB 2; Length 289;  
 Best Local Similarity 66.7%; Pred. No. 4.8;  
 Matches 10; Conservative 1; Mismatches 2; Indels 2; Gaps 1;

OY 4 KDTPEG--AELEKPMY 16  
 Db 197 KDTPEANAPLEKPMY 211

RESULT 13  
 T36649  
 probable transposase - Streptomyces coelicolor  
 C:Species: Streptomyces coelicolor  
 C>Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 21-Jan-2000  
 C:Accession: T36649  
 R:Oliver, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M  
 submitted to the EMBL Data Library, June 1999  
 A:Reference number: Z21610  
 A:Accession: T36649  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-407 <OLD>  
 A:Cross-references: EMBL:AL078610; PIDN:CAB44417.1; GSPDB:GN00070; SCOEDB:SCH35.10  
 A:Experimental source: strain A3(2)  
 C:Genetics:  
 A:Gene: SCOEDB:SCH35.10  
 C:Superfamily: hypothetical protein b1432

Query Match 45.4%; Score 49; DB 2; Length 407;  
 Best Local Similarity 41.2%; Pred. No. 9.5;  
 Matches 7; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

OY 1 CGPKTPGAELEKPMYC 17  
 Db 335 CGVKDGPKEPLOWREWTG 351

RESULT 14  
 S06192  
 tumor necrosis factor alpha precursor - goat (fragment)  
 N:Alternate names: cachectin; TNF alpha  
 C:Species: Capra aegagrus hircus (domestic goat)  
 C>Date: 28-Feb-1990 #sequence\_revision 28-Feb-1990 #text\_change 31-Jan-2000  
 C:Accession: S06192; S41867  
 R:Goldstein, I.M.; Henner, D.; Talhouk, A.  
 submitted to the EMBL Data Library, March 1989  
 A:Reference number: S06192  
 A:Accession: S06192  
 A:Molecule type: mRNA  
 A:Residues: 1-193 <COL>  
 A:Cross-references: EMBL:X14820; NID:g992; PIDN:CAA32937.1; PID:g993  
 R:Rimstad, E.  
 submitted to the EMBL Data Library, January 1994  
 A:Reference number: S41867  
 A:Accession: S41867

A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 36-38,'S',40-78,'A',80-88,'N',90-114,'Q',116-123,'D',125-144,'G',145-173,'L'  
 A:Cross-References: EMBL:X77317; NID:9452607; PIDN:CA54523.1; PID:9452608  
 C:Superfamily: tumor necrosis factor  
 C:Keywords: cytokine; cytotoxin; glycoprotein; lymphokine; macrophage; membrane protein  
 F:42/Binding site: carbohydrate (Ser) (covalent) #status predicted  
 F:106-138/Disulfide bonds: #status predicted

Query Match 44.9%; Score 48.5; DB 2; Length 193;  
 Best Local Similarity 69.2%; Pred. No. 5.5;  
 Matches 9; Conservative 2; Mismatches 1; Indels 1; Gaps 1;  
 Oy 4 KDTPEGAEKPMY 16  
 Db 140 RETPE-AEAKPMY 151

## RESULT 15

D69373  
 Immunogenic protein (bcsp31-3) homolog - Archaeoglobus fulgidus  
 C:Species: Archaeoglobus fulgidus  
 C:Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 17-Mar-2000  
 C:Accession: D69373  
 R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson  
 ; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.  
 Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.  
 Nature 390, 364-370, 1997  
 A:Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artlach, P.; Kalne, B.P.; Sykes, S.  
 Smith, H.O.; Moese, C.R.; Venter, J.C.  
 A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeo  
 A:Reference number: A69250; MUID:98049343; PMID:9389475  
 A:Accession: D69373  
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-347 <KLE>  
 A:Cross-References: GB:AF001036; GB:AF000782; NID:92689359; PIDN:AAB90255.1; PID:9264961  
 C:Superfamily: immunogenic protein BCSP31

Query Match 44.9%; Score 48.5; DB 2; Length 347;  
 Best Local Similarity 45.0%; Pred. No. 9.7;  
 Matches 9; Conservative 3; Mismatches 3; Indels 5; Gaps 1;  
 Oy 1 CGPKDTPGGA----ELKPM 15  
 Db 20 CAEEKPEGATPKVEVKPM 39

Search completed: April 4, 2003, 08:42:59  
 Job time : 13.3387 secs

GenCore version 5.1.4\_p5\_4578  
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OM protein - protein search, using sw model

Run on: April 4, 2003, 08:36:51 ; Search time 6.85484 Seconds

(without alignments)  
102.861 Million cell updates/sec

Title: US-09-779-703-5

Perfect score: 108

Sequence: 1 CGPKDPFGALKPWYC 17

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

## SUMMARIES

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	ID	Description
1	84	77.8	235	1 TNFA_MOUSE	P06804 mus muscula
2	84	77.8	235	1 TNFA_RAT	P16599 rattus norv
3	77	71.3	235	1 TNFA_PERLE	P36939 peromyscus
4	67	62.0	234	1 TNFA_CAVPO	P51435 cavia porce
5	65	60.2	232	1 TNFA_PIG	P23563 sus scrofa
6	65	60.2	233	1 TNFA_DELE	O8WMT1 delphinapte
7	65	60.2	233	1 TNFA_FELCA	P19101 felis silve
8	65	60.2	233	1 TNFA_HUMAN	P01375 homo sapien
9	65	60.2	233	1 TNFA_MACFA	P79337 macaca fasc
10	65	60.2	233	1 TNFA_MACMU	P48094 macaca mula
11	65	60.2	233	1 TNFA_PAPHU	O77510 papio hamad
12	65	60.2	233	1 TNFA_PAPSP	P33620 papio sp. (
13	65	60.2	233	1 TNFA_TURTR	O9B81 turlops tr
14	65	60.2	234	1 TNFA_CAPHI	P13286 capra hircu
15	62	57.4	233	1 TNFA_MARMO	O35734 marmota mon
16	61	56.5	233	1 TNFA_CANFA	P51742 canis fami
17	57	52.8	229	1 TNFA_CEREL	O06599 bos taurus
18	57	52.8	233	1 TNFA_BOVIN	O06599 bos taurus
19	55	50.9	234	1 TNFA_SHEEP	P23383 ovis aries
20	51	47.2	234	1 TNFA_HORSE	P29553 equus cabal
21	50	46.3	289	1 APFA_YERPE	O8Z1K7 yersinia pe
22	48	44.5	1236	1 SKIL_MOUSE	O60665 mus musculu
23	47	43.5	1236	1 POLS_WEBV	P13897 western equ
24	47	43.5	1240	1 POLS_EEEV3	P27884 eastern equ
25	47	43.5	1240	1 POLS_EEEV3	P27884 eastern equ
26	46	42.6	702	1 MLOS_ARATH	O22815 arabidopsis
27	46	42.6	702	1 D112_ANTCR	O16959 anthocidari
28	46	42.6	951	1 D298_HUMAN	P57071 homo sapien
29	45	41.7	593	1 PPO_MALDO	P43309 malus domes
30	45	41.7	684	1 SKIL_HUMAN	P12757 malus sapien
31	45	41.7	759	1 NHA2_SCHPO	O14123 schizosacch
32	44	40.7	198	1 C4BB_BOVIN	O28066 bos taurus
33	43.5	40.3	322	1 Y493_AQUAE	O66783 aquifex aeo

34	43	39.8	142	1 YFCC_CHREI	O06536 chromatium
35	43	39.8	259	1 APFA_KLEAE	P27510 klebsiella
36	43	39.8	748	1 MUTA_MOUSE	P16332 mus musculu
37	43	39.8	750	1 MUTA_HUMAN	P22033 homo sapien
38	43	39.8	2871	1 FBNI_PIG	O96130 sus scrofa
39	43	39.8	3298	1 PC16_HUMAN	O96130 sus sapien
40	42	38.9	250	1 HXD_MOUSE	P10628 mus musculu
41	42	38.9	712	1 MUTB_RHIME	O86028 rhizobium m
42	42	38.9	724	1 MALO_MYCTU	O35932 mycobacteri
43	42	38.9	812	1 EBN3_EBV	P12977 Epstein-Bar
44	42	38.9	2142	1 BAT2_HUMAN	P48634 homo sapien
45	41.5	38.4	516	1 YCP7_BRAVA	O45221 bradyrhizob

## ALIGNMENTS

RESULT 1  
TNFA\_MOUSE STANDARD: PRT: 235 AA.  
ID TNFA\_MOUSE AC P06804; Q62326; O35853;  
DT 01-JAN-1988 (Rel. 06, Created)  
DT 01-MAR-1989 (Rel. 10, Last sequence update)  
DE 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor  
DE ligand superfamily member 2) (Cachectin).  
GN TNF OR TNFSF2 OR TNFA.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murine; Mus.  
OX NCBI\_TaxID:10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE-8824564; PubMed-2836146;  
RA Shirai T., Shimizu N., Shiojiri S., Horiguchi S., Ito H.;  
RT "Cloning and expression in Escherichia coli of the gene for mouse  
RT tumor necrosis factor.";  
RL DNA 7:193-201(1988).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE-85298296; PubMed-3898078;  
RA Pennica D., Hayflick J.S., Brinman T.S., Palladino M.A.,  
RA Goeddel D.V.;  
RT "Cloning and expression in Escherichia coli of the cDNA for murine  
RT tumor necrosis factor.";  
RL Proc. Natl. Acad. Sci. U.S.A. 82:6060-6064(1985).  
RN [3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE-86149365; PubMed-2419912;  
RA Caput D., Beutler B., Hartog K., Thayer R., Brown-Shimer S.,  
RA Cerami A.;  
RT "Identification of a common nucleotide sequence in the  
RT 3'-untranslated region of mRNA molecules specifying inflammatory  
RT mediators.";  
RL Proc. Natl. Acad. Sci. U.S.A. 83:1670-1674(1986).  
RN [4]  
RP SEQUENCE FROM N.A.  
RX MEDLINE-85242112; PubMed-2989794;  
RA Franzen L., Mueller R., Marmenout A., Tavernier J., van der Heyden J.,  
RA Kawashima E., Chollat A., Tizard R., van Heuverswyn H., van Vliet A.,  
RA Rysschaert M.-R., Fiers W.;  
RT "Molecular cloning of mouse tumour necrosis factor cDNA and its  
RT eukaryotic expression.";  
RL Nucleic Acids Res. 13:4417-4429(1985).  
RN [5]  
RP SEQUENCE FROM N.A.  
RX MEDLINE-87298639; PubMed-3040015;  
RA Shakhov A.N., Nedospasov S.A.;  
RT "Molecular cloning of genes coding for tumor necrosis factor.  
RT Complete nucleotide sequence of the genome copy of TNF-alpha in  
RT mice.";  
RL Bioorg. Khim. 13:701-705(1987).  
RN [6]

RP SEQUENCE FROM N.A.  
 RX MEDLINE=88067722; PubMed=3684584;  
 RA Semon D., Kawashima E., Jongeneel C.V., Shakhov A.N., Nedospasov S.A.;  
 RT "Nucleotide sequence of the murine TNF locus, including the TNF-alpha  
 (tumor necrosis factor) and TNF-beta (lymphotoxin) genes.";   
 RL Nucleic Acids Res. 15:9083-9084(1987).  
 RN [17]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-CTS, AND NOD;  
 RX MEDLINE=96013654; PubMed=7560085;  
 RA Ikegami H., Makino S., Yamato E., Kawaguchi Y., Ueda H., Sakamoto T.,  
 RT Takekawa K., Ogihara T.;  
 RT "Identification of a new susceptibility locus for insulin-dependent  
 diabetes mellitus by ancestral haplotype congenic mapping.";   
 RL J. Clin. Invest. 96:1936-1942(1995).  
 RN [8]  
 RP SEQUENCE FROM N.A., AND VARIANTS THR-7 AND ALA-77.  
 RC STRAIN-A/J, BALB/c, and C57BL/6;  
 RX MEDLINE=97246744; PubMed=9089109;  
 RA Iraqi F., Teale A.;  
 RT "Cloning and sequencing of the Tnfa genes of three inbred mouse  
 strains";  
 RL Immunogenetics 45:459-461(1997).  
 RN [9]  
 RP SEQUENCE FROM N.A.  
 RA Rowen L., Qin S., Madan A., Abbas N., James R., Dickhoff R.,  
 RA Shaffer T., Ratcliffe A., Loretz C., Lasky S., Hood L.;  
 RT "Sequence of the mouse major histocompatibility class III region";  
 RL Submitted (Oct-1999) to the EMBL/Genbank/DBJ databases.  
 RN [10]  
 RP SEQUENCE OF 70-87.  
 RX MEDLINE=89380231; PubMed=2777790;  
 RA Cash K., Beutler B.;  
 RT "Alternative cleavage of the cachectin/tumor necrosis factor  
 propeptide results in a larger, inactive form of secreted protein.";   
 RL J. Biol. Chem. 264:16256-16260(1989).  
 RN [11]  
 RP SEQUENCE OF 80-99.  
 RX MEDLINE=91097531; PubMed=2268312;  
 RA Sherry B., Juc D.-M., Zentella A., Ceram A.;  
 RT "Characterization of high molecular weight glycosylated forms of  
 murine tumor necrosis factor";  
 RL Biochem. Biophys. Res. Commun. 173:1072-1078(1990).  
 RN [12]  
 RP IDENTIFICATION OF MEMBRANE-BOUND FORM.  
 RX MEDLINE=88165056; PubMed=349526;  
 RA Krieger M., Perez X., Defay K., Albert I., Lu S.D.;  
 RT "A novel form of TNF/cachectin is a cell surface cytotoxic  
 transmembrane protein: ramifications for the complex physiology of  
 TNF";  
 RL Cell 53:45-53(1988).  
 RN [13]  
 RP X-RAY CRYSTALLOGRAPHY (1.4 ANGSTROMS) OF 80-235.  
 RX MEDLINE=99190964; PubMed=10089307;  
 RA Baeyens K.J., De Bondt H.L., Raeymaekers A., Fiers W., De Ranter C.J.;  
 RT "The structure of mouse tumour-necrosis factor at 1.4 A resolution:  
 towards modulation of its selectivity and trimerization.";   
 RL Acta Crystallogr. D 55:772-778(1999).  
 CC -1- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and  
 TNFRSF1B/TNFR. It is mainly secreted by macrophages and can  
 induce cell death of certain tumor cell lines. It is potent  
 pyrogen causing fever by direct action or by stimulation of  
 interleukin 1 secretion and is implicated in the induction of  
 cachexia, under certain conditions it can stimulate cell  
 proliferation and induce cell differentiation.  
 CC -1- SUBUNIT: Homotrimer.  
 CC -1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN  
 EXTRACELLULAR SOLUBLE FORM.  
 CC -1- PTM: THE SOLUBLE FORM DERIVES FROM THE MEMBRANE FORM BY  
 PROTEOLYTIC PROCESSING.  
 CC -1- PTM: The membrane form, but not the soluble form, is  
 phosphorylated on serine residues. Dephosphorylation of the  
 membrane form occurs by binding to soluble TNFRSF1A/TNFR1 (By

CC similarity)  
 CC -1- DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF DISEASES, INCLUDING  
 CC CANCER AND INFECTION, AND IS CHARACTERIZED BY GENERAL ILL HEALTH  
 CC AND MALNUTRITION.  
 CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL; M20155; AAA40462.1; ALT\_SEQ.  
 DR EMBL; M1731; AAA40458.1; -  
 DR EMBL; M13049; AAA40457.1; -  
 DR EMBL; X02611; CAA26457.1; -  
 DR EMBL; M38296; AAA40459.1; -  
 DR EMBL; Y00467; CAA68530.1; -  
 DR EMBL; U06950; AAA18594.1; -  
 DR EMBL; D84196; BAA19512.1; -  
 DR EMBL; D84194; BAA19512.1; JOINED.  
 DR EMBL; D84195; BAA19512.1; JOINED.  
 DR EMBL; D84197; BAA19513.1; -  
 DR EMBL; D84197; BAA19513.1; JOINED.  
 DR EMBL; U68414; AAB65593.1; -  
 DR EMBL; AF109719; AAC82484.1; -  
 DR PIR; A23127; QWMSN.  
 DR PIR; A22908; A22908.  
 DR PIR; A25164; A25164.  
 DR PIR; A27303; A27303.  
 DR PIR; A34251; A34251.  
 DR PIR; S03791; S03791.  
 DR PDB; 2TNF; 12-OCT-99.  
 DR MGD; MGI:104798; TNF.  
 DR InterPro; IPR003636; TNF\_abc.  
 DR InterPro; IPR004478; TNF\_family.  
 DR Pfam; PF00229; TNF; 1.  
 DR PRINTS; PR01234; TNECROSISFCT.  
 DR ProDom; PD002012; TNF\_abc; 1.  
 DR SMART; SM00207; TNF; 1.  
 DR PROSITE; PS00251; TNF\_1; 1.  
 DR PROSITE; PS50049; TNF\_2; 1.  
 KM Cytokine; Cytotoxin; Transmembrane; Glycoprotein; Phosphorylation;  
 KV Signal-anchor; Polymorphism; 3D-structure.  
 FT CHAIN 1 235 TUMOR NECROSIS FACTOR, MEMBRANE FORM.  
 FT CHAIN 80 235 TUMOR NECROSIS FACTOR, SOLUBLE FORM.  
 FT DOMAIN 1 35 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 36 56 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)  
 FT DOMAIN 57 235 EXTRACELLULAR (POTENTIAL).  
 FT SITE 79 80 CLEAVAGE (BY ADAM17) (BY SIMILARITY).  
 FT MOD\_RES 2 2 PHOSPHORYLATION (BY CK1) (BY SIMILARITY).  
 FT DISULFID 148 179  
 FT CARBOHYD 86 86  
 FT VARIANT 7 7  
 FT VARIANT 77 77  
 FT CONFLICT 79 81  
 FT CONFLICT 231 231  
 FT SEQUENCE 235 AA; 25895 MW; 16DD2A9676D86CSD CMC64;  
 N-LINKED (GLCNAC...)  
 I -> T (IN STRAINS BALB/C AND C57BL/6).  
 T -> A (IN STRAINS BALB/C AND C57BL/6).  
 MISSING (IN REF. 8).  
 G -> R (IN REF. 3 AND 4).  
 16DD2A9676D86CSD CMC64;

Query Match 77.88; Score 84; DB 1; Length 235;  
 Best Local Similarity 100.08; Pred. No. 6,4e-06;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PKDTPGAEKLPWY 16  
 |||||  
 Db 180 PKDTPGAEKLPWY 193

RESULT 2



TNFA\_RAT  
ID TNFA\_RAT STANDARD: PRT; 235 AA.  
AC P16599;  
DT 01-AUG-1990 (Rel. 15, Created)  
DT 01-AUG-1990 (Rel. 15, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor ligand superfamily member 2) (cachectin).  
GN TNF OR TNFSF2 OR TNFA.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxId=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Sprague-Dawley; TISSUE=Testis;  
RX MEDLINE=94040766; PubMed=8224868;  
RA Kwon J., Chung I.Y., Benveniste E.N.;  
RT "Cloning and sequence analysis of the rat tumor necrosis factor-encoding genes.";  
RL Gene 132:227-236(1993).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Shirai T., Shimizu N., Horiguchi S., Ito H.;  
RT "Cloning and expression in Escherichia coli of the gene for rat tumor necrosis factor.";  
RL Agric. Biol. Chem. 53:1733-1736(1989).  
RN [3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=92329007; PubMed=1627266;  
RA Estler H.C., Grewe M., Gaussling R., Pavlovic M., Decker K.;  
RT "Rat tumor necrosis factor-alpha. Transcription in rat Kupffer cells and in vitro posttranslational processing based on a PCR-derived cDNA.";  
RL Biol. Chem. Hoppe-Seyler 373:271-281(1992).  
RN [4]  
RP SEQUENCE FROM N.A.  
RX STRAIN=Various;  
RX MEDLINE=21369712; PubMed=11477479;  
RA Furuya T., Joe B., Salstrom J.L., Hashiramoto A., Dobbins D.E., Wilder R.L., Remmers E.F.;  
RT "Polymorphisms of the tumor necrosis factor alpha locus among autoimmune disease susceptible and resistant inbred rat strains.";  
RL Genes Immun. 2:229-232(2001).  
RN [5]  
RP SEQUENCE FROM N.A.  
RA Decker K.F.;  
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.  
RN [6]  
RP SEQUENCE OF 1-231 FROM N.A.  
RC TISSUE=Tail;  
RA Kiritsis M.J., Vardimon D., Kunz H.W., Gill T.J. III;  
RT Submitted (JUN-1993) to the EMBL/GenBank/DBJ databases.  
RL FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and TNFRSF1B/TNFR. It is mainly secreted by macrophages and can induce cell death of certain tumor cell lines. It is potent pyrogen causing fever by direct action or by stimulation of interleukin 1 secretion and is implicated in the induction of cachexia, under certain conditions it can stimulate cell proliferation and induce cell differentiation.  
CC -1- SUBUNIT: Homotrimer (By similarity).  
CC -1- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an extracellular soluble form (By similarity).  
CC -1- PTM: The soluble form derives from the membrane form by proteolytic processing (By similarity).  
CC -1- PTM: The membrane form, but not the soluble form, is phosphorylated on serine residues. Dephosphorylation of the membrane form occurs by binding to soluble TNFRSF1A/TNFR1 (By similarity).  
CC -1- DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF DISEASES, INCLUDING CANCER AND INFECTION, AND IS CHARACTERIZED BY GENERAL ILL HEALTH AND MALNUTRITION.  
CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.

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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL: X66539; CAA47146.1; -;  
DR EMBL: L00981; AAA16275.1; -;  
DR EMBL: D00475; BAA00367.1; -;  
DR EMBL: AJ002278; CAA05290.1; -;  
DR EMBL: L19123; AAA42255.1; -;  
DR EMBL: AF329982; AAK53568.1; -;  
DR EMBL: AF329983; AAK53569.1; -;  
DR EMBL: AF329984; AAK53570.1; -;  
DR EMBL: AF329985; AAK53571.1; -;  
DR EMBL: AF329986; AAK53572.1; -;  
DR EMBL: AF329987; AAK53573.1; -;  
DR PIR: J00029; J00029.  
DR PIR: S21674; S21674.  
DR PIR: J00868; J00868.  
DR HSSP: P06804; 2TNF.  
DR InterPro: IPR003636; TNF\_abc.  
DR InterPro: IPR000478; TNF\_family.  
DR Pfam: PF00229; TNF\_1.  
DR PRINTS: PR01234; TNECROSISFCF.  
DR PRODOM: PD002012; TNF\_abc; 1.  
DR SMART: SM00207; TNF\_1.  
DR PROSITE: PS00251; TNF\_1; 1.  
DR PROSITE: PS50049; TNF\_2; 1.  
KM Cytokine; Cytotoxin; Transmembrane; Glycoprotein; Phosphorylation;  
KW Signal-anchor.  
FT CHAIN 1 235 TUMOR NECROSIS FACTOR, MEMBRANE FORM.  
FT CHAIN 80 235 TUMOR NECROSIS FACTOR, SOLUBLE FORM.  
FT DOMAIN 1 35 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 36 56 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN) (POTENTIAL).  
FT DOMAIN 57 235 EXTRACELLULAR (POTENTIAL).  
FT SITE 79 80 CLEAVAGE (BY ADAM17) (BY SIMILARITY).  
FT MOD\_RES 2 2 PHOSPHORYLATION (BY CK1) (BY SIMILARITY).  
FT DISULFID 148 179 BY SIMILARITY.  
FT CARBOHYD 86 86 N-LINKED GLYCAC. . . (POTENTIAL).  
FT CONFLICT 39 39 L -> P (IN REF. 3 AND 5).  
FT CONFLICT 163 163 I -> T (IN REF. 3 AND 5).  
FT CONFLICT 202 202 F -> S (IN REF. 3 AND 5).  
SQ SEQUENCE 235 AA; 25806 MW; B80BEC6D049C2F3B CRC64;  
Query Match 77.8%; Score 84; DB 1; Length 235;  
Best Local Similarity 100.0%; Pred. No. 6.4e-06;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps. 0;  
OY 3 PKDTPEGAEELKPMW 16  
DB 180 PKDTPEGAEELKPMW 193  
IIIIIIIIIIIIIIIIIIII  
RESULT 3  
ID TNFA\_PERLE STANDARD: PRT; 235 AA.  
AC P36939;  
DT 01-JUN-1994 (Rel. 29, Created)  
DT 01-JUN-1994 (Rel. 29, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor ligand superfamily member 2) (cachectin).  
GN TNF OR TNFSF2 OR TNFA.  
OS Peromyscus leucopus (White-footed mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae; Peromyscus.  
OX NCBI\_TaxId=10041;



```

RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-92218012; PubMed-1348497;
RA Crew M.D., Filipowicz M.E.;
RT "Sequence of the tumor necrosis factor/cachectin (TNF) gene from
RL Peromyscus leucopus (family Cricetidae).";
CC Immunogenetics 35:351-353(1992).
CC -1- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and
CC TNFRSF1B/TNFR. It is mainly secreted by macrophages and can
CC induce cell death of certain tumor cell lines. It is potent
CC pyrogen causing fever by direct action or by stimulation of
CC interleukin 1 secretion and is implicated in the induction of
CC cachexia. Under certain conditions it can stimulate cell
CC proliferation and induce cell differentiation.
CC -1- SUBUNIT: Homotrimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an
CC extracellular soluble form (By similarity).
CC -1- PTM: The soluble form derives from the membrane form by
CC proteolytic processing (By similarity).
CC -1- PTM: The membrane form, but not the soluble form, is
CC phosphorylated on serine residues. Dephosphorylation of the
CC membrane form occurs by binding to soluble TNFRSF1A/TNFR1 (By
CC similarity).
CC -1- DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF DISEASES, INCLUDING
CC CANCER AND INFECTION, AND IS CHARACTERIZED BY GENERAL ILL HEALTH
CC AND MALNUTRITION.
CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
CC -----
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CC -----
DR EMBL; M59233; AAA40596.1; -
DR HSSP; P06804; 2TNF.
DR InterPro; IPR003636; TNF_abc.
DR InterPro; IPR000478; TNF_family.
DR Pfam; PF00229; TNF; 1.
DR PRINTS; PR01234; TNECROSISFCT.
DR PRODOM; PD002012; TNF_abc; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS50049; TNF_2; 1.
KW Cytokine; Cytotoxin; Transmembrane; Glycoprotein; Phosphorylation;
KW Signal-anchor.
FT CHAIN 1 235 TUMOR NECROSIS FACTOR, MEMBRANE FORM.
FT CHAIN 80 235 TUMOR NECROSIS FACTOR, SOLUBLE FORM.
FT DOMAIN 1 35 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 36 56 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT (POTENTIAL).
FT DOMAIN 57 235 EXTRACELLULAR (POTENTIAL).
FT SITE 79 80 CLEAVAGE (BY ADAM17) (BY SIMILARITY).
FT MOD_RES 2 2 PHOSPHORYLATION (BY CK1) (BY SIMILARITY).
FT DISULFID 148 179 BY SIMILARITY.
FT CARBOHYD 86 86 N-LINKED (GLCNAc...) (POTENTIAL).
SQ SEQUENCE 235 AA; 25822 MW; 235A5CF9F9AC624 CRC64;

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Query Match 71.3%; Score 77; DB 1; Length 235;  
 Best Local Similarity 85.7%; Prcd. No. 7.9e-05;  
 Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 3 PKDTPGAGALKPMY 16  
 DB 180 KPEPGESEELKPMY 193

RESULT 4  
 TNFA\_CAVPO STANDARD; PRT; 234 AA.  
 ID TNFA\_CAVPO  
 AC P51435;

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DT 01-OCT-1996 (rel. 34, Created)
DT 01-OCT-1996 (rel. 34, Last sequence update)
DT 15-JUN-2002 (rel. 41, Last annotation update)
DE Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor
DE ligand superfamily member 2) (Cachectin).
GN TNF OR TNFSE2 OR TNFA.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystriocognathi; Cavidae; Cavia.
OC NCBI_Taxid=10141;
RP [1]
RP SEQUENCE FROM N.A.
RC STRAIN-Hartley; TISSUE-Lung;
RA Tuan H.T., Kelly F.J., Bingle C.D.;
RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
RL [2]
RP SEQUENCE FROM N.A.
RC STRAIN-Dunkin-Hartley;
RX MEDLINE-97462215; PubMed-9316485;
RA White A.M., Yoshimura T., Smith A.W., Westwick J., Watson M.L.;
RT "Airway inflammation induced by recombinant guinea pig tumor necrosis
RT factor-alpha.";
RL Am. J. Physiol. 273:L524-L530(1997).
CC -1- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and
CC TNFRSF1B/TNFR. It is mainly secreted by macrophages and can
CC induce cell death of certain tumor cell lines. It is potent
CC pyrogen causing fever by direct action or by stimulation of
CC interleukin 1 secretion and is implicated in the induction of
CC cachexia. Under certain conditions it can stimulate cell
CC proliferation and induce cell differentiation.
CC -1- SUBUNIT: Homotrimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an
CC extracellular soluble form (By similarity).
CC -1- PTM: The soluble form derives from the membrane form by
CC proteolytic processing (By similarity).
CC -1- PTM: The membrane form, but not the soluble form, is
CC phosphorylated on serine residues. Dephosphorylation of the
CC membrane form occurs by binding to soluble TNFRSF1A/TNFR1 (By
CC similarity).
CC -1- DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF DISEASES, INCLUDING
CC CANCER AND INFECTION, AND IS CHARACTERIZED BY GENERAL ILL HEALTH
CC AND MALNUTRITION.
CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
CC -----
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CC -----
DR EMBL; U39839; AAB06492.1; -
DR HSSP; P06804; 2TNF.
DR InterPro; IPR003636; TNF_abc.
DR InterPro; IPR000478; TNF_family.
DR Pfam; PF00229; TNF; 1.
DR PRINTS; PR01234; TNECROSISFCT.
DR PRODOM; PD002012; TNF_abc; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS50049; TNF_2; 1.
KW Cytokine; Cytotoxin; Transmembrane; Phosphorylation; Signal-anchor.
FT CHAIN 1 234 TUMOR NECROSIS FACTOR, MEMBRANE FORM.
FT CHAIN 80 234 TUMOR NECROSIS FACTOR, SOLUBLE FORM.
FT DOMAIN 1 35 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 36 56 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT (POTENTIAL).
FT DOMAIN 57 234 EXTRACELLULAR (POTENTIAL).
FT SITE 79 80 CLEAVAGE (BY ADAM17) (BY SIMILARITY).
FT MOD_RES 2 2 PHOSPHORYLATION (BY CK1) (BY SIMILARITY).
FT DISULFID 147 178 BY SIMILARITY.

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SQ SEQUENCE 234 AA: 25793 MW: 7272C940393E7E9B CRC64;  
 Query Match 62.0%; Score 67; DB 1; Length 234;  
 Best Local Similarity 84.6%; Pred. No. 0.0029;  
 Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 KOTPEGAEKPMY 16  
 1:||||| 1111  
 DB 180 KETPEGAEKPMY 192

RESULT 5  
 TNFA\_PIG STANDARD; PRT; 232 AA.  
 AC P23563;  
 DT 01-NOV-1991 (Rel. 20, Created)  
 DT 01-NOV-1991 (Rel. 20, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor  
 ligand superfamily member 2) (Cachectin).  
 GN TNF OR TNFSF2 OR TNFA.  
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.  
 NC NCB1\_TaxID=9823;  
 RX MEDLINE=91016861; PubMed=2216741;  
 RA Drews R.T., Coffee B.W., Prestwood A.K., McGraw R.A.;  
 RT "Gene sequence of porcine tumor necrosis factor alpha.";  
 RL Nucleic Acids Res. 18:5564-5564 (1990).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Liver;  
 RX MEDLINE=91340150; PubMed=1874444;  
 RA Kuhnert P., Wuehrlich C., Peterhans E., Pauli U.;  
 RT "The porcine tumor necrosis factor-encoding genes: sequence and  
 comparative analysis.";  
 RL Gene 102:171-178 (1991).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Macrophage;  
 RA Choi C.S., Mollitor T.W., Lin G.F., Murtough M.P.;  
 RT "Complete nucleotide sequence of a cDNA encoding porcine tumor  
 necrosis factor alpha.";  
 RL Anim. Biotechnol. 2:97-105 (1991).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Large white; TISSUE=Fibroblast;  
 RX MEDLINE=21108615; PubMed=11169259;  
 RA Charbon P., Rogel-Gallard C., Cattolico L., Duprat S., Vaiman M.,  
 RA Renard C.;  
 RT "Sequence of the swine major histocompatibility complex region  
 containing all non-classical class I genes.";  
 RL Tissue Antigens 57:55-65 (2001).  
 RN [5]  
 RP SEQUENCE OF 44-232 FROM N.A.  
 RX MEDLINE=90034181; PubMed=2478420;  
 RA Pauli U., Beutler B., Peterhans E.;  
 RT "Porcine tumor necrosis factor alpha: cloning with the polymerase  
 chain reaction and determination of the nucleotide sequence.";  
 RL Gene 81:185-191 (1989).  
 CC -1- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and  
 TNFRSF1B/TNFR2. It is mainly secreted by macrophages and can  
 induce cell death of certain tumor cell lines. It is potent  
 pyrogen causing fever by direct action or by stimulation of  
 interleukin 1 secretion and is implicated in the induction of  
 cachexia, under certain conditions it can stimulate cell  
 proliferation and induce cell differentiation.  
 CC -1- SUBUNIT: Homotrimer (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an  
 extracellular soluble form (By similarity).  
 CC -1- PTM: The soluble form derives from the membrane form by

CC proteolytic processing (By similarity).  
 CC -1- PTM: The membrane form, but not the soluble form, is  
 CC phosphorylated on serine residues. Dephosphorylation of the  
 CC membrane form occurs by binding to soluble TNFRSF1A/TNFR1 (By  
 CC similarity).  
 CC -1- DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF DISEASES, INCLUDING  
 CC CANCER AND INFECTION, AND IS CHARACTERIZED BY GENERAL ILL HEALTH  
 CC AND MALNUTRITION.  
 CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.  
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 CC -----  
 DR EMBL: X54001; CAA37949.1; -  
 DR EMBL: X54859; CAA38639.1; -  
 DR EMBL: X57321; CAA40591.1; -  
 DR EMBL: AJ251914; CAB63852.1; -  
 DR EMBL: M29079; AAA31128.1; -  
 DR PIR: S12606; S12606.  
 DR PIR: S17290; S17290.  
 DR PIR: S18965; S18965.  
 DR HSSP: P01375; 4TSV.  
 DR InterPro: IPR003636; TNF-abc.  
 DR InterPro: IPR000478; TNF-family.  
 DR Pfam: PR00229; TNF\_1.  
 DR PRINTS: PR01234; TNFECROSISFCT.  
 DR ProDom: PD002012; TNF-abc; 1.  
 DR SMART: SM00207; TNF; 1.  
 DR PROSITE: PS00251; TNF\_1; 1.  
 DR PROSITE: PS50049; TNF\_2; 1.  
 KW Cytokine; Cytotoxin; Transmembrane; Phosphorylation; Signal-anchor.  
 FT CHAIN 1 232  
 FT DOMAIN 77 232  
 FT TRANSMEM 1 35  
 FT TRANSMEM 36 56  
 FT FT  
 FT DOMAIN 57 232  
 FT SITE 76 77  
 FT MOD\_RES 2 2  
 FT DISULFID 144 176  
 FT FT  
 SQ SEQUENCE 232 AA: 25254 MW: 65828F702D99C8BE CRC64;  
 Query Match 60.2%; Score 65; DB 1; Length 232;  
 Best Local Similarity 76.9%; Pred. No. 0.0058;  
 Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 KOTPEGAEKPMY 16  
 178 KETPEGAEKPMY 190

RESULT 6  
 TNFA\_DELE STANDARD; PRT; 233 AA.  
 ID TNFA\_DELE  
 AC Q8WNR1;  
 DT 15-JUN-2002 (Rel. 41, Created)  
 DT 15-JUN-2002 (Rel. 41, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor  
 ligand superfamily member 2) (Cachectin).  
 GN TNF OR TNFSF2 OR TNFA.  
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Cetacea; Odontoceti;  
 CC Monodontidae; Delphinapterus.  
 CC NCB1\_TaxID=9749;  
 RX MEDLINE=9749;  
 RN [1]  
 RP SEQUENCE FROM N.A.

```

RX PubMed:11768130;
RA Denis F., Archambault D.;
RT "Molecular cloning and characterization of beluga whale
RT (Delphinapterus leucas) interleukin-1beta and tumor necrosis
RT factor-alpha.";
RL Can. J. Vet. Res. 65:233-240(2001).
CC -1- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and
CC TNFRSF1B/TNFR. It is mainly secreted by macrophages and can
CC induce cell death of certain tumor cell lines. It is potent
CC pyrogen causing fever by direct action or by stimulation of
CC interleukin 1 secretion and is implicated in the induction of
CC cachexia, under certain conditions it can stimulate cell
CC proliferation and induce cell differentiation (By similarity).
CC -1- SUBUNIT: Homotrimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an
CC extracellular soluble form (By similarity).
CC -1- PTM: The soluble form derives from the membrane form by
CC proteolytic processing (By similarity).
CC -1- PTM: The membrane form, but not the soluble form, is
CC phosphorylated on serine residues. Dephosphorylation of the
CC membrane form occurs by binding to soluble TNFRSF1A/TNFR1 (By
CC similarity).
CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
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-----
DR EMBL: AF320333; AAL56946.1; -
DR InterPro: IPR003636; TNF_abc.
DR InterPro: IPR000478; TNF_family.
DR Pfam: PF00229; TNF_1.
DR PRINTS: PR01234; TNECROSISFCT.
DR PRODOM: PD002012; TNF_abc; 1.
DR SMART: SM00207; TNF_1.
DR PROSITE: PS00251; TNF_1; 1.
DR PROSITE: PS50049; TNF_2; 1.
DR PROSITE: PS50049; TNF_2; 1.
KW Cytokine; Cytotoxin; Transmembrane; Glycoprotein; Phosphorylation;
KW Signal-anchor.
FT CHAIN 1 233 TUMOR NECROSIS FACTOR, MEMBRANE FORM.
FT CHAIN 1 35 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 78 233 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT TRANSMEM 36 56 (POTENTIAL).
FT DOMAIN 57 233 EXTRACELLULAR (POTENTIAL).
FT SITE 77 78 CLEAVAGE (BY ADAM17) (BY SIMILARITY).
FT MOD_RES 2 2 PHOSPHORYLATION (BY CK1) (BY SIMILARITY).
FT DISULFID 145 177 BY SIMILARITY.
FT CARBOHYD 95 95 N-LINKED (GLCNAC... ) (POTENTIAL).
SQ SEQUENCE 233 AA; 25420 MW; 2DR37DCB2HC9E961 CRC64;

Query Match 60.2%; Score 65; DB 1; Length 233;
Best Local Similarity 76.9%; Pred. No. 0.0058;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 KDPFGALKLPWY 16
Db 179 RETPGAKAKPWY 191

RESULT 7
TNFA_FELCA STANDARD; PRT; 233 AA.
AC P19101;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor
DE ligand superfamily member 2) (Cachectin).

```

```

GN TNF OR TNFSF2 OR TNFA.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=91016860; PubMed=2216740;
RA McGraw R.A., Coffee B.W., Otto C.M., Drews R.T., Rawlings C.A.;
RT "Gene sequence of feline tumor necrosis factor alpha.";
RL Nucleic Acids Res. 18:5563-5563(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Bone marrow;
RA Daniel S.L., Brenner C.A., Legendre A.M., Solomon A., Rouse B.T.;
RL Submitted (XXX-1993) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and
CC TNFRSF1B/TNFR. It is mainly secreted by macrophages and can
CC induce cell death of certain tumor cell lines. It is potent
CC pyrogen causing fever by direct action or by stimulation of
CC interleukin 1 secretion and is implicated in the induction of
CC cachexia, under certain conditions it can stimulate cell
CC proliferation and induce cell differentiation.
CC -1- SUBUNIT: Homotrimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an
CC extracellular soluble form (By similarity).
CC -1- PTM: The soluble form derives from the membrane form by
CC proteolytic processing (By similarity).
CC -1- PTM: The membrane form, but not the soluble form, is
CC phosphorylated on serine residues. Dephosphorylation of the
CC membrane form occurs by binding to soluble TNFRSF1A/TNFR1 (By
CC similarity).
CC -1- DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF DISEASES, INCLUDING
CC CANCER AND INFECTION, AND IS CHARACTERIZED BY GENERAL ILL HEALTH
CC AND MALNUTRITION.
CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
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DR EMBL: X54000; CAA37948.1; -
DR EMBL: M82061; AAA30818.1; -
DR PIR: S11688; S11688.
DR HSSP: P01375; 4TSV.
DR InterPro: IPR003636; TNF_abc.
DR InterPro: IPR000478; TNF_family.
DR Pfam: PF00229; TNF_1.
DR PRINTS: PR01234; TNECROSISFCT.
DR PRODOM: PD002012; TNF_abc; 1.
DR SMART: SM00207; TNF_1.
DR PROSITE: PS00251; TNF_1; 1.
DR PROSITE: PS50049; TNF_2; 1.
KW Cytokine; Cytotoxin; Transmembrane; Phosphorylation; Signal-anchor.
FT CHAIN 1 233 TUMOR NECROSIS FACTOR, MEMBRANE FORM.
FT CHAIN 1 35 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 77 233 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT TRANSMEM 36 56 (POTENTIAL).
FT DOMAIN 57 233 EXTRACELLULAR (POTENTIAL).
FT SITE 76 77 CLEAVAGE (BY ADAM17) (BY SIMILARITY).
FT MOD_RES 2 2 PHOSPHORYLATION (BY CK1) (BY SIMILARITY).
FT DISULFID 145 177 BY SIMILARITY.
FT CONFLICT 28 28 G -> R (IN REF. 2).
FT CONFLICT 104 104 R -> W (IN REF. 2).
FT CONFLICT 151 151 L -> H (IN REF. 2).
FT CONFLICT 155 155 A -> T (IN REF. 2).
FT CONFLICT 210 210 T -> A (IN REF. 2).

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SQ SEQUENCE 233 AA: 25322 MW: 434D239567862506 CRC64;  
 Query Match 60.2%; Score 65; DB 1; Length 233;  
 Best Local Similarity 76.9%; Pred. NO. 0.0058;  
 Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 QY 4 KDPFGAELKPMY 16  
 Db 179 RETPGAEAKPMY 191  
 RESULT 8  
 ID TNFA\_HUMAN STANDARD; PRT: 233 AA.  
 AC P01375;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor  
 ligand superfamily member 2) (Cachectin).  
 GN TNF OR TNFSF2 OR TNFA.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-87217060; PubMed-3555974;  
 RA Nedospasov S.A., Shakhov A.N., Turetskaya R.L., Mett V.A.,  
 RA Aalizov M.M., Georgiev G.P., Korobko V.G., Dobryln V.N.,  
 RA Filipov S.A., Bystrov N.S., Boldyreva E.F., Chuvpilo S.A.,  
 RA Chumakov A.M., Shingarova L.N., Ovchinnikov Y.A.,  
 RT "Random arrangement of genes coding for tumor necrosis factor (TNF-  
 alpha) and lymphotoxin (TNF-beta) in the human genome.";  
 RL Cold Spring Harb. Symp. Quant. Biol. 51:611-624(1986).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-85086244; PubMed-6392892;  
 RA Pallanca D., Nedwin G.E., Hayflick J.S., Seeburg P.H., Derynck R.,  
 RA Palladino M.A., Kohr W.J., Aggarwal B.B., Goeddel D.V.,  
 RT "Human tumor necrosis factor: precursor structure, expression and  
 homology to lymphotoxin.";  
 RL Nature 312:724-729(1984).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-85137898; PubMed-3883195;  
 RA Shirai T., Yamaguchi H., Ito H., Todd C.W., Wallace R.B.,  
 RT "Cloning and expression in Escherichia coli of the gene for human  
 tumor necrosis factor.";  
 RL Nature 313:803-806(1985).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-86016093; PubMed-2995927;  
 RA Nedwin G.E., Naylor S.L., Sakaguchi A.Y., Smith D.H.,  
 RA Jarrett-Nedwin J., Pennica D., Goeddel D.V., Gray P.W.,  
 RT "Human lymphotoxin and tumor necrosis factor genes: structure,  
 homology and chromosomal localization.";  
 RL Nucleic Acids Res. 13:6361-6373(1985).  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-85142190; PubMed-3856324;  
 RA Wang A.M., Creasey A.A., Laderer M.B., Lin L.S., Strickler J.,  
 RA van Arsdale J.N., Yamamoto R., Mark D.F.,  
 RT "Molecular cloning of the complementary DNA for human tumor necrosis  
 factor.";  
 RL Science 228:149-154(1985).  
 RN [6]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-86030296; PubMed-3932069;  
 RA Marneault A., Franssen L., Tavernier J., van der Heyden J., Tizard R.,  
 RA Kawashima E., Shaw A., Johnson M.J., Semon D., Mueller R.,  
 RA Ruysschaert M.R., van Vliet A., Fiers W.,  
 RT "Molecular cloning and expression of human tumor necrosis factor and

RT comparison with mouse tumor necrosis factor.";  
 RL Eur. J. Biochem. 152:515-522(1985).  
 RN [7]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-93272029; PubMed-8499947;  
 RA Iris F.J.M., Bougueleret L., Prieur S., Caterina D., Primas G.,  
 RA Perrot V., Jurka J., Rodriguez-Tome P., Claverie J.-M., Dausset J.,  
 RA Cohen D.,  
 RT "Dense Alu clustering and a potential new member of the NF kappa B  
 family within a 90 kilobase HLA class III segment.";  
 RL Nat. Genet. 3:137-145(1993).  
 RN [8]  
 RP SEQUENCE FROM N.A.  
 RA Rowen L., Madan A., Qin S., Shaffer T., James R., Ratcliffe A.,  
 RA Abbasi N., Dickhoff R., Loretz C., Madan A., Dors M., Young J.,  
 RA Lasky S., Hood L.,  
 RT "Sequence of the human major histocompatibility complex class III  
 region.";  
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.  
 RN [9]  
 RP SEQUENCE FROM N.A.  
 RA Shilina S., Tamiya G., Oka A., Inoko H.,  
 RT "Homo sapiens 2,229,817bp genomic DNA of 6p21.3 HLA class I region.";  
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.  
 RN [10]  
 RP SEQUENCE FROM N.A.  
 RA Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Yi Q.,  
 RA Nickerson D.A.,  
 RT Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.  
 RN [11]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Blood;  
 RL Strausberg R.,  
 RT Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.  
 RN [12]  
 RP PHOSPHORYLATION (MEMBRANE FORM).  
 RX PubMed-8597870;  
 RA Pocsik E., Duda E., Wallach D.,  
 RT "Phosphorylation of the 26 kDa TNF precursor in monocytic cells and in  
 transfected HeLa cells.";  
 RL J. Inflamm. 45:152-160(1995).  
 RN [13]  
 RP PHOSPHORYLATION BY CK1, AND DEPHOSPHORYLATION.  
 RX PubMed-10205166;  
 RA Watts A.D., Hunt N.H., Manjasekara Y., Bloomfield G., Wallach D.,  
 RA Roufogalis B.D., Chaudhuri G.,  
 RT "A casein kinase I motif present in the cytoplasmic domain of members  
 of the tumour necrosis factor ligand family is implicated in 'reverse  
 signalling'.";  
 RL EMBO J. 18:2119-2126(1999).  
 RN [14]  
 RP MUTAGENESIS.  
 RX MEDLINE-91184128; PubMed-2009660;  
 RA Ostrade X.V., Tavernier J., Prange T., Fiers W.,  
 RT "Localization of the active site of human tumour necrosis factor  
 (hTNF) by mutational analysis.";  
 RL EMBO J. 10:827-836(1991).  
 RN [15]  
 RP MYRISTOYLATION.  
 RX MEDLINE-93018820; PubMed-1402651;  
 RA Stevenson F.T., Bursten S.L., Locksley R.M., Lovett D.H.,  
 RT "Myristyl acylation of the tumor necrosis factor alpha precursor on  
 specific lysine residues.";  
 RL J. Exp. Med. 176:1053-1062(1992).  
 RN [16]  
 RP CLEAVAGE BY ADAM17.  
 RX MEDLINE-97186575; PubMed-9034191;  
 RA Moss M.L., Jin S.-L.C., Milla M.E., Burkhardt W., Carter H.L.,  
 RA Chen W.-J., Clay W.C., Didsbury J.R., Hassler D., Hoffman C.R.,  
 RA Kost T.A., Lambert M.H., Leesnitzer M.A., McCauley P., McGeehan G.,  
 RA Mitchell J., Moyer M., Patel G., Rocque W., Overton L.K., Schoenen F.,  
 RA Saxon T., Su J.-L., Warner J., Willard D., Becherer J.D.,  
 RT "Cloning of a disintegrin metalloproteinase that processes precursor

RT tumour-necrosis factor-alpha.";  
 RL Nature 385:733-736(1997).  
 RN [17]  
 RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).  
 RX MEDLINE=91159409; PubMed=2922050;  
 RA Jones E.Y., Stuart D.I., Walker N.P.;  
 RT "Structure of tumour necrosis factor.";  
 RL Nature 338:225-228(1989).  
 RN [18]  
 RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).  
 RX MEDLINE=91193276; PubMed=1964681;  
 RA Jones E.Y., Stuart D.I., Walker N.P.;  
 RT "The structure of tumour necrosis factor -- implications for biological function.";  
 RL J. Cell Sci. Suppl. 13:11-18(1990).  
 RN [19]  
 RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).  
 RX MEDLINE=90008932; PubMed=2551905;  
 RA Eck M.J., Sprang S.R.;  
 RT "The structure of tumor necrosis factor-alpha at 2.6-A resolution. Implications for receptor binding.";  
 RL J. Biol. Chem. 264:17595-17605(1989).  
 RN [20]  
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF MUTANT ARG-107.  
 RX MEDLINE=98147459; PubMed=9488135;  
 RA Reed C., Fu Z.Q., Wu J., Xue Y.N., Harrison R.W., Chen M.J., Weber I.F.;  
 RT "Crystal structure of TNF-alpha mutant R31D with greater affinity for receptor R1 compared with R2.";  
 RL Protein Eng. 10:1101-1107(1997).  
 RN [21]  
 RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF MUTANT M35.  
 RX MEDLINE=98113178; PubMed=9442056;  
 RA Cha S.S., Kim J.S., Cho H.S., Shin N.K., Jeong W., Shin H.C., Kim Y.J., Hahn J.H., Oh B.H.;  
 RT "High resolution crystal structure of a human tumor necrosis factor-alpha mutant with low systemic toxicity.";  
 RL J. Biol. Chem. 273:2153-2160(1998).  
 CC -1- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and TNFRSF1B/TNFR. It is mainly secreted by macrophages and can induce cell death of certain tumor cell lines. It is potent pyrogen causing fever by direct action or by stimulation of interleukin 1 secretion and is implicated in the induction of cachexia, under certain conditions it can stimulate cell proliferation and induce cell differentiation.  
 CC -1- SUBUNIT: Homotrimer.  
 CC -1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN EXTRACELLULAR SOLUBLE FORM.  
 CC -1- PTM: THE SOLUBLE FORM DERIVES FROM THE MEMBRANE FORM BY PROTEOLYTIC PROCESSING.  
 CC -1- PTM: The membrane form, but not the soluble form, is phosphorylated on serine residues. Dephosphorylation of the membrane form occurs by binding to soluble TNFRSF1A/TNFR1.  
 CC -1- DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF DISEASES, INCLUDING CANCER AND INFECTION, AND IS CHARACTERIZED BY GENERAL ILL HEALTH AND MALNUTRITION.  
 CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.  
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 DR EMBL: X02910; CAA26669.1; -

Query Match 60.2%; Score 65; DB 1; Length 233;  
 Best Local Similarity 76.9%; Pred. No. 0.0058;  
 Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 4 KOTPECAELKPMY 16

Db 179 RETPECAELKPMY 191  
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 RESULT 9  
 ID TNFA\_MACFA STANDARD; PRT; 233 AA.  
 AC P79337;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor ligand superfamily member 2) (Cachectin).  
 GN TNF OR TNFSF2 OR TNFA.  
 OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Cercopithecinae; Macaca.  
 OC NCBI\_TaxID=9541;  
 OX [1]  
 RN SEQUENCE FROM N.A.  
 RP TISSUE=Lymphocytes;  
 RA Tatsumi M.;  
 RE Submitted (JAN-1997) to the EMBL/Genbank/DBJ databases.  
 CC -1- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and TNFRSF1B/TNFR. It is mainly secreted by macrophages and can induce cell death of certain tumor cell lines. It is potent pyrogen causing fever by direct action or by stimulation of interleukin 1 secretion and is implicated in the induction of cachexia, under certain conditions it can stimulate cell proliferation and induce cell differentiation.  
 CC -1- SUBUNIT: Homotrimer (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an extracellular soluble form (By similarity).  
 CC -1- PTM: The soluble form derives from the membrane form by proteolytic processing (By similarity).  
 CC -1- PTM: The membrane form, but not the soluble form, is phosphorylated on serine residues. Dephosphorylation of the membrane form occurs by binding to soluble TNFRSF1A/TNFR1 (By similarity).  
 CC -1- DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF DISEASES, INCLUDING CANCER AND INFECTION, AND IS CHARACTERIZED BY GENERAL ILL HEALTH AND MALNUTRITION.  
 CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.  
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 DR EMBL: AB000513; BAA19131.1; -  
 DR HSSP: P01375; 4TSV.  
 DR InterPro: IPR003636; TNF\_abc.  
 DR InterPro: IPR000478; TNF\_family.  
 DR Pfam: PF00229; TNF\_1.  
 DR PRINTS: PR01234; TNFCROSISFCT.  
 DR PRODOM: PD002012; TNF\_abc; 1.  
 DR SMART: SM0207; TNF; 1.  
 DR PROSITE: PS00251; TNF\_1; 1.  
 DR PROSITE: PS50049; TNF\_2; 1.  
 KW Cytokine; Cytotoxin; Transmembrane; Phosphorylation; Signal-anchor.  
 FT CHAIN 1 233  
 FT CHAIN 77 233  
 FT DOMAIN 1 35  
 FT TRANSMEM 36 56  
 FT SIGNAL-ANCHOR (POTENTIAL).  
 FT SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN) (POTENTIAL).  
 FT EXTRACELLULAR (POTENTIAL).  
 FT CLEAVAGE (BY ADAM17) (BY SIMILARITY).  
 FT PHOSPHORYLATION (BY CK1) (BY SIMILARITY).  
 FT BY SIMILARITY.  
 FT DISULFID 145 177

SQ SEQUENCE 233 AA; 25558 MW; 6ABF2C3AB132C217 CRC64;  
 Query Match 60.2%; Score 65; DB 1; Length 233;  
 Best Local Similarity 76.9%; Pred. No. 0.0058;  
 Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 KDPREGAEKPMY 16  
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 Db 179 RETEGAEKPMY 191

RESULT 10  
 TNFA\_MACMU STANDARD; PRT; 233 AA.  
 ID TNFA\_MACMU  
 AC P48094;  
 DT 01-FEB-1996 (Rel. 33, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor ligand superfamily member 2) (cachectin).  
 GN TNF OR TNFSF2 OR TNFA.  
 OS Macaca mulatta (Rhesus macaque).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Macaca.  
 OC Cercopithecoidea; Macaca.  
 OX NCBI\_TaxID=9344;  
 RN [1]  
 RP MEDLINE=96003435; PubMed=7561102;  
 RA Villinger F.J., Brar S.S., Mayne A.E., Chikkala N., Ansari A.A.;  
 RT "Comparative sequence analysis of cytokine genes from human and nonhuman primates."  
 RL J. Immunol. 155:3946-3954(1995).  
 CC -1- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and TNFSF1B/TNFR. It is mainly secreted by macrophages and can induce cell death of certain tumor cell lines. It is potent pyrogen causing fever by direct action or by stimulation of interleukin 1 secretion and is implicated in the induction of cachexia, under certain conditions it can stimulate cell proliferation and induce cell differentiation.  
 CC -1- SUBUNIT: Homotrimer (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an extracellular soluble form (By similarity).  
 CC -1- PTM: The soluble form derives from the membrane form by proteolytic processing (By similarity).  
 CC -1- PTM: The membrane form, but not the soluble form, is phosphorylated on serine residues. Dephosphorylation of the membrane form occurs by binding to soluble TNFRSF1A/TNFR1 (By similarity).  
 CC -1- DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF DISEASES, INCLUDING CANCER AND INFECTION, AND IS CHARACTERIZED BY GENERAL ILL HEALTH AND MALNUTRITION.  
 CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.  
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 CC EMBL: U19850; AAA6712.1; -.  
 DR HSSP: P01375; 4TSV.  
 DR InterPro: IPR003636; TNF\_abc.  
 DR InterPro: IPR00478; TNF\_family.  
 DR Pfam: PF00229; TNF\_1.  
 DR PRINTS: PR01234; TNECROSISFCT.  
 DR PRODOM: PD002012; TNF\_abc; 1.  
 DR SMART: SM00207; TNF\_1.  
 DR SMART: PS00251; TNF\_1; 1.  
 DR PROSITE: PS0049; TNF\_2; 1.  
 KW Cytokine; Cytotoxin; Transmembrane; Phosphorylation; Signal-anchor.

FT CHAIN 1 233 TUMOR NECROSIS FACTOR, MEMBRANE FORM.  
 FT CHAIN 77 233 TUMOR NECROSIS FACTOR, SOLUBLE FORM.  
 FT DOMAIN 1 35 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 36 56 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN) (POTENTIAL).  
 FT DOMAIN 57 233 EXTRACELLULAR (POTENTIAL).  
 FT SITE 76 77 CLEAVAGE (BY ADAM17) (BY SIMILARITY).  
 FT MOD\_RES 2 2 PHOSPHORYLATION (BY CK1) (BY SIMILARITY).  
 FT DISULFID 145 177 BY SIMILARITY.  
 SQ SEQUENCE 233 AA; 25630 MW; 9F6F85050595FD59 CRC64;  
 Query Match 60.2%; Score 65; DB 1; Length 233;  
 Best Local Similarity 76.9%; Pred. No. 0.0058;  
 Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 KDPREGAEKPMY 16  
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 Db 179 RETEGAEKPMY 191

RESULT 11  
 TNFA\_PAPHU STANDARD; PRT; 233 AA.  
 ID TNFA\_PAPHU  
 AC G77510;  
 DT 15-DEC-1998 (Rel. 37, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor ligand superfamily member 2) (cachectin).  
 GN TNF OR TNFSF2 OR TNFA.  
 OS Papio hamadryas ursinus (Chacma baboon).  
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Macaca.  
 OC Cercopithecoidea; Papio.  
 OX NCBI\_TaxID=36229;  
 RN [1]  
 RP MEDLINE=98147379; PubMed=9488055;  
 RA Haudek S.B., Redl H., Schleg G., Giroit B.P.;  
 RT "Complementary DNA (cDNA) sequence of baboon tumor necrosis factor alpha."  
 RL Mol. Immunol. 34:1041-1042(1997).  
 CC -1- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and TNFSF1B/TNFR. It is mainly secreted by macrophages and can induce cell death of certain tumor cell lines. It is potent pyrogen causing fever by direct action or by stimulation of interleukin 1 secretion and is implicated in the induction of cachexia, under certain conditions it can stimulate cell proliferation and induce cell differentiation.  
 CC -1- SUBUNIT: Homotrimer (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an extracellular soluble form (By similarity).  
 CC -1- PTM: The soluble form derives from the membrane form by proteolytic processing (By similarity).  
 CC -1- PTM: The membrane form, but not the soluble form, is phosphorylated on serine residues. Dephosphorylation of the membrane form occurs by binding to soluble TNFRSF1A/TNFR1 (By similarity).  
 CC -1- DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF DISEASES, INCLUDING CANCER AND INFECTION, AND IS CHARACTERIZED BY GENERAL ILL HEALTH AND MALNUTRITION.  
 CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.  
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 CC EMBL: AF019963; AAC31675.1; -.  
 DR HSSP: P01375; 4TSV.



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DR InterPro: IPR003636; TNF_abc.
DR InterPro: IPR000478; TNF_family.
DR Pfam: PF00229; TNF; 1.
DR PRINTS: PR01234; TNECROSISFCT.
DR PRODOM: PD002012; TNF_abc; 1.
DR SMART: SM00207; TNF; 1.
DR PROSITE: PS00251; TNF_1; 1.
DR PROSITE: PS50049; TNF_2; 1.
DR Cytokine; Cytotoxin; Transmembrane; Phosphorylation; Signal-anchor.
KW CHAIN 1 233 TUMOR NECROSIS FACTOR, MEMBRANE FORM.
FT CHAIN 77 233 TUMOR NECROSIS FACTOR, SOLUBLE FORM.
FT DOMAIN 1 35 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 36 56 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
(POTENTIAL).
FT DOMAIN 57 233 EXTRACELLULAR (POTENTIAL).
FT SITE 76 77 CLEAVAGE (BY ADAM17) (BY SIMILARITY).
FT MOD_RES 2 2 PHOSPHORYLATION (BY CK1) (BY SIMILARITY).
FT DISULFID 145 177 BY SIMILARITY.
SQ SEQUENCE 233 AA; 25658 MW; B940325058DA03 CRC64;

Query Match 60.2%; Score 65; DB 1; Length 233;
Best Local Similarity 76.9%; Pred. No. 0.0058;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 KOTPEGAELKPMY 16
Db 179 RETPEGAELKPMY 191
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RESULT 12
TNFA_PAPSP STANDARD; PRT; 233 AA.
ID TNFA_PAPSP
AC P33620;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor
DE ligand superfamily member 2) (Cachectin).
GN TNF OR TNFSF2 OR TNFA.
OS Papio sp. (Baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoinae; Papio.
NCBI_TaxID=61183;
[1]
SEQUENCE FROM N.A.
RA Sanjanwala M., Edwards A.;
RL Submitted (SEP-1991) to the EMBL/Genbank/DBJ databases.
CC -1- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and
CC TNFRSF1B/TNFR. It is mainly secreted by macrophages and can
CC induce cell death of certain tumor cell lines. It is potent
CC pyrogen causing fever by direct action or by stimulation of
CC interleukin 1 secretion and is implicated in the induction of
CC cachexia. Under certain conditions it can stimulate cell
CC proliferation and induce cell differentiation.
CC -1- SUBUNIT: Homotrimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an
CC extracellular soluble form (By similarity).
CC -1- PTM: The soluble form derives from the membrane form by
CC proteolytic processing (By similarity).
CC -1- PTM: The membrane form, but not the soluble form, is
CC phosphorylated on serine residues. Dephosphorylation of the
CC membrane form occurs by binding to soluble TNFRSF1A/TNFR1 (By
CC similarity).
CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
CC -----
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
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CC -----
CC EMBL: Y62141; CAA44068.1; -
CC PIR: S22052; S22052.
CC HSSP: P01375; IABM.
CC InterPro: IPR003636; TNF_abc.
CC InterPro: IPR000478; TNF_family.
CC Pfam: PF00229; TNF; 1.
CC PRINTS: PR01234; TNECROSISFCT.
CC PRODOM: PD002012; TNF_abc; 1.
CC SMART: SM00207; TNF; 1.
CC PROSITE: PS00251; TNF_1; 1.
CC PROSITE: PS50049; TNF_2; 1.
CC Cytokine; Cytotoxin; Transmembrane; Phosphorylation; Signal-anchor;
KW Myristate.
FT CHAIN 1 233 TUMOR NECROSIS FACTOR, MEMBRANE FORM.
FT CHAIN 77 233 TUMOR NECROSIS FACTOR, SOLUBLE FORM.
FT DOMAIN 1 35 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 36 56 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
(POTENTIAL).
FT DOMAIN 57 233 EXTRACELLULAR (POTENTIAL).
FT SITE 76 77 CLEAVAGE (BY ADAM17) (BY SIMILARITY).
FT MOD_RES 2 2 PHOSPHORYLATION (BY CK1) (BY SIMILARITY).
FT LIPID 19 19 MYRISTATE (BY SIMILARITY).
FT LIPID 20 20 MYRISTATE (BY SIMILARITY).
FT DISULFID 145 177 BY SIMILARITY.
SQ SEQUENCE 233 AA; 25557 MW; 455360B48C74173 CRC64;

Query Match 60.2%; Score 65; DB 1; Length 233;
Best Local Similarity 76.9%; Pred. No. 0.0058;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 KOTPEGAELKPMY 16
Db 179 RETPEGAELKPMY 191
:::|||||::|

RESULT 13
TNFA_TURTR STANDARD; PRT; 233 AA.
ID TNFA_TURTR
AC Q9BEA1;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor
DE ligand superfamily member 2) (Cachectin).
GN TNF OR TNFSF2 OR TNFA.
OS Tursiops truncatus (Atlantic bottle-nosed dolphin).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Cetacea; Odontoceti; Delphinidae;
OC Tursiops.
NCBI_TaxID=9739;
[1]
SEQUENCE FROM N.A.
RA Shoji Y., Inoue Y., Sugisawa H., Itou T., Endo T., Sakai T.;
RX PubMed-11587733;
RT "Molecular cloning and functional characterization of bottlenose
RT dolphin (Tursiops truncatus) tumor necrosis factor alpha.";
RL Vet. Immunol. Immunopathol. 82:183-192(2001).
CC -1- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and
CC TNFRSF1B/TNFR. It is mainly secreted by macrophages and can
CC induce cell death of certain tumor cell lines. It is potent
CC pyrogen causing fever by direct action or by stimulation of
CC interleukin 1 secretion and is implicated in the induction of
CC cachexia. Under certain conditions it can stimulate cell
CC proliferation and induce cell differentiation (By similarity).
CC -1- SUBUNIT: Homotrimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an
CC extracellular soluble form (By similarity).
CC -1- PTM: The soluble form derives from the membrane form by
CC proteolytic processing (By similarity).
CC -1- PTM: The membrane form, but not the soluble form, is
CC phosphorylated on serine residues. Dephosphorylation of the
CC membrane form occurs by binding to soluble TNFRSF1A/TNFR1 (By
CC similarity).
```

CC similarity). BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.  
 CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 CC EMBL: AB049358; BAB39855.1; -  
 CC HSSP: P01375; 4TSV.  
 CC InterPro: IPR003636; TNF\_abc.  
 CC InterPro: IPR000478; TNF\_family.  
 CC Pfam: PF00229; TNF\_1.  
 CC PRINTS: PR01234; TNECROSISFCT.  
 CC PRODOM: PD002012; TNF\_abc; 1.  
 CC SMART: SM00207; TNF; 1.  
 CC PROSITE: PS00251; TNF\_1; 1.  
 CC PROSITE: PS50049; TNF\_2; 1.  
 CC Cytokine; Cytotoxin; Transmembrane; Glycoprotein; Phosphorylation;  
 CC Signal-anchor.  
 CC CHAIN 1 233 TUMOR NECROSIS FACTOR, MEMBRANE FORM.  
 CC FT CHAIN 78 233 TUMOR NECROSIS FACTOR, SOLUBLE FORM.  
 CC FT DOMAIN 1 35 CYTOPLASMIC (POTENTIAL).  
 CC FT TRANSMEM 36 56 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)  
 CC FT (POTENTIAL).  
 CC FT DOMAIN 57 233 EXTRACELLULAR (POTENTIAL).  
 CC FT SITE 77 78 CLEAVAGE (BY ADAM17) (BY SIMILARITY).  
 CC FT MOD\_RES 42 2 PHOSPHORYLATION (BY CK1) (BY SIMILARITY).  
 CC FT DISULFID 145 177 BY SIMILARITY.  
 CC FT CARBOHYD 95 95 N-LINKED (GLCNAC... ) (POTENTIAL).  
 CC SQ SEQUENCE 233 AA; 25404 MW; 71CC39689CC49D9 CRC64;  
 CC  
 CC Query Match 60.2%; Score 65; DB 1; Length 233;  
 CC Best Local Similarity 76.9%; Pred. No. 0.0058;  
 CC Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 CC  
 CC 4 KDPGAEELKPMY 16  
 CC Db 179 REPPEGAELKPMY 191  
 CC  
 CC RESULT 14  
 CC TNFA.CAPHI STANDARD; PRT; 234 AA.  
 CC ID TNFA\_CAPHI Q28320; Q9MYE2;  
 CC AC P13296; Q28320; Q9MYE2;  
 CC DT 01-JAN-1990 (Rel. 13, Created)  
 CC DT 15-JUN-2002 (Rel. 41, Last sequence update)  
 CC DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 CC DE Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor  
 CC DE ligand superfamily member 2) (Cachectin).  
 CC GN TNF OR TNFSF2 OR TNFA.  
 CC OS Capra hircus (Goat).  
 CC CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 CC CC Bovidae; Caprinae; Capra.  
 CC CC NCBI\_TaxID=9925;  
 CC OK NCBI\_TaxID=9925;  
 CC RN (1)  
 CC RP SEQUENCE FROM N.A.  
 CC RC TISSUE=Splenocyte;  
 CC RA Takakura H., Mori Y., Tatsumi M.;  
 CC RT "Molecular cloning of caprine TNF-alpha cDNA and its expression in  
 CC RT E.coli and insect cells.";  
 CC RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.  
 CC RN [2]  
 CC RP SEQUENCE OF 41-234 FROM N.A.  
 CC RA Goldstein I.M., Henner D., Talhouk A.;  
 CC RL Submitted (MAR-1989) to the EMBL/GenBank/DBJ databases.  
 CC RN [3]  
 CC RP SEQUENCE OF 44-234 FROM N.A.  
 CC RC TISSUE=Ovarian follicle;

RA Wang B., Zhang Y.;  
 RT "Goat ovarian TNF alpha cDNA sequence."  
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.  
 RP SEQUENCE OF 75-234 FROM N.A.  
 RC TISSUE=Blood;  
 RA Rüstad E.;  
 RL Submitted (JAN-1994) to the EMBL/GenBank/DBJ databases.  
 CC  
 CC -1- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and  
 CC TNFRSF1B/TNFR. It is mainly secreted by macrophages and can  
 CC induce cell death of certain tumor cell lines. It is potent  
 CC pyrogen causing fever by direct action or by stimulation of  
 CC interleukin 1 secretion and is implicated in the induction of  
 CC cachexia. Under certain conditions it can stimulate cell  
 CC proliferation and induce cell differentiation.  
 CC  
 CC -1- SUBUNIT: Homotrimer (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an  
 CC extracellular soluble form (By similarity).  
 CC -1- PTM: The soluble form derives from the membrane form by  
 CC proteolytic processing (By similarity).  
 CC -1- PTM: The membrane form, but not the soluble form, is  
 CC phosphorylated on serine residues. Dephosphorylation of the  
 CC membrane form occurs by binding to soluble TNFRSF1A/TNFR1 (By  
 CC similarity).  
 CC -1- DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF DISEASES, INCLUDING  
 CC CANCER AND INFECTION, AND IS CHARACTERIZED BY GENERAL ILL HEALTH  
 CC AND MALNUTRITION.  
 CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.  
 CC -1- CAUTION: Ref.2 sequence differs from that shown due to a  
 CC frameshift in position 60.  
 CC  
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 CC  
 CC EMBL: D86587; BAA13130.1; -  
 CC DR EMBL: X14828; CAA32937.1; ALT\_FRAME.  
 CC DR EMBL: AF276985; AAR87741.1; -  
 CC DR EMBL: X77317; CAA54523.1; -  
 CC DR PIR: S06192; S06192.  
 CC DR HSSP: P01375; 4TSV.  
 CC DR InterPro: IPR003636; TNF\_abc.  
 CC DR InterPro: IPR000478; TNF\_family.  
 CC DR Pfam: PF00229; TNF\_1.  
 CC DR PRODOM: PD002012; TNF\_abc; 1.  
 CC DR SMART: SM00207; TNF; 1.  
 CC DR PROSITE: PS00251; TNF\_1; 1.  
 CC DR PROSITE: PS50049; TNF\_2; 1.  
 CC KW Cytokine; Cytotoxin; Transmembrane; Signal-anchor.  
 CC FT CHAIN 1 234  
 CC FT DOMAIN 79 234  
 CC FT TRANSMEM 36 56  
 CC FT (POTENTIAL).  
 CC FT DOMAIN 57 233  
 CC FT MOD\_RES 78 79  
 CC FT SITE 146 178  
 CC FT CARBOHYD 96 96  
 CC FT CONFLICT 79 79  
 CC FT CONFLICT 119 119  
 CC FT CONFLICT 129 129  
 CC FT CONFLICT 155 155  
 CC FT CONFLICT 164 164  
 CC FT CONFLICT 184 184  
 CC FT CONFLICT 185 185  
 CC FT CONFLICT 215 215  
 CC SQ SEQUENCE 234 AA; 25519 MW; 9768E33BBAB041 CRC64;  
 CC  
 CC EXTRACELLULAR (POTENTIAL).  
 CC CLEAVAGE (BY ADAM17) (BY SIMILARITY).  
 CC BY SIMILARITY.  
 CC N-LINKED (GLCNAC... ) (POTENTIAL).  
 CC T. -> N (IN REF. 4).  
 CC Y. -> Q (IN REF. 4).  
 CC H. -> D (IN REF. 4).  
 CC E -> EG (IN REF. 4).  
 CC MISSING (IN REF. 2).  
 CC Q -> L (IN REF. 3 AND 4).  
 CC  
 CC TUMOR NECROSIS FACTOR, MEMBRANE FORM.  
 CC TUMOR NECROSIS FACTOR, SOLUBLE FORM.  
 CC CYTOPLASMIC (POTENTIAL).  
 CC SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)  
 CC (POTENTIAL).



Query Match 60.2%; Score 65; DB 1; Length 234;  
 Best Local Similarity 76.9%; Pred. No. 0.0059;  
 Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 KDTPEGAELKPMY 16  
 Db 180 RETPEGAELKPMY 192

RESULT 15  
 ID TNFA\_MARMO STANDARD: PRT; 233 AA.  
 AC 035734;  
 DT 15-JUL-1999 (Rel. 38, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last sequence update)  
 DE 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor  
 ligand superfamily member 2) (Cachectin).  
 GN TNF OR TNFSF2 OR TNFA.  
 OS Marmota monax (Woodchuck).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;  
 OC Marmota.  
 OC NCBI\_TaxID:9995;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-Peripheral blood;  
 RX MEDLINE-98139533; PubMed-9472070;  
 RA Lohrengel B., Lu M., Roggendorf M.;  
 RT "Molecular cloning of the woodchuck cytokines: TNF-alpha, IFN-gamma,  
 and IL-6."  
 RL Immunogenetics 47:332-335(1996).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-Peripheral blood;  
 RX MEDLINE-20184748; PubMed-10721723;  
 RA Li D.H., Haveli E.A., Brown C.L., Cullen J.M.;  
 RT "Woodchuck lymphotoxin-alpha, -beta and tumor necrosis factor genes:  
 structure, characterization and biological activity."  
 RL Gene 242:295-305(2000).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-Peripheral blood;  
 RX MEDLINE-20184748; PubMed-10721723;  
 RA Li D.H., Haveli E.A., Brown C.L., Cullen J.M.;  
 RT "Woodchuck lymphotoxin-alpha, -beta and tumor necrosis factor genes:  
 structure, characterization and biological activity."  
 RL Gene 242:295-305(2000).  
 CC -1- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and  
 TNFRSF1B/TNFR2. It is mainly secreted by macrophages and can  
 induce cell death of certain tumor cell lines. It is potent  
 pyrogen causing fever by direct action or by stimulation of  
 interleukin 1 secretion and is implicated in the induction of  
 cachexia. Under certain conditions it can stimulate cell  
 proliferation and induce cell differentiation.  
 CC -1- SUBUNIT: Homotrimer (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an  
 extracellular soluble form (By similarity).  
 CC -1- PTM: The soluble form derives from the membrane form by  
 proteolytic processing (By similarity).  
 CC -1- PTM: The membrane form, but not the soluble form, is  
 phosphorylated on serine residues. Dephosphorylation of the  
 membrane form occurs by binding to soluble TNFRSF1A/TNFR1 (By  
 similarity).  
 CC -1- DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF DISEASES, INCLUDING  
 CANCER AND INFECTION, AND IS CHARACTERIZED BY GENERAL ILL HEALTH  
 AND MALNUTRITION.  
 CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.  
 CC -----  
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CC -----  
 DR EMBL: Y14137; CAA74569.1; -  
 DR EMBL: AF082491; AAC32615.1; -  
 DR EMBL: AF012910; AAF34863.1; -  
 DR HSSP: P06804; 2TNF.  
 DR InterPro: IPR003636; TNF\_abg.  
 DR InterPro: IPR000478; TNF\_family.  
 DR Pfam: PF00229; TNF\_1.  
 DR PRINTS: PR01234; TNECROSISFCT.  
 DR PRODOM: PD002012; TNF\_abg; 1.  
 DR SMART: SM00207; TNF\_1.  
 DR PROSITE: PS00251; TNF\_2; 1.  
 DR PROSITE: PS0049; TNF\_2; 1.  
 KW Cytokine; Cytotoxin; Transmembrane; Phosphorylation; Signal-anchor.  
 FT CHAIN 1 233  
 FT CHAIN 78 233  
 FT DOMAIN 1 35  
 FT TRANSMEM 36 56  
 FT DOMAIN 57 233  
 FT SITE 77 78  
 FT MOD\_RES 2 2  
 FT DISULFID 146 177  
 SO SEQUENCE 233 AA; 25764 MW; 34D3D1965DAAE07 CRC64;

Query Match 57.4%; Score 62; DB 1; Length 233;  
 Best Local Similarity 71.4%; Pred. No. 0.017;  
 Matches 10; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 KDTPEGAELKPMY 16  
 Db 178 KESTLEGAELKPMY 191

Search completed: April 4, 2003, 08:40:28  
 Job time : 7.85484 secs

GenCore version 5.1.4.p5.4578  
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OM protein - protein search, using sw model

Run on: April 4, 2003, 08:37:16 ; Search time 24.6774 Seconds

(without alignments)  
141.944 Million cell updates/sec

Title: US-09-779-703-5

Perfect score: 108

Sequence: 1 GGPKPDPGAELEKPMYC 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPREMBL\_21.\*  
1: sp\_archaea.\*  
2: sp\_bacteria.\*  
3: sp\_fungi.\*  
4: sp\_human.\*  
5: sp\_invertebrate.\*  
6: sp\_mammal.\*  
7: sp\_mhc.\*  
8: sp\_organelle.\*  
9: sp\_phage.\*  
10: sp\_plant.\*  
11: sp\_rodent.\*  
12: sp\_virus.\*  
13: sp\_vertebrate.\*  
14: sp\_unclassified.\*  
15: sp\_virus.\*  
16: sp\_bacteriophage.\*  
17: sp\_archaeal.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	84	77.8	235	11	09J126
2	80	74.1	235	11	09J127
3	77	71.3	156	11	09J124
4	77	71.3	217	11	09ERG6
5	75	69.4	216	11	070332
6	65	60.2	66	4	09P102
7	65	60.2	149	6	097543
8	65	60.2	217	6	09BEF4
9	65	60.2	232	4	09UTV3
10	62	57.4	215	11	09JND1
11	62	57.4	216	6	09BEC4
12	62	57.4	157	6	043647
13	60	55.6	215	6	09BEE8
14	60	55.6	217	6	09BEG0
15	58	53.7	217	6	09BEG1

17	57	52.8	104	6	027978	027978	bos taurus
18	51	47.2	138	6	09TTC7	09TTC7	actus lemur
19	51	47.2	149	6	09T538	09T538	actus vocif
20	51	47.2	149	6	09TTC8	09TTC8	actus nigri
21	51	47.2	234	6	09TTC3	09TTC3	equus caball
22	49	45.4	407	16	09X826	09X826	streptomyce
23	49	45.4	656	5	09N342	09N342	caenorhabdi
24	48.5	44.9	347	17	029274	029274	archaeoglob
25	48	44.4	216	6	09BEC9	09BEC9	ochotona pr
26	48	44.4	433	16	09RD01	09RD01	streptomyce
27	48	44.4	674	11	060979	060979	mus musc
28	48	44.4	1234	2	09AES2	09AES2	clostridium
29	48	44.4	1649	16	09CFA2	09CFA2	lactococcus
30	48	44.4	2157	11	09ZIR1	09ZIR1	mus musc
31	47.5	44.0	551	2	09RH54	09RH54	pantoea agg
32	47	43.5	259	12	086972	086972	western equ
33	47	43.5	1235	12	09IBP3	09IBP3	western equ
34	47	43.5	1241	12	066579	066579	eastern equ
35	47	43.5	1242	12	086578	086578	eastern equ
36	47	43.5	1242	12	09PZX7	09PZX7	eastern equ
37	47	43.5	1242	12	09PZX6	09PZX6	eastern equ
38	47	43.5	1242	12	09PZX5	09PZX5	eastern equ
39	47	43.5	1242	12	09PZX4	09PZX4	eastern equ
40	47	43.5	1242	12	09PZX3	09PZX3	eastern equ
41	47	43.5	1242	12	09PZX2	09PZX2	eastern equ
42	47	43.5	1242	12	09PZX1	09PZX1	eastern equ
43	47	43.5	1242	12	09PZX0	09PZX0	eastern equ
44	47	43.5	1242	12	09PZX9	09PZX9	eastern equ
45	47	43.5	1242	12	09PZX8	09PZX8	eastern equ

## ALIGNMENTS

## RESULT 1

09J126 PRELIMINARY; PRT; 235 AA.  
ID 09J126  
AC 09J126;  
DT 01-OCT-2000 (TREMBlrel. 15, Created)  
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
DE TNF-alpha propeptide 3 (Fragment).  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
CX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=DARK AGOUTI;  
RA Seidel M.F., Junier M.-P., Vetter H.;  
RT "TNF-alpha polymorphism in rats with collagen-induced arthritis.";  
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF269160; AAF82568.1; -;  
DR HSSP; P06804; TNF;  
DR InterPro; IPR003636; TNF\_abc.  
DR InterPro; IPR000478; TNF\_family.  
DR Pfam; PF00229; TNF; 1.  
DR PRINTS; PR01234; TNFCROSISFCT.  
DR PRODOM; PD002012; TNF\_abc; 1.  
DR SMART; SM00207; TNF; 1.  
DR PROSITE; PS00251; TNF\_1; 1.  
DR PROSITE; PS50049; TNF\_2; 1.  
FT NOE\_TER 235  
SQ SEQUENCE 235 AA; 25789 MW; C801B92D049C2F2E CRC64;

Query Match 77.8%; Score 84; DB 11; Length 235;  
Best Local Similarity 100.0%; Pred. No. 2.7e-05;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 3 PKDTPGAELEKPMY 16  
DB 180 PKDTPGAELEKPMY 193

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RESULT 2
09J127 ID 09J127 PRELIMINARY; PRT; 235 AA.
AC 09J127;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE TNF-alpha propeptide 5 (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DARK AGOUTI;
RA Seidel M.F., Junter M.-P., Vetter H.;
RT "TNF-alpha polymorphism in rats with collagen-induced arthritis.";
RL Submitted (MAY-2000) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF269159; AAF82567.1; -.
DR HSSP; P06804; 2TNF.
DR InterPro; IPR003636; TNF_abc.
DR InterPro; IPR000478; TNF_family.
DR Pfam; PF00229; TNF; 1.
DR PRINTS; PR01234; TNECROSISFCT.
DR PRODOM; PD002012; TNF_abc; 1.
DR SMART; SM00207; TNF_1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS50049; TNF_2; 1.
FT NON_TER 235
SQ SEQUENCE 235 AA; 25806 MW; 12A8EC6D0491428D CRC64;

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Query Match
Best Local Similarity 74.1%; Score 80; DB 11; Length 235;
Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 3 PKDTPGAEKPMY 16
Db 180 PKDTPGAEKPMY 193

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RESULT 3
09J124 ID 09J124 PRELIMINARY; PRT; 156 AA.
AC 09J124;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Tumor necrosis factor alpha (Fragment).
OS Sigmodon hispidus (Hispid cotton rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
OC Sigmodon.
OX NCBI_TaxID=42415;
RN [1]
RP SEQUENCE FROM N.A.
RA Bianco J.C., Pietneva L.M., Prince G.A.;
RT "Sigmodon hispidus cytokines, chemokines and interferons.";
RL Submitted (SEP-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF421388; AAL18818.1; -.
DR InterPro; IPR003636; TNF_abc.
DR InterPro; IPR000478; TNF_family.
DR Pfam; PF00229; TNF; 1.
DR PRODOM; PD002012; TNF_abc; 1.
DR PROSITE; PS00251; TNF_1; UNKNOWN_1.
DR PROSITE; PS50049; TNF_2; 1.
FT NON_TER 1
SQ SEQUENCE 156 AA; 17303 MW; DC565F3BC3C82654 CRC64;

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Query Match
Best Local Similarity 71.3%; Score 77; DB 11; Length 156;
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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QY 3 PKDTPGAEKPMY 16
Db 101 PKDTPGAEKPMY 114

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RESULT 4
09ERG6 ID 09ERG6 PRELIMINARY; PRT; 217 AA.
AC 09ERG6;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Tumor necrosis factor alpha (Fragment).
OS Peromyscus maniculatus (Deer mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
OC Peromyscus.
OX NCBI_TaxID=10042;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=SPLEEN;
RA Herbst M.M., Schountz T.;
RT "Cloning of the deer mouse interferon gamma, interleukin-10 and tumor
necrosis factor genes.";
RL Submitted (SEP-2000) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF307013; AAG30264.1; -.
DR HSSP; P06804; 2TNF.
DR InterPro; IPR003636; TNF_abc.
DR InterPro; IPR000478; TNF_family.
DR Pfam; PF00229; TNF; 1.
DR PRINTS; PR01234; TNECROSISFCT.
DR PRODOM; PD002012; TNF_abc; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS50049; TNF_2; 1.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 217 AA; 23964 MW; D6F90C74C0B3021F CRC64;

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Query Match
Best Local Similarity 71.3%; Score 77; DB 11; Length 217;
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 3 PKDTPGAEKPMY 16
Db 172 PKDTPGAEKPMY 185

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RESULT 5
070332 ID 070332 PRELIMINARY; PRT; 216 AA.
AC 070332;
DT 01-AUG-1998 (TREMBlrel. 07, Created)
DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)
DT 01-OCT-2001 (TREMBlrel. 18, Last annotation update)
DE Tumor necrosis factor-alpha (Fragment).
OS Mesocricetus auratus (Golden hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Mesocricetus.
OX NCBI_TaxID=10036;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=SPLEEN;
RX MEDLINE=98234044; PubMed=9573100;
RA Melby P.C., Tryon V.V., Chandrasekar B., Freeman G.L.;
RT "Cloning of Syrian hamster (Mesocricetus auratus) cytokine cDNAs and
RT analysis of cytokine mRNA expression in experimental visceral
leishmaniasis.";
RL Infect. Immun. 66:2135-2142(1998).
DR EMBL; AF046215; AAC40100.1; -.
DR HSSP; P06804; 2TNF.
DR InterPro; IPR003636; TNF_abc.

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DR InterPro: IPR000478; TNF_family.
DR Pfam: PF00229; TNF_1.
DR PRINTS: PRO1234; TNECROSISFCT.
DR ProDom: PD002012; TNF_abc; 1.
DR SMART: SM00207; TNF_1.
DR PROSITE: PS00251; TNF_1; 1.
DR PROSITE: PS50049; TNF_2; 1.
DR NON_TER 1
FT NON_TER 1
SO SEQUENCE 216 AA; 23793 MW; BADAE3F83F45B533 CRC64;

Query Match
Best Local Similarity 69.4%; Score 75; DB 11; Length 216;
Matches 12; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 3 KDPREGAELKPMY 16
DB 170 KETPEGEELKPMY 183
:::|||||

RESULT 6
O9PIQ2 PRELIMINARY; PRT; 66 AA.
ID O9PIQ2
AC O9PIQ2
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DE APO1 protein (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Carnivora; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PROSTATE TUMOR;
RA Shao C., Yan W., Zhu F., Yue W., Chai Y., Zhao Z., Wang C.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF098751; AAF71992.1; -
DR HSSP: P01375; STSW.
DR InterPro: IPR003636; TNF_abc.
DR Pfam: PF00229; TNF_1.
DR PRINTS: PRO1234; TNECROSISFCT.
DR ProDom: PD002012; TNF_abc; 1.
DR PROSITE: PS50049; TNF_2; 1.
FT NON_TER 66
SQ SEQUENCE 66 AA; 7300 MW; C58DC35377E6D368 CRC64;

Query Match
Best Local Similarity 76.9%; Score 65; DB 4; Length 66;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 4 KDPREGAELKPMY 16
DB 31 KETPEGEELKPMY 43
:::|||||

RESULT 7
O97543 PRELIMINARY; PRT; 149 AA.
ID O97543
AC O97543
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DE Tumor necrosis factor alpha (Fragment).
OS Aotus naucymae (Owl monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.
OX NCBI_TaxID=37293;
RN [1]
RP SEQUENCE FROM N.A.
RA Echeverry S.J., Hernandez E., Moreno A., Patarro M.E., Murillo L.A.;

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RT "Identification, cloning and sequencing of different interleukin genes
in Aotus species."
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF014513; AAD01539.1; -
DR HSSP: P01375; 4TSV.
DR InterPro: IPR003636; TNF_abc.
DR Pfam: PF00229; TNF_1.
DR PRINTS: PRO1234; TNECROSISFCT.
DR ProDom: PD002012; TNF_abc; 1.
DR SMART: SM00207; TNF_1.
DR PROSITE: PS00251; TNF_1; 1.
DR PROSITE: PS50049; TNF_2; 1.
FT NON_TER 1
FT NON_TER 1
SO SEQUENCE 149 AA; 16466 MW; 3C2A6140778EFA8A CRC64;

Query Match
Best Local Similarity 60.2%; Score 65; DB 6; Length 149;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 4 KDPREGAELKPMY 16
DB 96 KETPEGEELKPMY 108
:::|||||

RESULT 8
O9BEF4 PRELIMINARY; PRT; 217 AA.
ID O9BEF4
AC O9BEF4
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DE Tumor necrosis factor (Fragment).
OS Cabassous unicinctus (Southern naked-tailed armadillo).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Edentata; Dasypodidae; Cabassous.
OX NCBI_TaxID=48852;
RN [1]
RP SEQUENCE FROM N.A.
RA van Dijk M.A.M., de Jong W.W.;
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ268829; CAC28518.1; -
DR HSSP: P01375; 4TSV.
DR InterPro: IPR003636; TNF_abc.
DR Pfam: PF00229; TNF_1.
DR PRINTS: PRO1234; TNECROSISFCT.
DR ProDom: PD002012; TNF_abc; 1.
DR SMART: SM00207; TNF_1.
DR PROSITE: PS00251; TNF_1; 1.
DR PROSITE: PS50049; TNF_2; 1.
FT NON_TER 1
FT NON_TER 1
SO SEQUENCE 217 AA; 23742 MW; 83C591DD6883FD86 CRC64;

Query Match
Best Local Similarity 76.9%; Score 65; DB 6; Length 217;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 4 KDPREGAELKPMY 16
DB 171 KETPEGEELKPMY 183
:::|||||

RESULT 9
O9UIV3 PRELIMINARY; PRT; 232 AA.
ID O9UIV3
AC O9UIV3
DT 01-MAY-2000 (TREMBLrel. 13, Created)

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DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE Tumor necrosis factor.  
 GN TNF.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=93272029; PubMed=8499947;  
 RA Irits F., Bougueret L., Prieur S., Caterina D., Prims G., Perrot V.,  
 RA Jurka J., Rodriguez-Tome P., Clavierie J., Cohen D., Dussset J.,  
 RT "dense A1u clustering and a potential new member of the NFkappa  
 RT family within a 90 kilobase HLA class III segment.";  
 RL Nat. Genet. 3:137-145(1993).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=96215741; PubMed=86293307;  
 RA Utans U., Quist W.C., McManus B.W., Wilson J.E., Arceci R.J.,  
 RA Wallace A.F., Russell M.E.;  
 RT "Allograft inflammatory factor-1. A cytokine-responsive macrophage  
 RT molecule expressed in transplanted human hearts.";  
 RL Transplantation 61:1387-1392(1996).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=96006565; PubMed=7590964;  
 RA Holzinger I., de Baey A., Messer G., Kick G., Zwierzina H.,  
 RA Weiss S.H.;  
 RT "Cloning and genomic characterization of Lst1: a new gene in the human  
 RT TNF region.";  
 RL Immunogenetics 42:315-322(1995).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=93208881; PubMed=7916555;  
 RA Browning J.L., Ngam-ek A., Lawton P., Dekarinis J., Tizard R.,  
 RA Chow E.P., Hession C., O'Brine-Greco B., Royle S.F., Ware C.F.;  
 RT "lymphotoxin-beta: A new member of the TNF family that forms a  
 RT heteromeric complex with lymphotoxin on the cell surface.";  
 RL Cell 72:847-856(1993).  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=86016093; PubMed=2995927;  
 RA Nedwin G.E., Naylor S.L., Sakaguchi A.Y., Smith D., Jarrett-Nedwin J.,  
 RA Pennica D., Goeddel D.V., Gray P.W.;  
 RT "Human lymphotoxin and tumor necrosis factor genes: structure,  
 RT homology and chromosomal localization.";  
 RL Nucleic Acids Res. 13:6361-6373(1985).  
 RN [6]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=91086846; PubMed=1670638;  
 RA Messer G., Spengler U., Jung M.C., Honold G., Bloemer K., Page G.R.,  
 RA Riethmuller G., Weiss E.H.;  
 RT "Polymorphic structure of the Tumor Necrosis Factor (TNF) Locus: An  
 RT Ncol Polymorphism in the First Intron of the human TNF-beta Gene  
 RT Correlates with A Variant Amino Acid in Position 26 and a Reduced  
 RT Level of TNF-beta Production.";  
 RL J. Exp. Med. 173:209-219(1991).  
 RN [7]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=91139175; PubMed=1671667;  
 RA Abraham L.V., Du D.C., Zahedi K., Dawkins R.L., Whitehead A.S.;  
 RT "Haplotype polymorphisms of the TNFB gene.";  
 RL Immunogenetics 33:50-53(1991).  
 RN [8]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=94362679; PubMed=8081366;  
 RA Albertella M.R., Campbell D.R.;  
 RT "Characterization of a novel gene in the human major  
 RT histocompatibility complex that encodes a potential new member of the  
 RT I kappa B family of proteins.";  
 RL Hum. Mol. Genet. 3:793-799(1994).  
 RN [9]

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RP      SEQUENCE FROM N.A.
RX      MEDLINE=95324911; PubMed=7601445;
RA      Peelman L., Chardon P., Nunes M., Renard C., Gelfroin C., Vaiman M.,
RA      Van Zeveren A., Coppieters W., Van de Weghe A., Bouquet Y., Choy W.,
RA      Strominger J., Spies T.;
RT      "The BAT1 Gene in the MHC Encodes an Evolutionarily Conserved Putative
RT      Nuclear RNA Helicase of the D-B-A-D Family.";
RL      Genomics 26:210-218(1995).
RN      [10]
RN      SEQUENCE FROM N.A.
RX      MEDLINE=20132445; PubMed=10668961;
RA      Neville M.J., Campbell R.D.;
RT      "Alternative splicing of the LST-1 gene located in the major
RT      histocompatibility complex on human chromosome 6.";
RL      DNA Seq. 8:155-160(1997).
RN      [11]
RN      SEQUENCE FROM N.A.
RX      MEDLINE=98035883; PubMed=9367684;
RA      de Baey A., Fellerhoff B., Walter S., Martinozzi S., Weidte U.,
RA      Weiss E.H.;
RT      "Complex expression pattern of the TNF region gene LST1 through
RT      differential regulation, initiation, and alternative splicing.";
RL      Genomics 45:591-600(1997).
RN      [12]
RN      SEQUENCE FROM N.A.
RX      MEDLINE=96149885; PubMed=9480751;
RA      Shina T., Taniya G., Oka A., Yamagata T., Yamagata N., Kikkawa E.,
RA      Goto K., Mizuki N., Watanabe K., Fukuzumi Y., Taguchi S., Sugawara C.,
RA      Ono A., Chen L., Yamazaki M., Tashiro H., Ando A., Ikemura T.,
RA      Kimura M., Inoko H.;
RT      "Nucleotide sequencing analysis of the 146-kilobase segment around the
RT      IkB and MICA genes at the centromeric end of the HLA class I
RT      region.";
RL      Genomics 47:372-382(1998).
RX      EMBL, Y14768; CAA75070.1; -.
DR      HSSP; P01375; 4TSV.
DR      InterPro; IPR003636; TNF_abc.
DR      InterPro; IPR000478; TNF_family.
DR      Pfam; PF00229; TNF_1.
DR      PRINTS; PR01234; TNECROSISFCT.
DR      ProDom; PD002012; TNF_abc; 1.
DR      SMART; SM00207; TNF_1.
DR      ProSITE; PS00251; TNF_1; 1.
DR      ProSITE; PS50049; TNF_2; 1.
SQ      SEQUENCE 232 AA; 23446 MW; EAD71B19C6AE0D03 CRC64;

Query Match          60.2%; Score 65; DB 4; Length 232;
Best Local Similarity 76.9%; Pred. No. 0.025;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY      4 KDTPEGAELKPWY 16
          :::::|||||
Db       178 RETPEGAELKPWY 190

RESULT 10
O99ND1 ID O99ND1 PRELIMINARY; PRT; 215 AA.
AC O99ND1;
DT 01-JUN-2001 (TREMblrel. 17, Created)
DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)
DE 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE Tumor necrosis factor (Fragment).
GN TNFA.
OS Taniasciurus hudsonicus (American red squirrel).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathu; Sciuridae; Sciurinae;
OC Taniasciurus.
OX NCBI TaxID=10009;
[1]
RP      SEQUENCE FROM N.A.
RA      van Dijk W.A.M., de Jong W.W.;
RT      "Indels indicate that rodents are monophyletic and lagomorphs are
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RT their sister group";  
 RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AJ286824; CAC28540.1; -  
 DR HSP: P06804; 2TNE.  
 DR InterPro: IPR003636; TNE\_abc.  
 DR InterPro: IPR000478; TNE\_family.  
 DR Pfam: PF00229; TNE\_1.  
 DR PRINTS: PR01234; TNECROSISFCT.  
 DR PRODOM: PD002012; TNE\_abc; 1.  
 DR SMART: SM00207; TNE\_1.  
 DR PROSITE: PS00251; TNE\_1; 1.  
 DR PROSITE: PS50049; TNE\_2; 1.  
 FT NON\_TER 1  
 FT 1  
 SQ SEQUENCE 215 AA; 23739 MW; 36441309CA5E9898 CRC64;  
 Query Match  
 Best Local Similarity 57.4%; Score 62; DB 11; Length 215;  
 Matches 10; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

DB 168 PKESLGAEKPMY 181  
 QY 3 PKDPEGAELKPMY 16  
 ID 09BEC4 PRELIMINARY; PRT; 216 AA.  
 AC 09BEC4;  
 DT 01-JUN-2001 (TRENBLREL. 17, Created)  
 DT 01-JUN-2001 (TRENBLREL. 17, Last sequence update)  
 DE Tumor necrosis factor (Fragment).  
 GN TNEA.  
 OS Talpa europaea (European mole).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Insectivora; Talpidae; Talpa.  
 OX NCBI\_TaxID=9375;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA van Dijk M.A.M., de Jong W.W.;  
 RT "Indels indicate that rodents are monophyletic and lagomorphs are  
 RT their sister group."  
 RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AJ286831; CAC28539.1; -  
 DR HSP: P01375; 1ABM.  
 DR InterPro: IPR003636; TNE\_abc.  
 DR InterPro: IPR000478; TNE\_family.  
 DR Pfam: PF00229; TNE\_1.  
 DR PRINTS: PR01234; TNECROSISFCT.  
 DR PRODOM: PD002012; TNE\_abc; 1.  
 DR SMART: SM00207; TNE\_1.  
 DR PROSITE: PS00251; TNE\_1; 1.  
 DR PROSITE: PS50049; TNE\_2; 1.  
 FT NON\_TER 1  
 FT 1  
 SQ SEQUENCE 216 AA; 23542 MW; FFFEE8DBBD27836 CRC64;  
 Query Match  
 Best Local Similarity 57.4%; Score 62; DB 6; Length 216;  
 Matches 9; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

DT 01-DEC-2001 (TRENBLREL. 19, Last annotation update)  
 DE Tumor necrosis factor (Fragment).  
 GN TNEA.  
 OS Tenrec ecaudatus (tailess tenrec).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Insectivora; Tenrecidae; Tenrecinae; Tenrec.  
 OX NCBI\_TaxID=94439;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA van Dijk M.A.M., de Jong W.W.;  
 RT "Indels indicate that rodents are monophyletic and lagomorphs are  
 RT their sister group."  
 RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AJ286826; CAC28538.1; -  
 DR HSP: P01375; 4TSV.  
 DR InterPro: IPR003636; TNE\_abc.  
 DR InterPro: IPR000478; TNE\_family.  
 DR Pfam: PF00229; TNE\_1.  
 DR PRINTS: PR01234; TNECROSISFCT.  
 DR PRODOM: PD002012; TNE\_abc; 1.  
 DR SMART: SM00207; TNE\_1.  
 DR PROSITE: PS00251; TNE\_1; 1.  
 DR PROSITE: PS50049; TNE\_2; 1.  
 FT NON\_TER 1  
 FT 1  
 SQ SEQUENCE 217 AA; 23845 MW; 1C5013E9B777B54A CRC64;  
 Query Match  
 Best Local Similarity 57.4%; Score 62; DB 6; Length 217;  
 Matches 9; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

DB 171 RETPGESEKPMY 183  
 QY 4 KDPPEGAELKPMY 16  
 ID 043647 PRELIMINARY; PRT; 157 AA.  
 AC 043647;  
 DT 01-JUN-1998 (TRENBLREL. 06, Created)  
 DT 01-JUN-1998 (TRENBLREL. 06, Last sequence update)  
 DE Tumor necrosis factor alpha (Fragment).  
 GN TNFA.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Jang J.S., Kim B.E.;  
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF043342; AAC03542.1; -  
 DR HSP: P01375; 1ABM.  
 DR InterPro: IPR003636; TNE\_abc.  
 DR InterPro: IPR000478; TNE\_family.  
 DR Pfam: PF00229; TNE\_1.  
 DR PRINTS: PR01234; TNECROSISFCT.  
 DR PRODOM: PD002012; TNE\_abc; 1.  
 DR SMART: SM00207; TNE\_1.  
 DR PROSITE: PS00251; TNE\_1; 1.  
 DR PROSITE: PS50049; TNE\_2; 1.  
 FT NON\_TER 1  
 FT 1  
 SQ SEQUENCE 157 AA; 17380 MW; D1344822267E9F20 CRC64;  
 Query Match  
 Best Local Similarity 55.6%; Score 60; DB 4; Length 157;  
 Matches 9; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

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RESULT 14
Q9BEE8      PRELIMINARY;      PRT;      215 AA.
AC Q9BEE8;
DT 01-JUN-2001 (TREMBLERL. 17, Created)
DT 01-JUN-2001 (TREMBLERL. 17, Last sequence update)
DE Tumor necrosis factor (Fragment).
GN TNFA.
OS Erinaceus europaeus (Western European hedgehog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Insectivora; Erinaceidae; Erinaceinae; Erinaceus.
OX NCBI_TaxID=9365;
RN [1]
RP SEQUENCE FROM N.A.
RA van Dijk M.A.M.; de Jong W.W.;
RT "Indels indicate that rodents are monophyletic and lagomorphs are
RL their sister group."
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ286830; CAC28522.1; -.
DR HSSP; P01375; 4TSV.
DR InterPro: IPR003636; TNF_abc.
DR InterPro: IPR000478; TNF_family.
DR Pfam; PF00229; TNF; 1.
DR PRINTS; PR01234; TNECROSISFCT.
DR PRODOM; PD002012; TNF_abc; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS50049; TNF_2; 1.
FT NON_TER
FT SEQUENCE 215 AA; 23696 MW; 3E337E7E65F074EA CRC64;

Query Match      55.6%; Score 60; DB 6; Length 215;
Best Local Similarity 75.0%; Pred. No. 0.14;
Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 5 DYPEGAEILKPMY 16
Db 170 ETPEGAEARPMY 181

RESULT 15
Q9BEG0      PRELIMINARY;      PRT;      217 AA.
AC Q9BEG0;
DT 01-JUN-2001 (TREMBLERL. 17, Created)
DT 01-JUN-2001 (TREMBLERL. 17, Last sequence update)
DE Tumor necrosis factor (Fragment).
GN TNFA.
OS Cyclopes didactylus (silky anteater).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Edentata; Myrmecophagidae; Cyclopes.
OX NCBI_TaxID=84074;
RN [1]
RP SEQUENCE FROM N.A.
RA van Dijk M.A.M.; de Jong W.W.;
RT "Indels indicate that rodents are monophyletic and lagomorphs are
RL their sister group."
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ286828; CAC28514.1; -.
DR HSSP; P01375; 1A8M.
DR InterPro: IPR003636; TNF_abc.
DR InterPro: IPR000478; TNF_family.
DR Pfam; PF00229; TNF; 1.
DR PRINTS; PR01234; TNECROSISFCT.
DR PRODOM; PD002012; TNF_abc; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS50049; TNF_2; 1.

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FT NON_TER 1 1
FT NON_TER 217 217
SQ SEQUENCE 217 AA; 23753 MW; F760E887F6C29EBB CRC64;

Query Match      55.6%; Score 60; DB 6; Length 217;
Best Local Similarity 69.2%; Pred. No. 0.14;
Matches 9; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 4 KDTPEGAEILKPMY 16
Db 171 REPPEGPEAKPMY 183

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Search completed: April 4, 2003, 08:42:07  
Job time : 24.6774 secs

GenCore version 5.1.4\_p5\_4578  
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OM protein - protein search, using sw model

Run on: April 4, 2003, 08:37:56 ; Search time 10.9677 Seconds  
(without alignments)

45,606 Million cell updates/sec

Title: US-09-779-703-5  
108  
Perfect score: 1 CGPKDPGEALRPMYC 17  
Sequence:

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: Issued\_Patents\_AA:\*  
2: /cgn2\_6/prodata/1/1aa/5A.COMB.pep.\*  
3: /cgn2\_6/prodata/1/1aa/5B.COMB.pep.\*  
4: /cgn2\_6/prodata/1/1aa/6A.COMB.pep.\*  
5: /cgn2\_6/prodata/1/1aa/6B.COMB.pep.\*  
6: /cgn2\_6/prodata/1/1aa/6C.COMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	108	100.0	17	2	US-08-500-860A-24	Sequence 24, Appl
2	88	81.5	17	2	US-08-500-860A-25	Sequence 25, Appl
3	84	77.8	156	2	US-08-500-860A-36	Sequence 36, Appl
4	84	77.8	157	5	PCT-US93-02475-8	Sequence 8, Appl
5	84	77.8	157	5	PCT-US93-02475-9	Sequence 9, Appl
6	84	77.8	235	4	US-08-883-086-7	Sequence 7, Appl
7	65	60.2	147	1	US-07-668-517-1	Sequence 1, Appl
8	65	60.2	147	1	US-07-668-517-2	Sequence 2, Appl
9	65	60.2	148	1	US-07-668-517-15	Sequence 15, Appl
10	65	60.2	149	1	US-07-668-517-16	Sequence 16, Appl
11	65	60.2	149	1	US-07-668-517-17	Sequence 17, Appl
12	65	60.2	150	1	US-07-668-517-4	Sequence 4, Appl
13	65	60.2	150	1	US-07-668-517-5	Sequence 5, Appl
14	65	60.2	150	1	US-07-668-517-6	Sequence 6, Appl
15	65	60.2	150	1	US-07-668-517-8	Sequence 8, Appl
16	65	60.2	150	1	US-07-668-517-9	Sequence 9, Appl
17	65	60.2	150	1	US-07-668-517-10	Sequence 10, Appl
18	65	60.2	150	1	US-07-668-517-11	Sequence 11, Appl
19	65	60.2	150	1	US-07-668-517-12	Sequence 12, Appl
20	65	60.2	150	1	US-07-668-517-13	Sequence 13, Appl
21	65	60.2	150	1	US-07-668-517-14	Sequence 14, Appl
22	65	60.2	150	1	US-07-668-517-17	Sequence 17, Appl
23	65	60.2	150	1	US-07-668-517-19	Sequence 19, Appl
24	65	60.2	150	1	US-07-668-517-29	Sequence 29, Appl
25	65	60.2	150	1	US-07-668-517-31	Sequence 31, Appl
26	65	60.2	150	1	US-07-668-517-35	Sequence 35, Appl
27	65	60.2	150	1	US-07-668-517-37	Sequence 37, Appl
			150	1	US-07-994-469A-6	Sequence 6, Appl

28	65	60.2	150	1	US-07-994-469A-7	Sequence 7, Appl
29	65	60.2	150	1	US-07-994-469A-8	Sequence 8, Appl
30	65	60.2	150	1	US-07-994-469A-57	Sequence 57, Appl
31	65	60.2	150	4	US-09-286-529-25	Sequence 25, Appl
32	65	60.2	151	1	US-07-668-517-7	Sequence 7, Appl
33	65	60.2	151	1	US-07-668-517-18	Sequence 18, Appl
34	65	60.2	151	1	US-07-668-517-19	Sequence 19, Appl
35	65	60.2	151	1	US-07-668-517-20	Sequence 20, Appl
36	65	60.2	151	1	US-07-668-517-22	Sequence 22, Appl
37	65	60.2	151	1	US-07-668-517-23	Sequence 23, Appl
38	65	60.2	151	1	US-07-668-517-24	Sequence 24, Appl
39	65	60.2	151	1	US-07-668-517-25	Sequence 25, Appl
40	65	60.2	151	1	US-07-668-517-26	Sequence 26, Appl
41	65	60.2	151	1	US-07-668-517-27	Sequence 27, Appl
42	65	60.2	151	1	US-07-668-517-28	Sequence 28, Appl
43	65	60.2	151	1	US-07-668-517-30	Sequence 30, Appl
44	65	60.2	151	1	US-07-668-517-32	Sequence 32, Appl
45	65	60.2	151	1	US-07-668-517-36	Sequence 36, Appl

## ALIGNMENTS

RESULT 1  
US-08-500-860A-24  
Sequence 24, Application US/08500860A  
Patent No. 5891679.  
GENERAL INFORMATION:  
APPLICANT: LUCAS, RUDOLPH  
APPLICANT: DE BAETSELIER, PATRICK  
APPLICANT: FRANSEN, LUCIE  
APPLICANT: SABON, ERWIN  
TITLE OF INVENTION: TNF-MOTIFINS, A PROCESS FOR PREPARING THEM AND  
TITLE OF INVENTION: THEIR USE AS ACTIVE SUBSTANCES IN PHARMACEUTICAL COMPOSIT:  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: NIXON & VANDERHIE P.C.  
STREET: 1100 NORTH GLEBE ROAD  
CITY: ARLINGTON  
STATE: VIRGINIA  
COUNTRY: U.S.A.  
ZIP: 22201-4714  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/500, 860A  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: BYRNE, THOMAS E.  
REGISTRATION NUMBER: 32,205  
REFERENCE/DOCKET NUMBER: 1487-8  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703)816-4000  
TELEFAX: (703)816-4100  
TELEX: 200797 NIXN UR  
INFORMATION FOR SEQ ID NO: 24:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 1  
OTHER INFORMATION: /note- "Biotin-Gly-Gly is coupled  
OTHER INFORMATION: to the N-terminus of the peptide"  
US-08-500-860A-24



Query Match 100.0%; Score 108; DB 2; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.2e-10;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CGPKDPGEGALRPMYC 17  
| | | | | | | | | | | | | | | | | | |  
Db 1 CGPKDPGEGALRPMYC 17

## RESULT 2

US-08-500-860A-25  
; Sequence 25, Application US/08500860A  
; Patent No. 5891679  
; GENERAL INFORMATION:  
; APPLICANT: LUCAS, RUDOLPH  
; APPLICANT: DE BAETSELIER, PATRICK  
; APPLICANT: FRANSSEN, LUCIE  
; APPLICANT: SALON, ERWIN  
; TITLE OF INVENTION: TNF-INHIBITORS, A PROCESS FOR PREPARING THEM AND  
; TITLE OF INVENTION: THEIR USE AS ACTIVE SUBSTANCES IN PHARMACEUTICAL COMPOSITIONS  
; NUMBER OF SEQUENCES: 36  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: NIXON & VANDERHAYE P.C.  
; STREET: 1100 NORTH GLEBE ROAD  
; CITY: ARLINGTON  
; STATE: VIRGINIA  
; COUNTRY: U.S.A.  
; ZIP: 22201-4714

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/500,860A  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: BYRNE, THOMAS E.  
REGISTRATION NUMBER: 32,205  
REFERENCE/DOCKET NUMBER: 1487-8  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703)816-4000  
TELEFAX: (703)816-4100  
TELEX: 200797 NIXN UR  
INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Binding-site  
LOCATION: 1  
OTHER INFORMATION: /note= "Biotin-Gly-Gly is coupled  
; OTHER INFORMATION: to the N-terminus of the peptide"  
US-08-500-860A-25

Query Match 81.5%; Score 88; DB 2; Length 17;  
Best Local Similarity 76.5%; Pred. No. 1.5e-07;  
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 CGPKDPGEGALRPMYC 17  
| | : | | | | | | | | | | | | | | | | | |  
Db 1 CGORETEGAEAKRPMYC 17

RESULT 3  
US-08-500-860A-36  
; Sequence 36, Application US/08500860A  
; Patent No. 5891679  
; GENERAL INFORMATION:

APPLICANT: LUCAS, RUDOLPH  
APPLICANT: DE BAETSELIER, PATRICK  
APPLICANT: FRANSSEN, LUCIE  
APPLICANT: SALON, ERWIN  
TITLE OF INVENTION: TNF-INHIBITORS, A PROCESS FOR PREPARING THEM AND  
TITLE OF INVENTION: THEIR USE AS ACTIVE SUBSTANCES IN PHARMACEUTICAL COMPOSITIO  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: NIXON & VANDERHAYE P.C.  
STREET: 1100 NORTH GLEBE ROAD  
CITY: ARLINGTON  
STATE: VIRGINIA  
COUNTRY: U.S.A.  
ZIP: 22201-4714

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/500,860A  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: BYRNE, THOMAS E.  
REGISTRATION NUMBER: 32,205  
REFERENCE/DOCKET NUMBER: 1487-8  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703)816-4000  
TELEFAX: (703)816-4100  
TELEX: 200797 NIXN UR  
INFORMATION FOR SEQ ID NO: 36:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 156 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-500-860A-36

Query Match 77.8%; Score 84; DB 2; Length 156;  
Best Local Similarity 100.0%; Pred. No. 7.5e-06;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 PKDPGEGALRPMYC 16  
| | | | | | | | | | | | | | | | | | |  
Db 101 PKDPGEGALRPMYC 114

## RESULT 4

PCT-US93-02475-8  
; Sequence 8, Application PC/TUS9302475  
; GENERAL INFORMATION:  
; APPLICANT: Wisniewski, Bernadine J.  
; TITLE OF INVENTION: Tumor Necrosis Factor with Modified  
; TITLE OF INVENTION: Ion Channel  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Donald G. Lewis  
; STREET: 8328 Regents Road #1E  
; CITY: San Diego  
; STATE: California  
; COUNTRY: USA  
; ZIP: 92122  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 M storage  
; COMPUTER: VE System 386  
; OPERATING SYSTEM: MS-DOS 5  
; SOFTWARE: Word Perfect  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US93/02475  
; FILING DATE: 19930412  
; CLASSIFICATION:

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/852,625  
 FILING DATE: 12 March 1992  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Donald G. Lewis  
 REGISTRATION NUMBER: 28636  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (619) 554-2421  
 TELEFAX: (619) 554-2421  
 INFORMATION FOR SEQ ID NO: 8:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 157 amino acids  
 TYPE: AMINO ACIDS  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 FEATURE:  
 NAME/KEY: Tumor Necrosis Factor (rat)  
 OTHER INFORMATION: A blank residue designated by "Xaa" is inserted after residue No. 70 of rat TNF  
 OTHER INFORMATION: TNF and the sequence numbering is augmented by 1  
 OTHER INFORMATION: starting with residue No. 71 in order to maximize  
 PUBLICATION INFORMATION: the sequence homology with human TNF.  
 AUTHORS: Shirai, T., Shimizu, N., Horiguchi,  
 AUTHORS: S., and Ito, H.  
 TITLE: Cloning and Expression in  
 TITLE: Escherichia coli of the gene for  
 TITLE: Rat  
 JOURNAL: Agric. Biol. Chem.  
 VOLUME: 53  
 PAGES: 1733-1736  
 DATE: 1989  
 RELEVANT RESIDUES IN SEQ ID NO: 8: 1-157 (includes  
 RELEVANT RESIDUES IN SEQ ID NO: one blank)  
 PCT-US93-02475-8

## Query Match

Best Local Similarity 77.8%; Score 84; DB 5; Length 157;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PKDTPEGAELKPMY 16  
 |||||

DB 102 PKDTPEGAELKPMY 115

## RESULT 5

Sequence 9, Application PC/TUS9302475  
 GENERAL INFORMATION:  
 APPLICANT: Wisniewski, Bernadine J.  
 TITLE OF INVENTION: Tumor Necrosis Factor with Modified  
 NUMBER OF SEQUENCES: 13  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Donald G. Lewis  
 STREET: 8328 Regents Road #1E  
 CITY: San Diego  
 STATE: California  
 COUNTRY: USA  
 ZIP: 92122  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette, 3.5 inch, 1.44 M storage  
 COMPUTER: VE System 386  
 OPERATING SYSTEM: MS-DOS 5  
 SOFTWARE: Word Perfect  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: PCT/US93/02475  
 FILING DATE: 19930412  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/852,625  
 FILING DATE: 12 March 1992

## ATTORNEY/AGENT INFORMATION:

NAME: Donald G. Lewis  
 REGISTRATION NUMBER: 28636  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (619) 554-2421  
 TELEFAX: (619) 554-2421  
 INFORMATION FOR SEQ ID NO: 9:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 157 amino acids  
 TYPE: AMINO ACIDS  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 FEATURE:  
 NAME/KEY: Tumor Necrosis Factor (murine)  
 OTHER INFORMATION: A blank residue designated by "Xaa" is inserted after residue No. 70 of murine  
 OTHER INFORMATION: TNF and the sequence numbering is augmented by 1  
 OTHER INFORMATION: starting with residue No. 71 in order to maximize  
 PUBLICATION INFORMATION: the sequence homology with human TNF.  
 AUTHORS: Caput, D., Beutler, B., Hartog, K.  
 AUTHORS: Thayer, R., Brown-Shimer, S. and  
 AUTHORS: Cerami, A.  
 TITLE: Identification of a Common Nucleotide  
 TITLE: Sequence in the 3'-untranslated Region of mRNA  
 TITLE: Molecules Specifying Inflammatory Mediators.  
 JOURNAL: U.S.A.  
 VOLUME: 83  
 PAGES: 1670-1674  
 DATE: 1986  
 RELEVANT RESIDUES IN SEQ ID NO: 9: 1-157 (includes  
 RELEVANT RESIDUES IN SEQ ID NO: one blank)  
 PCT-US93-02475-9

## Query Match

Best Local Similarity 77.8%; Score 84; DB 5; Length 157;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PKDTPEGAELKPMY 16  
 |||||

DB 102 PKDTPEGAELKPMY 115

## RESULT 6

Sequence 7, Application US/0883086  
 Patent No. 6171787  
 GENERAL INFORMATION:  
 APPLICANT: WILEY, STEVEN  
 TITLE OF INVENTION: MEMBER OF THE TNF FAMILY USEFUL  
 NUMBER OF SEQUENCES: 13  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Abbott Laboratories  
 STREET: 100 Abbott Park Road  
 CITY: Abbott Park  
 STATE: IL  
 COUNTRY: USA  
 ZIP: 60064-3500  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: DOS  
 SOFTWARE: FASTSEQ Version 2.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/883,086  
 FILING DATE:  
 CLASSIFICATION: 424  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER:  
 FILING DATE:

ATTORNEY/AGENT INFORMATION:  
NAME: POREMBSKI, PISCILLA E.  
REGISTRATION NUMBER: 33,207  
REFERENCE/DOCKET NUMBER: 6134 US-01  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 847-937-0378  
TELEFAX: 847-938-2623  
TELEX:  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 235 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-883-086-7

Query Match 77.8%; Score 84; DB 4; Length 235;  
Best Local Similarity 100.0%; Pred. No. 1.2e-05;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 KDTPEGAELKPMY 16  
|||  
Db 180 PKDTPEGAELKPMY 193

RESULT 7  
US-07-668-517-1  
Sequence 1, Application US/07668517  
Patent No. 5262309  
GENERAL INFORMATION:  
APPLICANT: SATOSHI NAKAMURA et al.  
TITLE OF INVENTION: No. 5262309el Physiologically Active  
TITLE OF INVENTION: Polypeptide, Recombinant Plasmid, Recombinant Microorganism  
TITLE OF INVENTION: Cell, Pharmaceutical Composition and Method of Recovering  
NUMBER OF SEQUENCES: 50  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wenderoth, Lind & Ponack  
STREET: 805 Fifteenth Street, N.W., #700  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch, 500 KB  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: DisplayWrite  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/668, 517  
FILING DATE: 19910322  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Matthew Jacob  
REGISTRATION NUMBER: 25,154  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-8850  
TELEFAX: 202-371-8856  
TELEX:  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 147 amino acids  
TYPE: AMINO ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY:  
LOCATION:  
IDENTIFICATION METHOD:  
OTHER INFORMATION:

OTHER INFORMATION:  
US-07-668-517-1

Query Match 60.2%; Score 65; DB 1; Length 147;  
Best Local Similarity 76.9%; Pred. No. 0.0064;  
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 4 KDTPEGAELKPMY 16  
:|||  
Db 93 RETPEGAELKPMY 105

RESULT 8  
US-07-668-517-2  
Sequence 2, Application US/07668517  
Patent No. 5262309  
GENERAL INFORMATION:  
APPLICANT: SATOSHI NAKAMURA et al.  
TITLE OF INVENTION: No. 5262309el Physiologically Active  
TITLE OF INVENTION: Polypeptide, Recombinant Plasmid, Recombinant Microorganism  
TITLE OF INVENTION: Cell, Pharmaceutical Composition and Method of Recovering  
NUMBER OF SEQUENCES: 50  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wenderoth, Lind & Ponack  
STREET: 805 Fifteenth Street, N.W., #700  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch, 500 KB  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: DisplayWrite  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/668, 517  
FILING DATE: 19910322  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Matthew Jacob  
REGISTRATION NUMBER: 25,154  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-8850  
TELEFAX: 202-371-8856  
TELEX:  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 148 amino acids  
TYPE: AMINO ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY:  
LOCATION:  
IDENTIFICATION METHOD:  
OTHER INFORMATION:

US-07-668-517-2

Query Match 60.2%; Score 65; DB 1; Length 148;  
Best Local Similarity 76.9%; Pred. No. 0.0064;  
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 4 KDTPEGAELKPMY 16  
:|||  
Db 94 RETPEGAELKPMY 106

RESULT 9  
US-07-668-517-15

Sequence 15, Application US/07668517  
Patent No. 5262309  
GENERAL INFORMATION:  
APPLICANT: Satoshi NAKAMURA et al.  
TITLE OF INVENTION: No. 5262309el Physiologically Active  
TITLE OF INVENTION: Polypeptide, Recombinant Plasmid, Recombinant Microorganism  
NUMBER OF SEQUENCES: Cell, Pharmaceutical Composition and Method of Recovering  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wenderoth, Lind & Ponack  
STREET: 805 Fifteenth Street, N.W., #700  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch, 500 KB  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: DisplayWrite  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/668,517  
FILING DATE: 19910322  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Matthew Jacob  
REGISTRATION NUMBER: 25,154  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-8850  
TELEFAX: 202-371-8856  
TELEX:  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 148 amino acids  
TYPE: AMINO ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY:  
LOCATION:  
IDENTIFICATION METHOD:  
OTHER INFORMATION:  
US-07-668-517-15

Query Match  
Best Local Similarity 60.2%; Score 65; DB 1; Length 148;  
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
QY 4 KDTPEGAEKPKMY 16  
::||||| |||  
DB 94 RETPEGAEKPKMY 106

RESULT 10  
US-07-668-517-3  
Sequence 3, Application US/07668517  
Patent No. 5262309  
GENERAL INFORMATION:  
APPLICANT: Satoshi NAKAMURA et al.  
TITLE OF INVENTION: No. 5262309el Physiologically Active  
TITLE OF INVENTION: Polypeptide, Recombinant Plasmid, Recombinant Microorganism  
NUMBER OF SEQUENCES: Cell, Pharmaceutical Composition and Method of Recovering  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wenderoth, Lind & Ponack  
STREET: 805 Fifteenth Street, N.W., #700  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.

ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch, 500 KB  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: DisplayWrite  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/668,517  
FILING DATE: 19910322  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Matthew Jacob  
REGISTRATION NUMBER: 25,154  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-8850  
TELEFAX: 202-371-8856  
TELEX:  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 149 amino acids  
TYPE: AMINO ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY:  
LOCATION:  
IDENTIFICATION METHOD:  
OTHER INFORMATION:  
US-07-668-517-3

Query Match  
Best Local Similarity 60.2%; Score 65; DB 1; Length 149;  
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
QY 4 KDTPEGAEKPKMY 16  
::||||| |||  
DB 95 RETPEGAEKPKMY 107

RESULT 11  
US-07-668-517-16  
Sequence 16, Application US/07668517  
Patent No. 5262309  
GENERAL INFORMATION:  
APPLICANT: Satoshi NAKAMURA et al.  
TITLE OF INVENTION: No. 5262309el Physiologically Active  
TITLE OF INVENTION: Polypeptide, Recombinant Plasmid, Recombinant Microorganism  
NUMBER OF SEQUENCES: Cell, Pharmaceutical Composition and Method of Recovering  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wenderoth, Lind & Ponack  
STREET: 805 Fifteenth Street, N.W., #700  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch, 500 KB  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: DisplayWrite  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/668,517  
FILING DATE: 19910322  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:

NAME: Matthew Jacob  
REGISTRATION NUMBER: 25,154  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-8850  
TELEFAX: 202-371-8856  
TELEX:  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 149 amino acids  
TYPE: AMINO ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY:  
LOCATION:  
IDENTIFICATION METHOD:  
OTHER INFORMATION:  
US-07-668-517-16

Query Match 60.2%; Score 65; DB 1; Length 149;  
Best Local Similarity 76.9%; Pred. No. 0.0064;  
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 4 KDTPEGAEKPKMY 16  
Db 95 RETPEGAEKPKMY 107

RESULT 12  
US-07-668-517-4  
Sequence 4, Application US/07668517  
Patent No. 5262309  
GENERAL INFORMATION:  
APPLICANT: Satoshi NAKAMURA et al.  
TITLE OF INVENTION: No. 5262309el Physiologically Active  
TITLE OF INVENTION: Polypeptide, Recombinant Plasmid, Recombinant Microorganism  
TITLE OF INVENTION: Cell, Pharmaceutical Composition and Method of Recovering  
NUMBER OF SEQUENCES: 50  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wenderoth, Lind & Ponack  
STREET: 805 Fifteenth Street, N.W., #700  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch, 500 Kb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: DisplayWrite  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/668,517  
FILING DATE: 19910322  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Matthew Jacob  
REGISTRATION NUMBER: 25,154  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-8850  
TELEFAX: 202-371-8856  
TELEX:  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 150 amino acids  
TYPE: AMINO ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:

NAME/KEY:  
LOCATION:  
IDENTIFICATION METHOD:  
OTHER INFORMATION:  
US-07-668-517-4

Query Match 60.2%; Score 65; DB 1; Length 150;  
Best Local Similarity 76.9%; Pred. No. 0.0065;  
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 4 KDTPEGAEKPKMY 16  
Db 96 RETPEGAEKPKMY 108

RESULT 13  
US-07-668-517-5  
Sequence 5, Application US/07668517  
Patent No. 5262309

GENERAL INFORMATION:  
APPLICANT: Satoshi NAKAMURA et al.  
TITLE OF INVENTION: No. 5262309el Physiologically Active  
TITLE OF INVENTION: Polypeptide, Recombinant Plasmid, Recombinant Microorganism  
TITLE OF INVENTION: Cell, Pharmaceutical Composition and Method of Recovering  
NUMBER OF SEQUENCES: 50  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wenderoth, Lind & Ponack  
STREET: 805 Fifteenth Street, N.W., #700  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch, 500 Kb

COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: DisplayWrite  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/668,517  
FILING DATE: 19910322  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Matthew Jacob  
REGISTRATION NUMBER: 25,154  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-8850  
TELEFAX: 202-371-8856  
TELEX:

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:  
LENGTH: 150 amino acids  
TYPE: AMINO ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:

NAME/KEY:  
LOCATION:  
IDENTIFICATION METHOD:  
OTHER INFORMATION:  
US-07-668-517-5

Query Match 60.2%; Score 65; DB 1; Length 150;  
Best Local Similarity 76.9%; Pred. No. 0.0065;  
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 4 KDTPEGAEKPKMY 16  
Db 96 RETPEGAEKPKMY 108

## RESULT 14

US-07-668-517-6  
Sequence 6, Application US/07668517  
Patent No. 5262309

## GENERAL INFORMATION:

APPLICANT: Satoshi NAKAMURA et al.  
TITLE OF INVENTION: No. 5262309el Physiologically Active  
TITLE OF INVENTION: Polypeptide, Recombinant Plasmid, Recombinant Microorganism  
NUMBER OF SEQUENCES: Cell, Pharmaceutical Composition and Method of Recovering  
CORRESPONDENCE ADDRESS: 50

ADDRESSEE: Wenderoth, Lind & Ponack  
STREET: 805 Fifteenth Street, N.W., #700  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005

## COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 5.25 inch, 500 Kb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Displaywrite

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/668,517  
FILING DATE: 19910322  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:

APPLICATION NUMBER:  
FILING DATE:

## ATTORNEY/AGENT INFORMATION:

NAME: Matthew Jacob  
REGISTRATION NUMBER: 25,154  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-8850  
TELEFAX: 202-371-8856  
TELEX:

## INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:  
LENGTH: 150 amino acids  
TYPE: AMINO ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY:  
LOCATION:  
IDENTIFICATION METHOD:  
OTHER INFORMATION:

US-07-668-517-6

Query Match 60.2%; Score 65; DB 1; Length 150;  
Best Local Similarity 76.9%; Pred. No. 0.0065;  
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 4 KDPGGAELKPY 16  
:::|||||  
DB 96 RETPGAEAKPY 108

## RESULT 15

US-07-668-517-8

Sequence 8, Application US/07668517  
Patent No. 5262309

## GENERAL INFORMATION:

APPLICANT: Satoshi NAKAMURA et al.  
TITLE OF INVENTION: No. 5262309el Physiologically Active  
TITLE OF INVENTION: Polypeptide, Recombinant Plasmid, Recombinant Microorganism  
NUMBER OF SEQUENCES: Cell, Pharmaceutical Composition and Method of Recovering  
CORRESPONDENCE ADDRESS: 50

ADDRESSEE: Wenderoth, Lind & Ponack  
STREET: 805 Fifteenth Street, N.W., #700

CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005

## COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 5.25 inch, 500 Kb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Displaywrite

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/668,517  
FILING DATE: 19910322  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:

APPLICATION NUMBER:  
FILING DATE:

## ATTORNEY/AGENT INFORMATION:

NAME: Matthew Jacob  
REGISTRATION NUMBER: 25,154  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-8850  
TELEFAX: 202-371-8856  
TELEX:

## INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:  
LENGTH: 150 amino acids  
TYPE: AMINO ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY:  
LOCATION:  
IDENTIFICATION METHOD:  
OTHER INFORMATION:

US-07-668-517-8

Query Match 60.2%; Score 65; DB 1; Length 150;  
Best Local Similarity 76.9%; Pred. No. 0.0065;  
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 4 KDPGGAELKPY 16  
:::|||||  
DB 96 RETPGAEAKPY 108

Search completed: April 4, 2003, 08:43:41  
Job time: 10.9677 secs

GenCore version 5.1.4-p5\_4578  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 4, 2003, 08:42:11

Search time 10.6935 Seconds

(without alignments)

97.191 Million cell updates/sec

Title: US-09-779-703-5  
Sequence: 108  
1 CGPRTPEGAELKPMYC 17

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 248812 seqs, 61136040 residues

Total number of hits satisfying chosen parameters: 248812

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 08

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications\_AA:\*

- 1: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep:\*
- 2: /cgn2\_6/ptodata/2/pubpaa/PCP\_NEW\_PUB.pep:\*
- 3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep:\*
- 4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep:\*
- 5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep:\*
- 6: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep:\*
- 7: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep:\*
- 8: /cgn2\_6/ptodata/2/pubpaa/PCPUS\_PUBCOMB.pep:\*
- 9: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep:\*
- 10: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep:\*
- 11: /cgn2\_6/ptodata/2/pubpaa/US09\_PUBCOMB.pep:\*
- 12: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep:\*
- 13: /cgn2\_6/ptodata/2/pubpaa/US10\_PUBCOMB.pep:\*
- 14: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	84	77.8	151	9	US-09-779-050A-40
2	84	77.8	233	9	US-10-017-910-8
3	84	77.8	268	9	US-10-185-425-6
4	65	60.2	150	10	US-09-877-156-25
5	65	60.2	150	12	US-10-116-378-28
6	65	60.2	152	9	US-09-779-050A-24
7	65	60.2	157	9	US-09-903-327A-7
8	65	60.2	157	9	US-10-043-432-1
9	65	60.2	157	10	US-09-756-301A-1
10	65	60.2	157	10	US-09-927-703-1
11	65	60.2	157	10	US-09-854-280-19
12	65	60.2	157	10	US-09-934-465-13
13	65	60.2	157	10	US-09-766-535A-13
14	65	60.2	157	10	US-09-854-208-19
15	65	60.2	157	10	US-09-756-161A-1
16	65	60.2	157	12	US-10-010-229-1
17	65	60.2	157	12	US-10-043-450-1
18	65	60.2	157	12	US-10-044-534-1
19	65	60.2	164	10	US-09-798-789-2

20	65	60.2	164	10	US-09-981-289-2	Sequence 2, Appl1
21	65	60.2	193	9	US-10-145-014-3	Sequence 3, Appl1
22	65	60.2	193	10	US-09-982-308-3	Sequence 3, Appl1
23	65	60.2	233	8	US-08-971-317A-5	Sequence 5, Appl1
24	65	60.2	233	9	US-10-136-511-3	Sequence 5, Appl1
25	65	60.2	233	9	US-10-145-014-22	Sequence 22, Appl1
26	65	60.2	233	9	US-09-131-237-3	Sequence 9, Appl1
27	65	60.2	233	9	US-10-174-654-9	Sequence 9, Appl1
28	65	60.2	233	9	US-10-151-882-42	Sequence 42, Appl1
29	65	60.2	233	10	US-09-193-663-5	Sequence 5, Appl1
30	65	60.2	233	10	US-09-879-919-5	Sequence 5, Appl1
31	65	60.2	233	10	US-09-782-980-43	Sequence 14, Appl1
32	65	60.2	233	10	US-09-840-707A-14	Sequence 3, Appl1
33	65	60.2	233	10	US-09-446-1298-3	Sequence 3, Appl1
34	65	60.2	233	10	US-09-345-790-3	Sequence 3, Appl1
35	65	60.2	233	10	US-09-829-493-3	Sequence 3, Appl1
36	65	60.2	233	10	US-09-899-059-3	Sequence 3, Appl1
37	65	60.2	233	12	US-10-082-260-5	Sequence 3, Appl1
38	65	60.2	233	12	US-10-012-452-10	Sequence 10, Appl1
39	65	60.2	233	9	US-09-903-327A-11	Sequence 11, Appl1
40	49	45.4	104	9	US-09-911-777-5	Sequence 5, Appl1
41	46	42.6	104	10	US-09-738-626-5707	Sequence 5707, Ap
42	46	42.6	104	9	US-09-770-517C-2	Sequence 2, Appl1
43	44	40.7	522	9	US-09-764-868-1138	Sequence 1138, Ap
44	44	40.7	524	9	US-09-764-868-761	Sequence 761, App
45	43.5	40.3	229	9	US-09-992-598-281	Sequence 281, App

## ALIGNMENTS

RESULT 1  
US-09-779-050A-40  
Sequence 40, Application US/09779050A  
Patent No. US20020160416A1  
GENERAL INFORMATION:  
APPLICANT: BOYLE, WILLIAM  
APPLICANT: HSU, HAILING  
FILE REFERENCE: A-570B  
CURRENT APPLICATION NUMBER: US/09/779, 050A  
CURRENT FILING DATE: 2001-02-12  
PRIOR APPLICATION NUMBER: 60/181,800  
NUMBER OF SEQ ID NOS: 52  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 40  
LENGTH: 151  
TYPE: PRT  
ORGANISM: Mus musculus  
US-09-779-050A-40

Query Match 77.8%; Score 84; DB 9; Length 151;  
Best Local Similarity 100.0%; Pred. No. 3.5e-05;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Db 96 PKDTPGAEELKPMYC 109  
|||||

## RESULT 2

US-10-017-910-8  
Sequence 8, Application US/10017910  
Patent No. US20020159970A1  
GENERAL INFORMATION:  
APPLICANT: Choi, Yongwon  
Wong, Brian  
Joesten, Regis  
Steinman, Ralph

TITLE OF INVENTION: A PROTEIN BELONGING TO THE TNF SUPERFAMILY  
INVOLVED IN SIGNAL TRANSDUCTION, NUCLEIC ACIDS ENCODING  
METHODS OF USE THEREOF

```

:      NUMBER OF SEQUENCES: 14
:      CORRESPONDENCE ADDRESS:
:      ADDRESSEE: Klauber & Jackson
:      STREET: 411 Hackensack Avenue, 4th Floor
:      CITY: Hackensack
:      STATE: New Jersey
:      COUNTRY: USA
:      ZIP: 07601
:
:      COMPUTER READABLE FORM:
:      MEDIUM TYPE: Floppy disk
:      COMPUTER: IBM PC compatible
:      OPERATING SYSTEM: PC-DOS/MS-DOS
:      SOFTWARE: PatentIn Release #1.0, Version #1.30
:
:      CURRENT APPLICATION DATA:
:      APPLICATION NUMBER: US/10/017,910
:      FILING DATE: 14-Dec-2001
:      CLASSIFICATION: <Unknown>
:
:      PRIOR APPLICATION DATA:
:      APPLICATION NUMBER: US 09/447,035
:      FILING DATE: 1999-11-22
:
:      ATTORNEY/AGENT INFORMATION:
:      NAME: Jackson Esq., David A.
:      REGISTRATION NUMBER: 26,742
:      REFERENCE/DOCKET NUMBER: 600-1-200
:      TELECOMMUNICATION INFORMATION:
:      TELEPHONE: 201-487-5800
:      TELEFAX: 201-343-1684
:      TELEX: 133521
:
:      INFORMATION FOR SEQ ID NO: 8:
:      SEQUENCE CHARACTERISTICS:
:      LENGTH: 235 amino acids
:      TYPE: amino acid
:      STRANDEDNESS: Single
:      TOPOLOGY: linear
:      MOLECULE TYPE: protein
:      HYPOTHETICAL: NO
:      ORIGINAL SOURCE:
:      ORGANISM: Mus musculus
:
:      SEQUENCE DESCRIPTION: SEQ ID NO: 8:
:      US-10-017-910-8
:
:      Query Match      77.8%; Score 84; DB 9; Length 235;
:      Best Local Similarity 100.0%; Pred. No. 5.4e-05;
:      Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
:
:      QY      3 PKDPEGAELKPMY 16
:              |||||
:      Db      180 PKDPEGAELKPMY 193
:
:      RESULT 3
:      US-10-185-425-6
:      Sequence 6, Application US/10185425
:      Publication No. US20030053984A1
:      GENERAL INFORMATION:
:      APPLICANT: Apotech Research and Development Ltd.
:      APPLICANT: Tschopp, Jürg
:      APPLICANT: Schneider, Pascal
:      APPLICANT: Holler, Nils
:      TITLE OF INVENTION: A dimer or an oligomer of a dimer, trimer, quadrimer, or pentamer
:      TITLE OF INVENTION: Recombinant Fusion Proteins
:      FILE REFERENCE: 1708.0010SI
:      CURRENT APPLICATION NUMBER: US/10/185,425
:      CURRENT FILING DATE: 2002-06-28
:      PRIOR APPLICATION NUMBER: PCT/EP00/13032
:      PRIOR FILING DATE: 2000-12-20
:      PRIOR APPLICATION NUMBER: DE 199 63 859.4
:      PRIOR FILING DATE: 1999-12-30
:      NUMBER OF SEQ ID NOS: 24
:      SOFTWARE: FastSeq for Windows Version 4.0
:      SEQ ID NO 6
:      LENGTH: 268
:      TYPE: PRT

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: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: TNFa-ACRP30
: FEATURE:
: NAME/KEY: DOMAIN
: LOCATION: (1)...(8)
: OTHER INFORMATION: Flag
: FEATURE:
: NAME/KEY: DOMAIN
: LOCATION: (9)...(16)
: OTHER INFORMATION: Linker
: FEATURE:
: NAME/KEY: DOMAIN
: LOCATION: (17)...(108)
: OTHER INFORMATION: mouseACRP30 aa 18-111
: FEATURE:
: NAME/KEY: DOMAIN
: LOCATION: (109)...(110)
: OTHER INFORMATION: Linker
: FEATURE:
: NAME/KEY: DOMAIN
: LOCATION: (111)...(268)
: OTHER INFORMATION: mouseTNFa aa 77-235
US-10-185-425-6

Query Match          77.8%; Score 84; DB 9; Length 268;
Best Local Similarity 100.0%; Pred. No. 6.2e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      3 PKDTPEGALRKPMY 16
        |||||||
DB      213 PKDTPEGALRKPMY 226

RESULT 4
US-09-877-156-25
: Sequence 25, Application US/09877156
: Patent No. US20020055625A1
: GENERAL INFORMATION:
: APPLICANT: Catherine Tribouley
: TITLE OF INVENTION: NEW MEMBERS OF TNF AND TNFR FAMILIES
: FILE REFERENCE: 1408.003/200130.439C1
: CURRENT APPLICATION NUMBER: US/09/877,156
: CURRENT FILING DATE: 2001-06-08
: PRIOR APPLICATION NUMBER: US 09/286,529
: PRIOR FILING DATE: 1998-04-05
: NUMBER OF SEQ ID NOS: 25
: SOFTWARE: FASTSEQ for Windows Version 3.0
: SEQ ID NO 25
: LENGTH: 150
: TYPE: PRT
: ORGANISM: Homo sapien
US-09-877-156-25

Query Match          60.2%; Score 65; DB 10; Length 150;
Best Local Similarity 76.9%; Pred. No. 0.021;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY      4 KDTPGAEALRKPMY 16
        ::|||
DB      96 RETPGAEALRKPMY 108

RESULT 5
US-10-116-378-28
: Sequence 28, Application US/10116378
: Patent No. US2002015093A1
: GENERAL INFORMATION:
: APPLICANT: Ashkenazi, Avi J.
: APPLICANT: Goddard, Audrey
: APPLICANT: Gurney, Austin
: APPLICANT: Marsters, Scott A.
: APPLICANT: Pitti, Robert M.

```



APPLICANT: Wood, William  
TITLE OF INVENTION: NOVEL TUMOR NECROSIS FACTOR RECEPTOR HOMOLOG AND  
TITLE OF INVENTION: NUCLEIC  
FILE REFERENCE: P1206R1  
CURRENT APPLICATION NUMBER: US/10/116,378  
PRIOR FILING DATE: 2002-04-04  
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/247,225  
PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-09  
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/074,087  
NUMBER OF SEQ ID NOS: 31  
SEQ ID NO 28  
LENGTH: 150  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-116-378-28

Query Match  
Best Local Similarity 60.2%; Score 65; DB 9; Length 150;  
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 KDTPEGALKPWY 16  
Db 96 RETPEGAEAKPWY 108  
:::|||||

RESULT 6  
US-09-779-050A-24  
Sequence 24, Application US/09779050A  
Patent No. US20020160416A1  
GENERAL INFORMATION:  
APPLICANT: BOYLE, WILLIAM  
APPLICANT: HSU, HAILING  
TITLE OF INVENTION: RECEPTOR FROM TNF FAMILY  
FILE REFERENCE: A-570B  
CURRENT APPLICATION NUMBER: US/09/779,050A  
PRIOR FILING DATE: 2001-02-12  
PRIOR APPLICATION NUMBER: 60/181,800  
PRIOR FILING DATE: 2000-02-11  
NUMBER OF SEQ ID NOS: 52  
SOFTWARE: Patentin version 3.0  
SEQ ID NO 24  
LENGTH: 152  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-779-050A-24

Query Match  
Best Local Similarity 60.2%; Score 65; DB 9; Length 152;  
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 KDTPEGALKPWY 16  
Db 98 RETPEGAEAKPWY 110  
:::|||||

US-09-903-327A-7  
Sequence 7, Application US/09903327A  
Patent No. US2002016433A1  
GENERAL INFORMATION:  
APPLICANT: Nemerow, Glen R.  
APPLICANT: Li, Eiguang  
TITLE OF INVENTION: BIFUNCTIONAL MOLECULES AND VECTORS COMPLEXED THEREWITH FOR TARGET  
TITLE OF INVENTION: GENE  
FILE REFERENCE: DELIVERY  
CURRENT APPLICATION NUMBER: US/09/903,327A  
PRIOR FILING DATE: 2001-07-10  
PRIOR APPLICATION NUMBER: 09/613,017  
NUMBER OF SEQ ID NOS: 33

SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 7  
LENGTH: 157  
TYPE: PRT  
ORGANISM: Human  
NAME/KEY: PEPTIDE  
LOCATION: (0)...(0)  
OTHER INFORMATION: Tumor necrosis factor-alpha (TNF alpha, mature  
US-09-903-327A-7

Query Match  
Best Local Similarity 60.2%; Score 65; DB 9; Length 157;  
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 KDTPEGALKPWY 16  
Db 103 RETPEGAEAKPWY 115  
:::|||||

RESULT 8  
US-10-043-432-1  
Sequence 1, Application US/10043432  
Publication No. US20030054004A1  
GENERAL INFORMATION:  
APPLICANT: Le, Junming  
APPLICANT: Vilcek, Jan  
APPLICANT: Daddona, Peter  
APPLICANT: Chrayed, John  
APPLICANT: Knight, David M.  
TITLE OF INVENTION: Anti-TNF Antibodies and Peptides of  
FILE REFERENCE: Human Tumor Necrosis Factor  
CURRENT APPLICATION NUMBER: US/10/043,432  
PRIOR FILING DATE: 2002-01-10  
PRIOR APPLICATION NUMBER: 09/927,703  
PRIOR FILING DATE: 2001-08-10  
PRIOR APPLICATION NUMBER: U.S. 09/756,398  
PRIOR FILING DATE: 2001-01-08  
PRIOR APPLICATION NUMBER: U.S. 09/133,119  
PRIOR FILING DATE: 1998-08-12  
PRIOR APPLICATION NUMBER: U.S. 08/570,674  
PRIOR FILING DATE: 1995-12-11  
PRIOR APPLICATION NUMBER: U.S. 08/324,799  
PRIOR FILING DATE: 1994-10-18  
PRIOR APPLICATION NUMBER: U.S. 08/192,102  
PRIOR FILING DATE: 1994-02-04  
PRIOR APPLICATION NUMBER: U.S. 08/192,861  
PRIOR FILING DATE: 1994-02-04  
PRIOR APPLICATION NUMBER: U.S. 08/192,093  
PRIOR FILING DATE: 1994-02-04  
PRIOR APPLICATION NUMBER: U.S. 08/010,406  
PRIOR FILING DATE: 1993-01-29  
PRIOR APPLICATION NUMBER: U.S. 08/013,413  
PRIOR FILING DATE: 1993-02-02  
PRIOR APPLICATION NUMBER: U.S. 07/943,852  
PRIOR FILING DATE: 1992-09-11  
PRIOR APPLICATION NUMBER: U.S. 07/853,606  
PRIOR FILING DATE: 1992-03-18  
PRIOR APPLICATION NUMBER: U.S. 07/670,827  
NUMBER OF SEQ ID NOS: 19  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 1  
LENGTH: 157  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-043-432-1

Query Match  
Best Local Similarity 60.2%; Score 65; DB 9; Length 157;  
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 QY 4 KDTPEGAELKPMY 16  
 Db 103 RETPEGAELKPMY 115

## RESULT 9

US-09-756-301A-1

; Sequence 1, Application US/09756301A  
 ; Patent No. US20010027249A1  
 ; GENERAL INFORMATION:

; APPLICANT: Vilcek, Jan  
 ; APPLICANT: Daddona, Peter  
 ; APPLICANT: Chirayeb, John  
 ; APPLICANT: Knight, David M.  
 ; APPLICANT: Siegel, Scott

; TITLE OF INVENTION: Anti-TNF Antibodies and Peptides of  
 ; FILE REFERENCE: 0975.1005-008  
 ; CURRENT APPLICATION NUMBER: US/09/756,301A

; CURRENT FILING DATE: 2001-01-08  
 ; PRIOR APPLICATION NUMBER: U.S. 09/133,119  
 ; PRIOR FILING DATE: 1998-08-12  
 ; PRIOR APPLICATION NUMBER: U.S. 08/570,674  
 ; PRIOR FILING DATE: 1995-12-11  
 ; PRIOR APPLICATION NUMBER: U.S. 08/324,799  
 ; PRIOR FILING DATE: 1994-10-18  
 ; PRIOR APPLICATION NUMBER: U.S. 08/192,102  
 ; PRIOR FILING DATE: 1994-02-04  
 ; PRIOR APPLICATION NUMBER: U.S. 08/192,861  
 ; PRIOR FILING DATE: 1994-02-04  
 ; PRIOR APPLICATION NUMBER: U.S. 08/192,093  
 ; PRIOR FILING DATE: 1994-02-04  
 ; PRIOR APPLICATION NUMBER: U.S. 08/010,406  
 ; PRIOR FILING DATE: 1993-01-29  
 ; PRIOR APPLICATION NUMBER: U.S. 08/013,413  
 ; PRIOR FILING DATE: 1993-02-02  
 ; PRIOR APPLICATION NUMBER: U.S. 07/943,852  
 ; PRIOR FILING DATE: 1992-09-11  
 ; PRIOR APPLICATION NUMBER: U.S. 07/853,606  
 ; PRIOR FILING DATE: 1992-03-18  
 ; PRIOR APPLICATION NUMBER: U.S. 07/670,827  
 ; PRIOR FILING DATE: 1991-03-18  
 ; NUMBER OF SEQ ID NOS: 19  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 1  
 ; LENGTH: 157  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-09-756-301A-1

Query Match 60.2%; Score 65; DB 10; Length 157;  
 Best Local Similarity 76.9%; Pred. No. 0.022;  
 Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 KDTPEGAELKPMY 16  
 Db 103 RETPEGAELKPMY 115

## RESULT 10

US-09-927-703-1

; Sequence 1, Application US/09927703  
 ; Patent No. US20020022720A1  
 ; GENERAL INFORMATION:

; APPLICANT: Le, Junning  
 ; APPLICANT: Vilcek, Jan  
 ; APPLICANT: Daddona, Peter  
 ; APPLICANT: Chirayeb, John  
 ; APPLICANT: Knight, David M.  
 ; APPLICANT: Siegel, Scott

; TITLE OF INVENTION: Anti-TNF Antibodies and Peptides of  
 ; FILE REFERENCE: 0975.1005-013  
 ; CURRENT APPLICATION NUMBER: US/09/927,703  
 ; CURRENT FILING DATE: 2001-08-10  
 ; PRIOR APPLICATION NUMBER: U.S. 09/756,398  
 ; PRIOR FILING DATE: 2001-01-08  
 ; PRIOR APPLICATION NUMBER: U.S. 09/133,119  
 ; PRIOR FILING DATE: 1998-08-12  
 ; PRIOR APPLICATION NUMBER: U.S. 08/570,674  
 ; PRIOR FILING DATE: 1995-12-11  
 ; PRIOR APPLICATION NUMBER: U.S. 08/324,799  
 ; PRIOR FILING DATE: 1994-10-18  
 ; PRIOR APPLICATION NUMBER: U.S. 08/192,102  
 ; PRIOR FILING DATE: 1994-02-04  
 ; PRIOR APPLICATION NUMBER: U.S. 08/192,861  
 ; PRIOR FILING DATE: 1994-02-04  
 ; PRIOR APPLICATION NUMBER: U.S. 08/192,093  
 ; PRIOR FILING DATE: 1994-02-04  
 ; PRIOR APPLICATION NUMBER: U.S. 08/010,406  
 ; PRIOR FILING DATE: 1993-01-29  
 ; PRIOR APPLICATION NUMBER: U.S. 08/013,413  
 ; PRIOR FILING DATE: 1993-02-02  
 ; PRIOR APPLICATION NUMBER: U.S. 07/943,852  
 ; PRIOR FILING DATE: 1992-09-11  
 ; PRIOR APPLICATION NUMBER: U.S. 07/853,606  
 ; PRIOR FILING DATE: 1992-03-18  
 ; PRIOR APPLICATION NUMBER: U.S. 07/670,827  
 ; PRIOR FILING DATE: 1991-03-18  
 ; NUMBER OF SEQ ID NOS: 19  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 1  
 ; LENGTH: 157  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-09-927-703-1

Query Match 60.2%; Score 65; DB 10; Length 157;  
 Best Local Similarity 76.9%; Pred. No. 0.022;  
 Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 KDTPEGAELKPMY 16  
 Db 103 RETPEGAELKPMY 115

## RESULT 11

US-09-854-280-19

; Sequence 19, Application US/09854280  
 ; Patent No. US20020052027A1  
 ; GENERAL INFORMATION:

; APPLICANT: Chen, Jian  
 ; APPLICANT: Filvaroff, Ellen  
 ; APPLICANT: Goddard, Audrey  
 ; APPLICANT: Gurney, Austyn  
 ; APPLICANT: Li, Hanzhong  
 ; APPLICANT: Wood, William I.

; TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF  
 ; FILE REFERENCE: P1381R1C2  
 ; CURRENT APPLICATION NUMBER: US/09/854,280  
 ; CURRENT FILING DATE: 2001-05-10  
 ; PRIOR APPLICATION NUMBER: US 09/311,832  
 ; PRIOR FILING DATE: 1999-05-14  
 ; PRIOR APPLICATION NUMBER: US 60/085,579  
 ; PRIOR FILING DATE: 1998-05-15  
 ; PRIOR APPLICATION NUMBER: US 60/113,621  
 ; PRIOR FILING DATE: 1998-12-23  
 ; NUMBER OF SEQ ID NOS: 26  
 ; SEQ ID NO 19  
 ; LENGTH: 157  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-09-854-280-19

Query Match 60.2%; Score 65; DB 10; Length 157;  
Best Local Similarity 76.9%; Pred. No. 0.022;  
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 KOTPEGAELKPMY 16  
:|||||  
Db 103 RETPEGAELKPMY 115

RESULT 12  
US-09-934-465-13  
; Sequence 13, Application US/09934465  
; Patent No. US20020102233A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; TITLE OF INVENTION: APO-2 LIGAND  
; FILE REFERENCE: 11669.22US03  
; CURRENT APPLICATION NUMBER: US/09/934,465  
; PRIOR FILING DATE: 2001-08-21  
; PRIOR APPLICATION NUMBER: 08/584,031  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: Patent Ver. 2.0  
; SEQ ID NO 13  
; LENGTH: 157  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-934-465-13

Query Match 60.2%; Score 65; DB 10; Length 157;  
Best Local Similarity 76.9%; Pred. No. 0.022;  
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 KOTPEGAELKPMY 16  
:|||||  
Db 103 RETPEGAELKPMY 115

RESULT 13  
US-09-766-535A-1  
; Sequence 1, Application US/09766535A  
; Patent No. US20020106372A1  
; GENERAL INFORMATION:  
; APPLICANT: Le, Junming  
; APPLICANT: Vilcek, Jan  
; APPLICANT: Daddona, Peter  
; APPLICANT: Ghayeb, John  
; APPLICANT: Siegel, Scott M.  
; TITLE OF INVENTION: Anti-TNF Antibodies and Peptides of  
; FILE REFERENCE: 0975.1005-010  
; CURRENT APPLICATION NUMBER: US/09/766,535A  
; PRIOR FILING DATE: 2001-01-18  
; PRIOR APPLICATION NUMBER: U.S. 09/133,119  
; PRIOR FILING DATE: 1998-08-12  
; PRIOR APPLICATION NUMBER: U.S. 08/570,674  
; PRIOR FILING DATE: 1995-12-11  
; PRIOR APPLICATION NUMBER: U.S. 08/324,799  
; PRIOR FILING DATE: 1994-10-18  
; PRIOR APPLICATION NUMBER: U.S. 08/192,102  
; PRIOR FILING DATE: 1994-02-04  
; PRIOR APPLICATION NUMBER: U.S. 08/192,861  
; PRIOR FILING DATE: 1994-02-04  
; PRIOR APPLICATION NUMBER: U.S. 08/192,093  
; PRIOR FILING DATE: 1994-02-04  
; PRIOR APPLICATION NUMBER: U.S. 08/010,406  
; PRIOR FILING DATE: 1993-01-29  
; PRIOR APPLICATION NUMBER: U.S. 08/013,413  
; PRIOR FILING DATE: 1993-02-02  
; PRIOR APPLICATION NUMBER: U.S. 07/943,852  
; PRIOR FILING DATE: 1992-09-11

; PRIOR APPLICATION NUMBER: U.S. 07/853,606  
; PRIOR FILING DATE: 1992-03-18  
; PRIOR APPLICATION NUMBER: U.S. 07/670,827  
; PRIOR FILING DATE: 1991-03-18  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 157  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-766-535A-1

Query Match 60.2%; Score 65; DB 10; Length 157;  
Best Local Similarity 76.9%; Pred. No. 0.022;  
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 KOTPEGAELKPMY 16  
:|||||  
Db 103 RETPEGAELKPMY 115

RESULT 14  
US-09-854-208-19  
; Sequence 19, Application US/09854208  
; Patent No. US20020106743A1  
; GENERAL INFORMATION:  
; APPLICANT: Chen, Jian  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Gurney, Austin  
; APPLICANT: Li, Hanzhong  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES  
; FILE REFERENCE: P1381-R1  
; CURRENT APPLICATION NUMBER: US/09/854,208  
; PRIOR FILING DATE: 2001-05-10  
; PRIOR APPLICATION NUMBER: US/09/311,832  
; PRIOR FILING DATE: 1999-05-14  
; PRIOR APPLICATION NUMBER: US 60/085,579  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: US 60/113,621  
; NUMBER OF SEQ ID NOS: 26  
; SEQ ID NO 19  
; LENGTH: 157  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-854-208-19

Query Match 60.2%; Score 65; DB 10; Length 157;  
Best Local Similarity 76.9%; Pred. No. 0.022;  
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 KOTPEGAELKPMY 16  
:|||||  
Db 103 RETPEGAELKPMY 115

RESULT 15  
US-09-756-161A-1  
; Sequence 1, Application US/09756161A  
; Patent No. US20020132307A1  
; GENERAL INFORMATION:  
; APPLICANT: Le, Junming  
; APPLICANT: Vilcek, Jan  
; APPLICANT: Daddona, Peter  
; APPLICANT: Ghayeb, John  
; APPLICANT: Siegel, Scott M.  
; TITLE OF INVENTION: Anti-TNF Antibodies and Peptides of  
; FILE REFERENCE: 0975.1005-007

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; CURRENT APPLICATION NUMBER: US/09/756,161A
; CURRENT FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: U.S. 09/133,119
; PRIOR FILING DATE: 1998-08-12
; PRIOR APPLICATION NUMBER: U.S. 08/570,674
; PRIOR FILING DATE: 1995-12-11
; PRIOR APPLICATION NUMBER: U.S. 08/324,799
; PRIOR FILING DATE: 1994-10-18
; PRIOR APPLICATION NUMBER: U.S. 08/192,102
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/192,861
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/192,093
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/010,406
; PRIOR FILING DATE: 1993-01-29
; PRIOR APPLICATION NUMBER: U.S. 08/013,413
; PRIOR FILING DATE: 1993-02-02
; PRIOR APPLICATION NUMBER: U.S. 07/943,852
; PRIOR FILING DATE: 1992-09-11
; PRIOR APPLICATION NUMBER: U.S. 07/853,606
; PRIOR FILING DATE: 1992-03-18
; PRIOR APPLICATION NUMBER: U.S. 07/670,827
; PRIOR FILING DATE: 1991-03-18
; SOFTWARE: FastSeq for Windows Version 4.0
; NUMBER OF SEQ ID NOS: 19
; SEQ ID NO 1
; LENGTH: 157
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-756-161A-1
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Query Match          60.2%; Score 65; DB 10; Length 157;
Best Local Similarity 76.9%; Pred. No. 0.022;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      4 KDTPEGALKPPY 16
      ::|||||
Db      103 RETPEGALKPPY 115
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Job time : 11.6935 secs